

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 6, 2005, 16:53:22 ; Search time 190 Seconds
(without alignments)
695.350 Million cell updates/sec

Title: US-09-646-835-1_COPY_384_641

Perfect score: 1314

Sequence: 1 KSENVQILLDVLAPLSGL.....FGAQGPKGSGSGPTIEVD 258

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1314	100.0	641	1	HS71_HUMAN
2	1296	98.6	641	2	Q6S4R2
3	1295	98.6	641	1	HS71_BOVIN
4	1295	98.6	641	1	HS72_BOVIN
5	1295	98.6	641	2	Q6DLW1
6	1295	98.6	641	2	Q7YQF7
7	1291	98.2	641	2	Q7YQF6
8	1279.5	97.4	638	1	HS71_CERAB
9	1279	97.3	641	1	HS71_PIG
10	1258.5	95.8	640	2	Q8WNS9
11	1258	95.7	641	1	HS71_RAT
12	1258	95.7	641	2	Q63256
13	1239	94.3	641	2	Q9QWU5
14	1236	94.1	641	2	Q7TQD8
15	1228.5	93.5	642	1	HS71_MOUSE
16	1216	92.5	420	1	HS1A_MOUSE
17	1109	84.4	641	1	HS7H_HUMAN
18	1108.5	84.4	650	2	Q6Q154
19	1108	84.3	649	2	Q8Q4B6
20	1102.5	83.9	646	2	Q7ZTK6
21	1101	83.8	649	1	HS7C_BRARE
22	1101	83.8	649	2	Q6NYF4
23	1100.5	83.8	646	1	HS7C_CRIGR
24	1100.5	83.8	646	1	HS7C_MOUSE
25	1100.5	83.8	646	1	HS7C_RAT
26	1100.5	83.8	646	2	Q6TDU0
27	1098	83.6	653	2	Q6TJ00
28	1097.5	83.5	269	2	Q96BE0
29	1097.5	83.5	586	2	Q96IS6
30	1097.5	83.5	646	1	HS7C_HUMAN
31	1097.5	83.5	646	1	HS7C_SAGOE
					Q7IU34 saguinus oe

ALIGNMENTS

32	1097	83.5	649	2	Q7ZVU1
33	1096.5	83.4	646	2	Q6NZD0
34	1096.5	83.4	650	2	Q8AVE2
35	1095	83.3	641	2	Q8NE72
36	1094	83.3	631	2	Q801X8
37	1092	83.1	282	2	Q91ZU5
38	1092	83.1	461	2	Q91ZU4
39	1092	83.1	552	2	Q9QWU1
40	1091.5	83.1	650	1	HS7C_BOVIN
41	1091	83.0	649	1	HS7C_BOVIN
42	1090.5	83.0	655	2	Q6XVG4
43	1089.5	82.9	650	2	Q76N60
44	1089	82.9	641	2	Q6MG67
45	1088	82.8	649	1	HS7C_ICTPU
46	1088	82.8	651	2	Q8UV14
47	1087	82.7	641	1	HS1A_RAT
48	1087	82.7	641	2	Q88686
49	1086	82.6	644	2	Q7SZM7
50	1086	82.6	659	2	Q6RYT8
51	1085	82.6	641	1	HS7T_MOUSE
52	1084	82.5	651	1	HS70_ONCMY
53	1078.5	82.1	646	2	Q73885
54	1077	82.0	659	2	Q9XZJ2
55	1074	81.7	345	2	Q23954
56	1073.5	81.7	650	2	Q73788
57	1073.5	81.7	652	2	Q6AZH8
58	1070	81.4	654	2	Q86QW8
59	1070	81.4	655	2	Q6WAW3
60	1069	81.4	643	2	Q6PH56
61	1067	81.2	658	2	Q7Z1W9
62	1066	81.1	490	2	Q6QAN5
63	1066	81.1	647	2	Q6PGX4
64	1064.5	81.0	656	2	Q81S62
65	1064	81.0	634	2	Q7SX63
66	1064	81.0	645	2	Q9NGK9
67	1064	81.0	649	2	Q79984
68	1063.5	80.9	652	2	Q6GUA8
69	1063.5	80.9	652	2	Q71KW5
70	1063	80.9	335	2	Q17267
71	1063	80.9	644	1	HS70_BRUMA
72	1060	80.7	583	2	Q6QAN4
73	1059.5	80.6	639	1	HS72_HUMAN
74	1059.5	80.6	658	2	Q271Z1
75	1058	80.5	645	1	HS70_PLEWA
76	1057.5	80.5	657	2	Q6RYT7
77	1056	80.4	228	2	Q61698
78	1056	80.4	645	2	Q96541
79	1055	80.3	649	2	Q6S4R6
80	1054.5	80.3	633	1	HS72_MOUSE
81	1054.5	80.3	633	2	Q99KD7
82	1054.5	80.3	633	2	Q66HL1
83	1054	80.2	645	2	Q9NJB7
84	1052.5	80.1	646	2	Q94614
85	1052.5	80.1	650	2	Q81860
86	1052.5	80.1	650	2	Q9GFK0
87	1051	80.0	636	2	Q9TUG3
88	1050	79.9	623	2	Q801X9
89	1050	79.9	634	1	HS70_CHICK
90	1049.5	79.9	640	2	Q93240
91	1049	79.8	634	2	Q8AYL6
92	1048	79.8	649	2	Q86MC3
93	1047.5	79.7	633	1	HS72_RAT
94	1045.5	79.6	656	2	Q7PYR5
95	1043.5	79.4	652	1	HS7D_MANSE
96	1043	79.4	631	1	HS73_BOVIN
97	1042.5	79.3	639	2	Q73922
98	1042.5	79.3	644	1	HS70_ONCTS
99	1042	79.3	653	2	Q17310
100	1041.5	79.3	650	2	Q8ITL5

Q7zv11	brachydanio
Q8nzD0	mus musculus
Q8ave2	xenopus lae
Q8ne72	homo sapien
Q801x8	carassius a
Q91zu5	mus musculus
Q91zu4	mus musculus
Q9quw1	mus musculus
P19120	bos taurus
Q6teq5	brachydanio
Q6xvg4	chlamyra far
Q76n60	paralichthy
Q6mg67	rattus norv
P47773	ictalurusa p
Q8uv14	ambystoma m
P55063	rattus norv
Q88686	mus musculus
Q7szm7	cyprinus ca
Q6ryt8	aequipetec
P16627	mus musculus
P08108	oncorhynch
Q73885	gallus gall
Q9xzi2	crassostrea
Q23954	dirofilaria
Q73788	paralichthy
Q6azh8	xenopus lae
Q86qm8	locusta mig
Q6waw3	locusta mig
Q6ph56	brachydanio
Q7z1w9	crassostrea
Q6qan5	megachile r
Q6pgx4	brachydanio
Q81s62	cotesia rub
Q7sx63	gallus gall
Q81s62	cotesia rub
Q9ngk9	wuchereria
P79984	brachydanio
Q6gua8	penaeus van
Q17kw5	penaeus mon
Q17267	brugia paha
Q27541	brugia mala
Q6qan4	megachile r
P54652	homo sapien
Q27121	urechis cau
Q1291	pleurodeles
Q6ryt7	patinopecte
Q61698	mus musculus
Q96541	setaria dig
Q6s4r6	macrobrachi
P17156	mus musculus
Q99kd7	mus musculus
Q66hl1	rattus norv
Q9njb7	wuchereria
Q94614	mesocetoid
Q81860	heterodera
Q9gpk0	heterodera
Q9tug3	capra hircu
Q801x9	carassius a
P08106	gallus gall
Q93240	paralichthy
Q8ayl6	numida mele
Q86mc3	balanus amp
P14659	rattus norv
Q7pyr5	anopheles g
Q9u639	manduca sex
P34933	bos taurus
Q73922	oreochromis
Q12333	oncorhynch
Q17310	ceratitis c
Q8itl5	chironomus

RESULT 1
 HS71_HUMAN STANDARD; PRT; 641 AA.
 AC P08107; P19790; Q9UOL9; Q9UQW0;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP70-2).
 GN Name=HSPA1A; Synonyms=HSPAL;
 GN and
 GN Name=HSPA1B;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (HSPA1A AND HSPA1B).
 RX MEDLINE=91055806; PubMed=1700760;
 RA Milner C.M., Campbell R.D.;
 RT "Structure and expression of the three MHC-linked HSP70 genes.";
 RL Immunogenetics 32:242-251(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86016721; PubMed=3931075;
 RA Hunt C., Morimoto R.I.;
 RT "Conserved features of eukaryotic hsp70 genes revealed by comparison with the nucleotide sequence of human hsp70.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).
 RN [3]
 RP SEQUENCE FROM N.A. (HSPA1A AND HSPA1B).
 RA Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,
 RA Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,
 RA Laskey S., Hood L.;
 RT "Sequence of the human major histocompatibility complex class III region.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (HSPA1A AND HSPA1B).
 RA Shiina S., Tamiya G., Oka A., Inoko H.;
 RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle, Pancreas, and Skin;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Tuchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalilus D.E.,
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE OF 1-36 AND 360-424 FROM N.A.
 RX MEDLINE=89184548; PubMed=2538825;
 RA Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.;
 RT "Human major histocompatibility complex contains genes for the major heat shock protein HSP70.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).
 [7]
 RN SEQUENCE OF 1-22 AND 618-641 FROM N.A.
 RX MEDLINE=87066768; PubMed=3786141;
 RA Drabent B., Genthe A., Benecke B.-J.;
 RT "In vitro transcription of a human hsp 70 heat shock gene by extracts prepared from heat-shocked and non-heat-shocked human cells.";
 RL Nucleic Acids Res. 14:8933-8948(1986).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.
 RX MEDLINE=99234376; PubMed=10216320; DOI=10.1107/S0907444999002103;
 RA Osiptuk J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;
 RT "Structure of a new crystal form of human hsp70 Arpase domain.";
 RL Acta Crystallogr. D 55:1105-1107(1999).
 CC -I- FUNCTION: In cooperation with other chaperones, HSP70s stabilize preexistent proteins against aggregation and mediate the folding of newly translated polypeptides in the cytosol as well as within organelles. The HSP70s in mitochondria and the endoplasmic reticulum play an additional role by providing a driving force for protein translocation. They are involved in signal transduction pathways in cooperation with HSP90. They participate in all these processes through their ability to recognize nonnative conformations of other proteins. They bind extended peptide segments with a net hydrophobic character exposed by polypeptides during translation and membrane translocation, or following stress-induced damage.
 CC -I- INDUCTION: By heat shock.
 CC -I- SIMILARITY: Belongs to the heat shock protein 70 family.
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 DR EMBL; M59828; AAA63226.1; -
 DR EMBL; M59830; AAA63227.1; -
 DR EMBL; AF134726; AAD21816.1; -
 DR EMBL; AF134726; AAD21815.1; -
 DR EMBL; AP000503; BAB63300.1; -
 DR EMBL; AP000503; BAB63399.1; -
 DR EMBL; M11717; AAA52697.1; -
 DR EMBL; BC002453; AAH02453.1; -
 DR EMBL; BC009322; AAH09322.1; -
 DR EMBL; BC018740; AAH18740.1; -
 DR EMBL; M24743; AAA59844.1; -
 DR EMBL; M24744; AAA59845.1; -
 DR EMBL; X04676; CAA28381.1; -
 DR EMBL; X04677; CAA28382.1; -
 DR PIR; A29160; A29160.
 DR PIR; A45871; A45871.
 DR PIR; I59139; I59139.
 DR PIR; I79540; I79540.
 DR PDB; 1H3O; X-ray; A=3-382.
 DR PDB; 1S3X; X-ray; A=1-382.
 DR SWISS-2DPAGE; P08107; HUMAN.
 DR OGP; P08107; -
 DR Genew; HGNC:5232; HSPA1A.
 DR Genew; HGNC:5233; HSPA1B.
 DR H-InvDB; HIX0005733; -
 DR H-InvDB; HIX0005734; -
 DR MIM; 140550; -
 DR GO; GO:0005737; C:cytoplasm; TAS.
 DR GO; GO:0005634; C:nucleus; TAS.
 DR GO; GO:0003773; F:heat shock protein activity; TAS.
 DR GO; GO:0006402; P:mRNA catabolism; TAS.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; Hsp70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR TIGRFAMs; TIGR01991; HscA; 1.

DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW 3D-structure; ATP-binding; Chaperone; Heat shock; Multigene family.
FT CONFLICT 7 7
FT CONFLICT 110 110
FT CONFLICT 370 370
FT CONFLICT 469 469
FT CONFLICT 499 499
FT STRAND 7 11
FT STRAND 15 22
FT TURN 23 24
FT STRAND 25 28
FT TURN 32 33
FT STRAND 38 39
FT STRAND 42 44
FT STRAND 49 51
FT TURN 52 52
FT HELIX 53 57
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FT HELIX 59 61
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FT STRAND 66 67
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FT TURN 74 75
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FT HELIX 230 248
FT TURN 254 255
FT HELIX 257 273
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FT TURN 289 290
FT STRAND 291 298
FT HELIX 299 312
FT TURN 313 313
FT HELIX 314 323

Query Match 100.0%; Score 1314; DB 1; Length 641;
Best Local Similarity 100.0%; Pred. No. 3.9e-73;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTTYSNQPGVLIQVY 60
Db 384 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTTYSNQPGVLIQVY 443

Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503

Qy 121 TNDKGRLSKEEIERMVQEAKEYKAEDVQRRVSAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 504 TNDKGRLSKEEIERMVQEAKEYKAEDVQRRVSAKNALESYAFNMKSAVEDEGLKGKIS 563

Qy 181 EADKKKVLDCQEVISWLDANTLAEKDFEHHKKELEQVCNPIISGLYQAGGPGGFG 240
Db 564 EADKKKVLDCQEVISWLDANTLAEKDFEHHKKELEQVCNPIISGLYQAGGPGGFG 623

Qy 241 AQPCKGSGSGPTIEVD 258
Db 624 AQPCKGSGSGPTIEVD 641

RESULT 2
Q6S4N2 ID Q6S4N2 PRELIMINARY; PRT; 641 AA.
AC Q6S4N2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heat shock protein 70.2.
GN Name=hsp70.2;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen M.Y., Lee W.C.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY466608; AAR30953.1; -.
DR HSP; P19120; IBA1.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock;
SQ SEQUENCE 641 AA; 70098 MW; 9B49BF380AF0E2A CRC64;

Query Match 98.6%; Score 1296; DB 2; Length 641;
Best Local Similarity 98.4%; Pred. No. 5.1e-72;
Matches 254; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTTYSNQPGVLIQVY 60
Db 384 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTTYSNQPGVLIQVY 443

Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503

Qy 121 TNDKGRLSKEEIERMVQEAKEYKAEDVQRRVSAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 504 TNDKGRLSKEEIERMVQEAKEYKAEDVQRRVSAKNALESYAFNMKSAVEDEGLKGKIS 563

Qy 181 EADKKKVLDCQEVISWLDANTLAEKDFEHHKKELEQVCNPIISGLYQAGGPGGFG 240
Db 564 EADKKKVLDCQEVISWLDANTLAEKDFEHHKKELEQVCNPIISGLYQAGGPGGFG 623

Qy 241 AQPCKGSGSGPTIEVD 258
Db 624 AQPCKGSGSGPTIEVD 641

RESULT 3
HS71_BOVIN
ID HS71_BOVIN STANDARD; PRT; 641 AA.
AC Q27975; Q27964;
DT 01-NOV-1997 (Rel. 35, Created)

DR ProDom; PD000089; Hsp70; 1.
 DR TIGRFAMs; TIGR01991; Hsca; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Chaperone; Heat shock; Multigene family.
 SQ SEQUENCE 641 AA; 70228 MW; 229C19EBB6F610DF CRC64;

Query Match 98.6%; Score 1295; DB 1; Length 641;
 Best Local Similarity 98.8%; Pred. No. 5.9e-72;
 Matches 255; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQTQFTTYSNQPGLVLIQVY 60
 Db 384 KSENVQDLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQTQFTTYSNQPGLVLIQVY 443

Qy 61 EGERAMTKONLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
 Db 444 EGERAMTRDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 503

Qy 121 TNDKGRLSKEEIERMVQEAERYKAEDVQERVSAKNALESYAFNMKSAYEDELGKGKIS 180
 Db 504 TNDKGRLSKEEIERMVQEAERYKAEDVQERVSAKNALESYAFNMKSAYEDELGKGKIS 563

Qy 181 EADKKVKLDKQCVISWLDANTLAEDKDEFEHKKELQVNCNPIISGLYQAGGPGGPGFG 240
 Db 564 EADKKVKLDKQCVISWLDANTLAEDKDEFEHKKELQVNCNPIISRLYQAGGPGGPGFG 623

Qy 241 AQPGKGGSGSGPTIEEVD 258
 Db 624 AQPGKGGSGSGPTIEEVD 641

RESULT 5
 Q6DLW1 PRELIMINARY; PRT; 641 AA.

AC Q6DLW1
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Heat shock protein 70 kDa.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cardiac muscle;
 RA LakshmiKuttyamma A., Selvakumar P., Anderson D.H., Datla R.S.,
 RA Sharma R.K.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
 DR EMBL; AY662497; AAT75223.1; -
 DR GO; GO:0006457; P:response to unfolded protein; IEA.
 DR GO; GO:0006986; P:proteome to unfolded protein; IEA.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Heat shock.
 SQ SEQUENCE 641 AA; 70231 MW; 6B3F9E6B8E8FDFB0 CRC64;

Query Match 98.6%; Score 1295; DB 2; Length 641;
 Best Local Similarity 98.8%; Pred. No. 5.9e-72;
 Matches 255; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQTQFTTYSNQPGLVLIQVY 60
 Db 384 KSENVQDLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQTQFTTYSNQPGLVLIQVY 443

Qy 61 EGERAMTKONLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
 Db 444 EGERAMTRDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 503

Qy 121 TNDKGRLSKEEIERMVQEAERYKAEDVQERVSAKNALESYAFNMKSAYEDELGKGKIS 180
 Db 504 TNDKGRLSKEEIERMVQEAERYKAEDVQERVSAKNALESYAFNMKSAYEDELGKGKIS 563

Qy 181 EADKKVKLDKQCVISWLDANTLAEDKDEFEHKKELQVNCNPIISGLYQAGGPGGPGFG 240
 Db 564 EADKKVKLDKQCVISWLDANTLAEDKDEFEHKKELQVNCNPIISRLYQAGGPGGPGFG 623

Qy 241 AQPGKGGSGSGPTIEEVD 258
 Db 624 AQPGKGGSGSGPTIEEVD 641

RESULT 6
 Q7YQF7 PRELIMINARY; PRT; 641 AA.

AC Q7YQF7
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Heat-shock 70-kilodalton protein 1A.
 GN Names-HSPA1A;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22640451; PubMed=12755819;
 RA Sugimoto M., Furuoka H., Sugimoto Y.;
 RT "Deletion of one of the duplicated Hsp70 genes causes hereditary
 myopathy of diaphragmatic muscles in Holstein-Friesian cattle.";
 RL Anim. Genet. 34:191-197(2003).
 CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
 DR EMBL; AY149618; AAN78092.1; -
 DR EMBL; AY149619; AAN78094.1; -
 DR HSP; P08107; IS3X.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding.
 SQ SEQUENCE 641 AA; 70258 MW; 6FAC1F30540E80F9 CRC64;

Query Match 98.6%; Score 1295; DB 2; Length 641;
 Best Local Similarity 98.8%; Pred. No. 5.9e-72;
 Matches 255; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQTQFTTYSNQPGLVLIQVY 60
 Db 384 KSENVQDLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQTQFTTYSNQPGLVLIQVY 443

Qy 61 EGERAMTKONLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
 Db 444 EGERAMTRDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 503

Qy 121 TNDKGRLSKEEIERMVQEAERYKAEDVQERVSAKNALESYAFNMKSAYEDELGKGKIS 180
 Db 504 TNDKGRLSKEEIERMVQEAERYKAEDVQERVSAKNALESYAFNMKSAYEDELGKGKIS 563

Qy 181 EADKKVKLDKQCVISWLDANTLAEDKDEFEHKKELQVNCNPIISGLYQAGGPGGPGFG 240
 Db 564 EADKKVKLDKQCVISWLDANTLAEDKDEFEHKKELQVNCNPIISRLYQAGGPGGPGFG 623

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Qy 241 AQP6KGGSGGPTIEVD 258
Db 624 AQP6KGGSGGPTIEVD 641

RESULT 7
Q7YQC6 PRELIMINARY; PRT; 641 AA.
ID Q7YQC6
AC Q7YQC6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heat shock protein 70.
GN Name=hsp70;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamasaki M., Tajima M., Yamato O., Jeong J., Maede Y.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AB114672; BAC79353.1; -
DR EMBL; AB114673; BAC79354.1; -
DR EMBL; AB114674; BAC79355.1; -
DR EMBL; AB114675; BAC79356.1; -
DR HSP; P08107; I53X.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:006457; P:protein folding; IEA.
DR GO; GO:006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 641 AA; 70070 MW; DID80C3689346C88 CRC64;

Query Match 98.2%; Score 1291; DB 2; Length 641;
Best Local Similarity 98.1%; Pred. No. 1e-71;
Matches 253; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTYSDNQPGVLIQVY 60
Db 384 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTYSDNQPGVLIQVY 443

Qy 61 EGERAMTKDNNLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTRDNNLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 503

Qy 121 TNDKGRLSKEEIERMWQAEKKAEDVQERVSAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 504 TNDKGRLSKEEIERMWQAEKKAEDVQERVSAKNALESYAFNMKSAVEDEGLKGKIS 563

Qy 181 EADKKVKLDKQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGGPGGFG 240
Db 564 EADKKVKLDKQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGGPGGFG 623

Qy 241 AQP6KGGSGGPTIEVD 258
Db 624 AQP6KGGSGGPTIEVD 641

RESULT 8
HS71_CERAE STANDARD; PRT; 638 AA.
ID HS71_CERAE
AC Q28222;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock 70 kDa protein 1.

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GN Name=HSPAL;
OS Cercopithecus aethiops (Green monkey) (Grivet);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=95080396; PubMed=7988690; DOI=10.1016/0014-5793(94)01210-5;
RA Sainis I., Angelidis C., Pagoulatos G., Lazaridis I.;
RT "The hsc70 gene which is slightly induced by heat is the main virus
RT inducible member of the hsp70 gene family.";
RL FEBS Lett. 355:282-286(1994).
CC -1- FUNCTION: In cooperation with other chaperones, HSP70s stabilize
CC preexistent proteins against aggregation and mediate the folding
CC of newly translated polypeptides in the cytosol as well as within
CC organelles. The HSP70s in mitochondria and the endoplasmic
CC reticulum play an additional role by providing a driving force for
CC protein translocation. They are involved in signal transduction
CC pathways in cooperation with HSP90. They participate in all these
CC processes through their ability to recognize nonnative
CC conformations of other proteins. They bind extended peptide
CC segments with a net hydrophobic character exposed by polypeptides
CC during translation and membrane translocation, or following
CC stress-induced damage.
CC -1- INDUCTION: By heat shock.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X70684; CAA50019.1; -
CC PIR; S31766; S31766.
CC HSP; P08107; IHJO.
CC InterPro; IPR001023; Hsp70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC ProDom; PD000089; Hsp70; 1.
CC TIGRfam; TIGR01991; HscA; 1.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family.
SQ SEQUENCE 638 AA; 69920 MW; D5076A0FFAB6AB3 CRC64;

Query Match 97.4%; Score 1279.5; DB 1; Length 638;
Best Local Similarity 98.1%; Pred. No. 5.3e-71;
Matches 253; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTYSDNQPGVLIQVY 60
Db 382 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTYSDNQPGVLIQVY 441

Qy 61 EGERAMTKDNNLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 442 EGERAMTKDNNLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 500

Qy 121 TNDKGRLSKEEIERMWQAEKKAEDVQERVSAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 501 TNDKGRLSKEEIERMWQAEKKAEDVQERVSAKNALESYAFNMKSAVEDEGLKGKIS 560

Qy 181 EADKKVKLDKQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGGPGGFG 240
Db 561 EADKKVKLDKQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGGPGGFG 620

Qy 241 AQP6KGGSGGPTIEVD 258
Db 624 AQP6KGGSGGPTIEVD 258

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Db 621 AQPCKGSGSGPTIEVD 638

RESULT 9

HS71_PIG

ID HS71_PIG STANDARD; PRT; 641 AA.

AC P34930;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Heat shock 70 kDa protein 1 (HSP70.1).

GN Name=HSPAL;

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92175874; PubMed=1339404;

RA Peelman L.J., de Weghe A.R., Coppieters W.R., van Zeveren A.J.,

RT Bouquet Y.H.;

RL "Complete nucleotide sequence of a porcine HSP70 gene.";

Immunogenetics 35:286-289(1992).

CC -1- FUNCTION: In cooperation with other chaperones, Hsp70s stabilize

CC of newly translated polypeptides in the cytosol as well as within

CC organelles. These chaperones participate in all these processes

CC through their ability to recognize nonnative conformations of

CC other proteins. They bind extended peptide segments with a net

CC hydrophobic character exposed by polypeptides during translation

CC and membrane translocation, or following stress-induced damage.

CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC entities requires a license agreement (See <http://www.isb-gib.ch/announce/>

CC or send an email to license@isb-sib.ch).

EMBL; M69100; -; NOT_ANNOTATED_CDS.

DR PIR; S35718; S35718.

DR HSP; P08107; IHJO.

DR InterPro; IPR001023; Hsp70.

DR Pfam; PF00012; HSP70; 1.

DR PRINTS; P00301; HEATSHOCK70.

DR PRODOM; PD000089; Hsp70; 1.

DR TIGRFAMs; TIGR01991; HscA; 1.

DR PROSITE; PS00297; HSP70_1; 1.

DR PROSITE; PS00329; HSP70_2; 1.

DR PROSITE; PS01036; HSP70_3; 1.

KW ATP-binding; Chaperone; Heat shock; Multigene family.

SQ SEQUENCE 641 AA; 70083 MW; FE77B20A03E0A33 CRC64;

Query Match 97.3%; Score 1279; DB 1; Length 641;

Best Local Similarity 97.3%; Pred. No. 5.7e-71;

Matches 251; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLDVAPLSLGLETAGVMTALIKRSTPTKQTQIFTTYSNDQPGVLIQVY 60

Db 384 KSENVQDLLLDVAPLSLGLETAGVMTALIKRSTPTKQTQIFTTYSNDQPGVLIQVY 443

Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120

Db 444 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 503

Qy 121 TNDKGRLSKEIERMVQEAERYKAEDVQERVSNAKNALESYAFNMKSAVEDEGLKGKIS 180

Db 504 TNDKGRLSKEIERMVQEAERYKAEDVQERVSNAKNALESYAFNMKSAVEDEGLKGKIS 563

Qy 181 EADKKKVLDCQEVISWLDANTLAEKDFEHRKELQVNCNPIISGLYQAGGPGGFG 240

Db 564 EADKKKVLDCQEVISWLDANTLAEKDFEHRKELQVNCNPIISGLYQAGGPGGFG 623

Qy 241 AQPCKGSGSGPTIEVD 258

Db 624 APDLKGGSGSGPTIEVD 641

RESULT 10

Q8WNS9

ID Q8WNS9 PRELIMINARY; PRT; 640 AA.

AC Q8WNS9;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Heat shock protein 70.

GN Name=hsp70;

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RA Abe K., Kano R., Hasegawa A.;

RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.

DR EMBL; AB075027; BAB78505.1; -.

DR HSP; P08107; IS3X.

DR GO; GO:0005524; P:ATP binding; IEA.

DR GO; GO:0006457; P:protein folding; IEA.

DR GO; GO:0006986; P:response to unfolded protein; IEA.

DR Pfam; PF00012; HSP70; 1.

DR PRINTS; PR00301; HEATSHOCK70.

DR PRODOM; PD000089; Hsp70; 1.

DR PROSITE; PS00297; HSP70_1; 1.

DR PROSITE; PS00329; HSP70_2; 1.

DR PROSITE; PS01036; HSP70_3; 1.

KW ATP-binding; Heat shock.

SQ SEQUENCE 640 AA; 69934 MW; 402F3E91871BF87F CRC64;

Query Match 95.8%; Score 1258.5; DB 2; Length 640;

Best Local Similarity 96.5%; Pred. No. 1.1e-69;

Matches 249; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Qy 1 KSENVQDLLLDVAPLSLGLETAGVMTALIKRSTPTKQTQIFTTYSNDQPGVLIQVY 60

Db 384 KSENVQDLLLDVAPLSLGLETAGVMTAL-SRNSTPTKQTQIFTTYSNDQPGVLIQVY 442

Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120

Db 444 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 502

Qy 121 TNDKGRLSKEIERMVQEAERYKAEDVQERVSNAKNALESYAFNMKSAVEDEGLKGKIS 180

Db 503 TNDKGRLSKEIERMVQEAERYKAEDVQERVSNAKNALESYAFNMKSAVEDEGLKGKIS 562

Qy 181 EADKKKVLDCQEVISWLDANTLAEKDFEHRKELQVNCNPIISGLYQAGGPGGFG 240

Db 563 EADKKKVLDCQEVISWLDGFTLAEKDFEHRKELQVNCNPIITGLYQAGGPGGFG 622

Qy 241 AQPCKGSGSGPTIEVD 258

Db 623 AQPCKGSGSGPTIEVD 640

RESULT 11

HS71_RAT

ID HS71_RAT STANDARD; PRT; 641 AA.

AC Q07439; P42853;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Heat shock 70 kDa protein 1/2 (HSP70.1/2).

GN Name=Hsp70-1;


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Db 504 TNDKRLSKKEIERMVOEAERYKAEDEVQVRRVAAKNALESYAFNMKSAVEDEGLKGKIS 563
Qy 181 EADKKKVLDKCOEIVSWLDANTLAEKDFEHRKKELEQVCNPIISGLYQGAGGPGGFG 240
Db 564 EADKKKVLDKCOEIVSWLDNSNTLAEKEEFVHKRELERVNCNPIISGLYQGAGGPGGFG 623
Qy 241 AQPCKGSGSGPTTIEVD 258
Db 624 AQPCKGSGSGPTTIEVD 641

RESULT 13
Q9QWJ5 PRELIMINARY; PRT; 641 AA.
ID Q9QWJ5
AC Q9QWJ5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE HSP70.
GN Name=H2-Bf;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX PubMed=14656967; DOI=10.1101/gr.1736803;
RA Xie T., Rowen L., Aquado B., Ahearn M.E., Madan A., Qin S.,
RA Campbell R.D., Hood L.;
RT "Analysis of the gene-dense major histocompatibility complex class III
RT region and its comparison to mouse.";
RL Genome Res. 13:2621-2636(2003).
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AF109906; AAC84169.1; -.
DR HSP; P08107; 1H7O.
DR MGD; MGI:105975; H2-Bf.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
SQ SEQUENCE 641 AA; 70079 MW; F49C333E602EAE334 CRC64;

Query Match 94.3%; Score 1239; DB 2; Length 641;
Best Local Similarity 93.4%; Pred. No. 1.7e-68;
Matches 241; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQTFTTYSNDQPGVLIQVY 60
Db 384 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQTFTTYSNDQPGVLIQVY 443
Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTFDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 503
Qy 121 TNDKRLSKKEIERMVOEAERYKAEDEVQVRRVAAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 504 TNDKRLSKKEIERMVOEAERYKAEDEVQVRRVAAKNALESYAFNMKSAVEDEGLKGKIS 563
Qy 181 EADKKKVLDKCOEIVSWLDANTLAEKDFEHRKKELEQVCNPIISGLYQGAGGPGGFG 240
Db 564 EADKKKVLDKCOEIVSWLDNSNTLAEKEEFVHKRELERVNCNPIISGLYQGAGGPGGFG 623
Qy 241 AQPCKGSGSGPTTIEVD 258
Db 624 AQPCKGSGSGPTTIEVD 641
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RESULT 14
Q7TQD8 PRELIMINARY; PRT; 641 AA.
ID Q7TQD8;
AC Q7TQD8;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Heat shock protein 1A.
GN Name=Hspalpa;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Richmond J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; BC054782; AH54782.1; -.
DR HSSP; P08107; 1H7O.
DR GO; GO:0006281; P:DNA repair; IMP.
DR GO; GO:0009408; P:response to heat; IMP.
DR GO; GO:0000723; P:telomere maintenance; IMP.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 641 AA; 70093 MW; F49B439372C8E364 CRC64;

Query Match 94.1%; Score 1236; DB 2; Length 641;
Best Local Similarity 93.0%; Pred. No. 2.6e-68;
Matches 240; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQTFTTYSNDQPGVLIQVY 60
Db 384 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQTFTTYSNDQPGVLIQVY 443
Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTRDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 503
Qy 121 TNDKRLSKKEIERMVOEAERYKAEDEVQVRRVAAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 504 TNDKRLSKKEIERMVOEAERYKAEDEVQVRRVAAKNALESYAFNMKSAVEDEGLKGKIS 563
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QY 181 EADKKVLDKQEVISWLDANTLAEDKFEHKKELBOVCNPIISGLYQAGGPGGFG 240
DB 564 EADKKVLDKQEVISWLDNTLADKEEFVHKREELERVCSPIISGLYQAGGPGGFG 623
QY 241 AQGPKGSGSGPTIEVD 258
DB 624 AQAPKGSGSGPTIEVD 641

RESULT 15
HS71_MOUSE
ID HS71_MOUSE STANDARD; PRT; 642 AA.
AC P17879; Q61689; Q925V6;
DT 01-AUG-1990 (Rel. 15, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP70-2).
GN Name=Hspal; Synonyms=Hsp70.1, Hsp70-1, Hsp70a1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90236310; PubMed=2332169; DOI=10.1016/0378-1119(90)90302-8;
RA Hunt C., Calderwood S.;
RT "Characterization and sequence of a mouse hsp70 gene and its
expression in mouse cell lines.";
RL Gene 87:199-204(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RX MEDLINE=94357449; PubMed=8076831; DOI=10.1016/0378-1119(94)90305-0;
RA Perry M.D., Aujame L., Shtang S., Moran L.A.;
RT "Structure and expression of an inducible HSP70-encoding gene from Mus
musculus.";
RL Gene 146:273-278(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=129;
RA Rowen L., Madan A., Qin S., Hall J., Dahl T., James R., Dickhoff R.,
Schaffer T., Ratcliffe A., Abbasi N., Loretz C., Lasky S., Hood L.;
RT "Sequence of the mouse MHC class III region.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: In cooperation with other chaperones, Hsp70s stabilize
of newly translated polypeptides in the cytosol as well as within
organelles. These chaperones participate in all these processes
through their ability to recognize nonnative conformations of
other proteins. They bind extended peptide segments with a net
hydrophobic character exposed by polypeptides during translation
and membrane translocation, or following stress-induced damage.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC EMBL; M35021; AAA37864.1; -.
CC EMBL; W76613; AAA57233.1; -.
CC EMBL; AF103906; AAC84168.1; -.
CC HSSP; P08107; IHJO.
CC MGD; MGI:99517; Hsp70-1.
CC GO; GO:0001719; P:inhibition of caspase activation; IDA.
CC InterPro; IPR001023; Hsp70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC ProDom; PD000089; Hsp70; 1.
CC TIGRfam; TIGR01991; HSCA; 1.

DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family.
FT CONFLICT 342 R->A (in Ref. 2).
FT CONFLICT 628 Missing (in Ref. 2).
SQ SEQUENCE 642 AA; 70176 MW; 4BB9B0B130C23D8B CRC64;

Query Match 93.5%; Score 1228.5; DB 1; Length 642;
Best Local Similarity 93.1%; Pred. No. 7 6e-68;
Matches 241; Conservative 11; Mismatches 6; Indels 1; Gaps 1;

QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVMTALIKRNSTIPKQIQIFFTYSDNQGVLIQVY 60
DB 384 KSENVQDLLLLDVAPLSGLGLETAGGVMTALIKRNSTIPKQIQIFFTYSDNQGVLIQVY 443
QY 61 EGERAMTKDNLLGRFELSGIPAPRGVQIQIEVTFDIDANGILNVTTATDKSTGKANKITI 120
DB 444 EGERAMTRDNLLGRFELSGIPAPRGVQIQIEVTFDIDANGILNVTTATDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQORERVSNAKNALESYAFNMKSAVEDGLKGKIS 180
DB 504 TNDKGRLSKEEIERMVOEAEKYKAEDVQORERVSNAKNALESYAFNMKSAVEDGLKGKLS 563
QY 181 EADKKVLDKQEVISWLDANTLAEDKFEHKKELBOVCNPIISGLYQAGGPGGFG 240
DB 564 EADKKVLDKQEVISWLDNTLADKEEFVHKREELERVCSPIISGLYQAGGPGGFG 623
QY 241 AQGPKGSGSGPTIEVD 258
DB 624 AQAPKGSGSGPTIEVD 642

RESULT 16
HS1A_MOUSE
ID HS1A_MOUSE STANDARD; PRT; 420 AA.
AC Q61696; Q61697;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock protein 1A (Heat shock 70 kDa protein 3) (HSP70.3)
DE (Fragment).
GN Name=Hspal; Synonyms=Hsp70-3, Hsp70a1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86111900; PubMed=2868009;
RA Lowe D.G., Moran L.A.;
RT "Molecular cloning and analysis of DNA complementary to three mouse Mr
= 68,000 heat shock protein mRNAs.";
RL J. Biol. Chem. 261:2102-2112(1986).
RN [2]
RP SEQUENCE OF 155-420 FROM N.A.
RX MEDLINE=94357449; PubMed=8076831; DOI=10.1016/0378-1119(94)90305-0;
RA Perry M.D., Aujame L., Shtang S., Moran L.A.;
RT "Structure and expression of an inducible HSP70-encoding gene from Mus
musculus.";
RL Gene 146:273-278(1994).
CC -!- FUNCTION: In cooperation with other chaperones, Hsp70s stabilize
preexistent proteins against aggregation and mediate the folding
of newly translated polypeptides in the cytosol as well as within
organelles. These chaperones participate in all these processes
through their ability to recognize nonnative conformations of
other proteins. They bind extended peptide segments with a net
hydrophobic character exposed by polypeptides during translation
and membrane translocation, or following stress-induced damage.
CC -!- INDUCTION: By heat shock.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
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```

located in the class III region of the major histocompatibility complex of mouse and man.;
 [3] J. Biochem. 124:347-353(1998).
 [3] SEQUENCE FROM N.A.
 Rowen L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hicks P., Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.;
 "Sequence of the human major histocompatibility complex class III region.";
 Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

[4] SEQUENCE FROM N.A.
 Shina S., Tamiya G., Oka A., Inoko H.;
 "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
 Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 [5] MEDLINE=92406261; PubMed=1356099;
 Milner C.M., Campbell R.D.;
 "Polymorphic analysis of the three MHC-linked HSP70 genes";
 Immunogenetics 36:357-362(1992).
 CC -!- INDUCTION: Not induced by heat shock.
 CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.

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 EMBL; M59829; AAA63228.1; --
 EMBL; D85730; BAA32521.1; --
 EMBL; AF134726; AAD21817.1; --
 EMBL; AP000503; BAB63301.1; --
 PIR; B45871; B45871.
 HSP; P08107; 1HJO.
 Genew; HGNC:5234; HSPALL.
 MIM; 140559; --
 GO; GO:0003773; P:heat shock protein activity; TAS.
 InterPro; IPR001023; Hsp70.
 Pfam; PF00012; HSP70; 1.
 PRINTS; PR00301; HEATSHOCK70.
 ProDom; PD000089; Hsp70; 1.
 TIGRfam; TIGR01991; HscA; 1.
 PROSITE; PS00297; HSP70_1; 1.
 PROSITE; PS00329; HSP70_2; 1.
 PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Multigene family; Polymorphism.
 FT VARIANT 493 493 T -> M.
 /FTID=VAR_003820.
 FT CONFLICT 408 408 A -> V (in Ref. 1).
 FT CONFLICT 424 424 T -> P (in Ref. 1).
 FT CONFLICT 627 627 V -> M (in Ref. 2).
 SQ SEQUENCE 641 AA; 70375 MW; A9339D7657166FF7 CRC64;

Query Match 84.4%; Score 1109; DB 1; Length 641;
 Best Local Similarity 82.6%; Pred. No. 1.9e-60;
 Matches 219; Conservative 16; Mismatches 14; Indels 16; Gaps 2;

Qy 1 KSENVQDLLLLDVAPLSGLTAGVMTALKRSTPTKTQITFTTYSNDQPGVLIQVY 60
 Db 386 KSEKVDLLLLDVAPLSGLTAGVMTALKRSTPTKTQITFTTYSNDQPGVLIQVY 445
 Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVPQIEVTFDANGILNVTATDKSTGKANKITI 120
 Db 446 EGERAMTKNNLLGRFELSGIPAPRGVPQIEVTFDANGILNVTATDKSTGKANKITI 505
 Qy 121 TNDGRSLKSEIERMVAEKYKAEDVQERVSAAKNALESYAFNMKSAVDEGLKGIS 180
 Db 506 TNDGRSLKSEIERMVAEKYKAEDVQERVSAAKNALESYAFNMKSAVDEGLKGIS 565

located in the class III region of the major histocompatibility complex of mouse and man.;
 [3] J. Biochem. 124:347-353(1998).
 [3] SEQUENCE FROM N.A.
 Rowen L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hicks P., Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.;
 "Sequence of the human major histocompatibility complex class III region.";
 Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

[4] SEQUENCE FROM N.A.
 Shina S., Tamiya G., Oka A., Inoko H.;
 "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
 Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 [5] MEDLINE=92406261; PubMed=1356099;
 Milner C.M., Campbell R.D.;
 "Polymorphic analysis of the three MHC-linked HSP70 genes";
 Immunogenetics 36:357-362(1992).
 CC -!- INDUCTION: Not induced by heat shock.
 CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.

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 EMBL; M12571; AAA57234.1; --
 EMBL; M12572; AAA57235.1; --
 PIR; A26283; A26283.
 HSP; P08107; 1HJO.
 MGI; 96244; Hspala.
 InterPro; IPR001023; Hsp70.
 Pfam; PF00012; HSP70; 1.
 PRINTS; PR00301; HEATSHOCK70.
 PROSITE; PS00297; HSP70_1; PARTIAL.
 PROSITE; PS00329; HSP70_2; PARTIAL.
 PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Chapterone; Heat shock; Multigene family.
 FT NON TER 1 1
 FT VARIANT 188 188 V -> G.
 SQ SEQUENCE 420 AA; 46292 MW; 5DA1C6155C7B16B5 CRC64;

Query Match 92.5%; Score 1216; DB 1; Length 420;
 Best Local Similarity 91.9%; Pred. No. 2.7e-67;
 Matches 237; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLLDVAPLSGLTAGVMTALKRSTPTKTQITFTTYSNDQPGVLIQVY 60
 Db 163 KSENVQDLLLLDVAPLSGLTAGVMTALKRSTPTKTQITFTTYSNDQPGVLIQVY 222
 Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVPQIEVTFDANGILNVTATDKSTGKANKITI 120
 Db 223 EGERAMTKNNLLGRFELSGIPAPRGVPQIEVTFDANGILNVTATDKSTGKANKITI 282
 Qy 121 TNDGRSLKSEIERMVAEKYKAEDVQERVSAAKNALESYAFNMKSAVDEGLKGIS 180
 Db 283 TNDGRSLKSEIERMVAEKYKAEDVQERVSAAKNALESYAFNMKSAVDEGLKGIS 342
 Qy 181 EADKKVLDKQEVISWLDANTLAEKDEFEHKKRLEQVCPNPIISGLYQAGAGPGPGGFG 240
 Db 343 EADKKVLDKQEVISWLDNTLADKEEFVHKRELEVCSPNPIISGLYQAGAGPGGFG 402
 Qy 241 AQPKGSGSGGPTIEVD 258
 Db 403 AQPKGSGSGGPTIEVD 420

located in the class III region of the major histocompatibility complex of mouse and man.;
 [3] J. Biochem. 124:347-353(1998).
 [3] SEQUENCE FROM N.A.
 Rowen L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hicks P., Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.;
 "Sequence of the human major histocompatibility complex class III region.";
 Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

[4] SEQUENCE FROM N.A.
 Shina S., Tamiya G., Oka A., Inoko H.;
 "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
 Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 [5] MEDLINE=91055806; PubMed=1700760;
 Milner C.M., Campbell R.D.;
 "Structure and expression of the three MHC-linked HSP70 genes.";
 Immunogenetics 32:242-251(1990).
 [2] SEQUENCE FROM N.A.
 Tissue-Testis;
 RX MEDLINE=98351992; PubMed=9685725;
 RA Ito Y., Ando A., Ando H., Ando J., Saijoh Y., Inoko H., Fujimoto H.;
 "Genomic structure of the spermatid-specific HSP70 homolog gene

located in the class III region of the major histocompatibility complex of mouse and man.;
 [3] J. Biochem. 124:347-353(1998).
 [3] SEQUENCE FROM N.A.
 Rowen L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hicks P., Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.;
 "Sequence of the human major histocompatibility complex class III region.";
 Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

[4] SEQUENCE FROM N.A.
 Shina S., Tamiya G., Oka A., Inoko H.;
 "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
 Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 [5] MEDLINE=92406261; PubMed=1356099;
 Milner C.M., Campbell R.D.;
 "Polymorphic analysis of the three MHC-linked HSP70 genes";
 Immunogenetics 36:357-362(1992).
 CC -!- INDUCTION: Not induced by heat shock.
 CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.

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 EMBL; M12571; AAA57234.1; --
 EMBL; M12572; AAA57235.1; --
 PIR; A26283; A26283.
 HSP; P08107; 1HJO.
 MGI; 96244; Hspala.
 InterPro; IPR001023; Hsp70.
 Pfam; PF00012; HSP70; 1.
 PRINTS; PR00301; HEATSHOCK70.
 PROSITE; PS00297; HSP70_1; PARTIAL.
 PROSITE; PS00329; HSP70_2; PARTIAL.
 PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Chapterone; Heat shock; Multigene family.
 FT NON TER 1 1
 FT VARIANT 188 188 V -> G.
 SQ SEQUENCE 420 AA; 46292 MW; 5DA1C6155C7B16B5 CRC64;


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Qy 181 EADKKVLDKQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGGPGPGFG 240
Db 566 ESDKNKILDKCNELLSWLVNQLAEKDFEHRKKELEQVNCNPIITKLYQG-----G 616

Qy 241 AQPCKGSG-----SGPTIEEVD 258
Db 617 CTGPACGTGYVPGRPATGPTIEEVD 641

RESULT 18
Q6Q1S4 PRELIMINARY; PRT; 650 AA.
AC Q6Q1S4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heat shock cognate 70 kDa protein.
GN Name=HSP70;
OS Pimphales promelas.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Pimphales.
OX NCBI_TaxID=90988;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Lynn S.G., Scholik A.R., Yan H.Y., Shepherd B.S.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY538777; AAS46619.1; -.
DR HSSP; P19120; IATR.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; Hsp70_1; 1.
DR PROSITE; PS00329; Hsp70_2; 1.
DR PROSITE; PS01036; Hsp70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 650 AA; 71316 MW; 60D538BA36A2EEF4 CRC64;

Query Match 84.4%; Score 1108.5; DB 2; Length 650;
Best Local Similarity 82.8%; Pred. No. 2e-60;
Matches 221; Conservative 17; Mismatches 20; Indels 9; Gaps 4;

Qy 1 KSENVQDLLLDVAPLSGLGTAGGVTALIKRNTIPTKTQTFTTYSNQPGVLIQVY 60
Db 384 KSENVQDLLLDVTPLSGLGTAGGVTILIKRNTIPTKTQTFTTYSNQPGVLIQVY 443

Qy 61 EGERAMTKDNNLLGRFELSGTIPAPRGVQPIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKDNNLLGKLFELTGIPAPRGVQPIEVTFDIDANGIMNVSAVDKSTGKANKITI 503

Qy 121 TNDKGRLSKEIERMVOEAEKYKAEDEVQERVSNAKNALESYAFNMKSADVEDEGLKGKIS 180
Db 504 TNDKGRLSKEDIERMVOEAEKYKSEDDVQREKVSANKNGLESYAFNMKSTVEDEKLKGKIS 563

Qy 181 EADKKVLDKQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGG-PG---- 235
Db 564 EEDKQILDKCNQEVISWLDKNQTAKEEFHQKELEKVCNPIITKLYQSAGGMPGGMPE 623

Qy 236 --PGGF-GAQG-PKGGSGSGPTIEEVD 258
Db 624 GMPGFFGAGAPGSGSGSGPTIEEVD 650

RESULT 19
Q804B6 PRELIMINARY; PRT; 649 AA.
ID Q804B6
AC Q804B6;
Qy 181 EADKKVLDKQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGG-PG---- 235
Db 564 EEDKQILDKCNQEVISWLDKNQTAKEEFHQKELEKVCNPIITKLYQSAGGMPGGMPE 623

Qy 236 --PGGF-GAQG-PKGGSGSGPTIEEVD 258
Db 624 GMPGFFGAGAPGSGSGSGPTIEEVD 650
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DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heat shock cognate 70 kDa protein.
OS Carassius auratus gibelio.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=101364;
RN [1]
RP SEQUENCE FROM N.A.
RA Shi Y., Gui J., Liu J., Xia J.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY195744; AAO43731.1; -.
DR HSSP; P19120; IATR.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; Hsp70_1; 1.
DR PROSITE; PS00329; Hsp70_2; 1.
DR PROSITE; PS01036; Hsp70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 649 AA; 71258 MW; ODA48D5B5A28DF5D CRC64;

Query Match 84.3%; Score 1108; DB 2; Length 649;
Best Local Similarity 82.3%; Pred. No. 2.2e-60;
Matches 219; Conservative 18; Mismatches 21; Indels 8; Gaps 3;

Qy 1 KSENVQDLLLDVAPLSGLGTAGGVTALIKRNTIPTKTQTFTTYSNQPGVLIQVY 60
Db 384 KSENVQDLLLDVTPLSGLGTAGGVTILIKRNTIPTKTQTFTTYSNQPGVLIQVY 443

Qy 61 EGERAMTKDNNLLGRFELSGTIPAPRGVQPIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKDNNLLGKLFELTGIPAPRGVQPIEVTFDIDANGIMNVSAVDKSTGKANKITI 503

Qy 121 TNDKGRLSKEIERMVOEAEKYKAEDEVQERVSNAKNALESYAFNMKSADVEDEGLKGKIS 180
Db 504 TNDKGRLSKEDIERMVOEAEKYKSEDDVQREKVSANKNGLESYAFNMKSTVEDEKLKGKIS 563

Qy 181 EADKKVLDKQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGG-PG---- 235
Db 564 EEDKQILDKCNQEVISWLDKNQTAKEEFHQKELEKVCNPIITKLYQSAGGMPGGMPE 623

Qy 236 --PGGF-GAQG-PKGGSGSGPTIEEVD 258
Db 624 GMPGFFGAGAPGSGSGSGPTIEEVD 649

RESULT 20
Q7ZTK6 PRELIMINARY; PRT; 646 AA.
ID Q7ZTK6
AC Q7ZTK6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC53952 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smalius D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX Klein S., Strausberg R.;
RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; BC046262; AAH46262.1; -;
DR HSSP; P19120; IATR.
DR GO; GO:0005524; P:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70_1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
SQ SEQUENCE 646 AA; 70791 MW; 08F72BEDD2C4D58D CRC64;

Query Match 83.9%; Score 1102.5; DB 2; Length 646;
Best Local Similarity 82.1%; Pred. No. 4.8e-60;
Matches 216; Conservative 22; Mismatches 20; Indels 5; Gaps 3;

Qy 1 KSENVQDLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTFTTYSNQPGLVLIQVY 60
Db 384 KSENVQDLLLLDVTPLSIGLETAGVMTVLKRNVTIPTKTQTFTTYSNQPGLVLIQVY 443

Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVQPEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKDNNLLGKFELTGIPPPAPRGVQPEVTFDIDANGILNVSADVSKTGKANKITI 503

Qy 121 TNDKGRLSKEIERMVOEAEKYKAEDVQERVSANNALESYAFNMKSAVEDEGLGKIS 180
Db 504 TNDKGRLSKEDIERMVOEAEKYKAEDQQRDKVSNNLSYAFNMKSTVDEKLGKIS 563

Qy 181 EADKKVLDKQCVISWLDANTLAEKDFEHRKLEQVNCNPIISGLYQAGG-PG--PG 237
Db 564 DEDKQKILEKNEVSWLDKNQTAERBEFHEQKELEKVCNPIITKLYQAGGPGGPNP 623

Qy 238 GFAGAG--PKGSGSGGPTIEVD 258
Db 624 GFGAGAGPAGSGSGSGGPTIEVD 646

RESULT 21
HS7C_BRARE

HS7C_BRARE STANDARD; PRT; 649 AA.
AC Q90473;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock cognate 71 kDa protein.
GN Name=hsc70;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97348566; PubMed=9204550;
RA Graser R.T., Malnar-Dragojevic D., Vincsek V.;
RT "Cloning and characterization of a 70 kd heat shock cognate (hsc70)
gene from the zebrafish (Danio rerio).";
RL Genetica 98:273-276(1996).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L77146; AB03704.1; -;
DR HSSP; P08109; ICKR.
DR ZFIN; ZDB-GENE-990415-92; hsc70.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70_1.
DR TIGRFAMs; TIGR01991; HscA; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock; Multigene family.
SQ SEQUENCE 649 AA; 70974 MW; D486B85CA8E8938C CRC64;

Query Match 83.8%; Score 1101; DB 1; Length 649;
Best Local Similarity 81.6%; Pred. No. 5.9e-60;
Matches 217; Conservative 19; Mismatches 22; Indels 8; Gaps 3;

Qy 1 KSENVQDLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTFTTYSNQPGLVLIQVY 60
Db 384 KSENVQDLLLLDVTPLSIGLETAGVMTVLKRNVTIPTKTQTFTTYSNQPGLVLIQVY 443

Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVQPEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKDNNLLGKFELTGIPPPAPRGVQPEVTFDIDANGIMNVSADVSKTGKANKITI 503

Qy 121 TNDKGRLSKEIERMVOEAEKYKAEDVQERVSANNALESYAFNMKSAVEDEGLGKIS 180
Db 504 TNDKGRLSKEDIERMVOEAEKYKAEDDQQRDKVSANNALESYAFNMKSTVDEKLGKIS 563

Qy 181 EADKKVLDKQCVISWLDANTLAEKDFEHRKLEQVNCNPIISGLYQAGG-PG----- 235
Db 564 DEDKQKILDKNEVSWLDKNQTAERBEFHEQKELEKVCNPIITKLYQAGGPGGMP 623

Qy 236 --PGGF--GAQPGKSGSGGPTIEVD 258
Db 624 GMPGFFGAGAPGSGSGGPTIEVD 649

RESULT 22
Q6NYR4
ID Q6NYR4 PRELIMINARY; PRT; 649 AA.
AC Q6NYR4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

05-JUL-2004 (TrEMBLrel. 27, last sequence update)
 25-OCT-2004 (TrEMBLrel. 28, last annotation update)
 Hsp88 protein.
 Name=hsp88;
 Brachydanio rerio (Zebrafish) (Danio rerio).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 Cyprinidae; Danio.
 NCBI_TaxID=7955;
 [1]
 SEQUENCE FROM N.A.
 TISSUE=Kidney, and Whole;
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie H.F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [2]
 SEQUENCE FROM N.A.
 TISSUE=Kidney;
 RA Strausberg R.;
 RA Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 [3]
 SEQUENCE FROM N.A.
 TISSUE=Whole;
 RA Strausberg R.;
 RA Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
 DR EMBL; BC066491; AAH6491.1; --
 DR EMBL; BC063228; AAH63228.1; --
 DR HSP; P19120; 1ATR.
 DR ZFIN; ZDB-GENE-990415-92; hsp88.
 DR GO; GO:005524; F:ATP binding; IEA.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70_1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR PRODOM; PD000089; Hsp70_1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding.
 SQ SEQUENCE 649 AA; 71180 MW; 18454BB693C838A9 CRC64;
 Query Match 83.8%; Score 1101; DB 2; Length 649;
 Best Local Similarity 81.6%; Pred. No. 5.9e-60;
 Matches 217; Conservative 19; Mismatches 22; Indels 8; Gaps 3;
 QY 1 KSNVQDLLLLVAPLSGLGTAGGVTALIKRNSTIPTKQTQIFTTYSNQPGLVIOVY 60
 DB 384 KSNVQDLLLLVAPLSGLGTAGGVTALIKRNSTIPTKQTQIFTTYSNQPGLVIOVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 444 EGERAMTKNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEDIERMVQEAKEYKAEDVDQVQDKVSARNGLESYAFNMKSTVEDEKLKGKIS 180

504 TNDKGRLSKEDIERMVQEAKEYKAEDVDQVQDKVSARNGLESYAFNMKSTVEDEKLKGKIS 563
 181 EADKKVLDKCOEVIISWLDANTLAKDPEHKKKELEQVCNPIISGLYQAGG-PG----- 235
 564 DEDQKILDKNEVIGWLDKNTQAREEFHQKLEKVCNPIIITKLYQSAGMFGGMPE 623
 236 --PGGF-GAQQPKGSGSGPTIEEVD 258
 624 GMPGFPAGAAAPGGSSGPTIEEVD 649

RESULT 23
 HS7C CRIGR STANDARD; PRT; 646 AA.
 AC P19378;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, last sequence update)
 DT 25-OCT-2004 (Rel. 45, last annotation update)
 DE Heat shock cognate 71 kDa protein.
 GN Name=HSP88; Synonyms=HSC70;
 OS Cricetus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 OC NCBI_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90377205; PubMed=1975944;
 RA Ahmad S., Ahuja R., Venner T.J., Gupta R.S.;
 RT "Identification of a protein altered in mutants resistant to
 RT microtubule inhibitors as a member of the major heat shock protein
 (hsp70) family.";
 RL Mol. Cell. Biol. 10:5160-5165 (1990).
 CC -1- FUNCTION: Chaperone.
 CC -1- SUBCELLULAR LOCATION: Translocates rapidly from the cytoplasm to
 the nuclei, and especially to the nucleoli, upon heat shock (By
 similarity).
 CC -1- INDUCTION: Constitutively synthesized.
 CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
 CC
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 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M34561; AAA36991.1; --
 DR PIR; A35922; A35922.
 DR HSP; P08109; 1CKR.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70_1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR PRODOM; PD000089; Hsp70_1.
 DR TIGRFAMs; TIGR01991; Hsca; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Chaperone; Heat shock; Multigene family; Nuclear protein.
 SQ SEQUENCE 646 AA; 70805 MW; FC65A2DC5095AD1C CRC64;
 Query Match 83.8%; Score 1100.5; DB 1; Length 646;
 Best Local Similarity 81.7%; Pred. No. 6.3e-60;
 Matches 215; Conservative 23; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSNVQDLLLLVAPLSGLGTAGGVTALIKRNSTIPTKQTQIFTTYSNQPGLVIOVY 60
 DB 384 KSNVQDLLLLVAPLSGLGTAGGVTALIKRNSTIPTKQTQIFTTYSNQPGLVIOVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 444 EGERAMTKNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 503

KW ATP-binding; Chaperone; Heat shock; Multigene family; Nuclear protein.
 FT CONFLICT 428 428 F -> L (in Ref. 2 and 3).
 SQ SEQUENCE 646 AA; 70871 MW; 03A27B30B6C076ED CRC64;

Query Match 83.8%; Score 1100.5; DB 1; Length 646;
 Best Local Similarity 81.7%; Pred. No. 6.3e-60;
 Matches 215; Conservative 23; Mismatches 20; Indels 5; Gaps 3;

Qy 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNTIPTKTQTFTTYSNDQPGVLIQVY 60
 Db 384 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNTIPTKTQTFTTYSNDQPGVLIQVY 443

Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVQIETVFDIDANGILNVATDKSTGKANKITI 120
 Db 444 EGERAMTKDNNLLGKLFELTGIPPPAPRGVQIETVFDIDANGILNVATDKSTGKANKITI 503

Qy 121 TNDKGRLSKEBIERMVQEAKEYKAEDVQRRVSAKNALESYAFNMKSASVEDEGLKGGKIS 180
 Db 504 TNDKGRLSKEBIERMVQEAKEYKAEDKQDKVSKNSLESYAFNMKATVDEKLGKIN 563

Qy 181 EADKKKVLDCQEVISWLDANTLAEKDFEHRKKELEOVNCPPIISGLYQAGG-PG--PG 237
 Db 564 DEDKQKILDKCNEIISWLDKNQTAKEBEFHEQKQLEKVCNPIITKLYQSAGGMPGMPG 623

Qy 238 GF--GAQGPKGSGSGPTIEVD 258
 Db 624 GFPGGAPPSGSGSGPTIEVD 646

RESULT 25
 ID_HSC RAT STANDARD; PRT: 646 AA.
 AC P63018; P08109; P12225; Q62373; Q62374; Q62375;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Heat shock cognate 71 kDa protein.
 GN Name=Hsp8; Synonyms=Hsc70, Hsc73;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87246537; PubMed=35955567;
 RA Sorger P.K., Pelham H.R.B.;
 RT "Cloning and expression of a gene encoding hsc73, the major hsp70-like
 RT protein in unstressed rat cells.";
 RL EMBO J. 6:993-998(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86310827; PubMed=3939319;
 RA O'Walley K., Mauron A., Barchas J.D., Keddes L.;
 RT "Constitutively expressed rat mRNA encoding a 70-kilodalton heat-
 RT shock-like protein.";
 RL Mol. Cell. Biol. 5:3476-3483(1985).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary;
 RG NIH - Mammalian Gene Collection (MGC) project;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP STRUCTURE BY NMR OF 385-543.
 RX MEDLINE=99303702; PubMed=10373374; DOI=10.1006/jmbi.1999.2776;
 RA Morshauser R.C., Hu W., Wang H., Pang Y., Flynn G.C.,
 RA Zunderweg E.R.P.;
 RT "High-resolution solution structure of the 18 kDa substrate-binding
 RT domain of the mammalian chaperone protein Hsc70.";
 RL J. Mol. Biol. 289:1387-1403(1999).
 CC -!- FUNCTION: Chaperone
 CC -!- SUBCELLULAR LOCATION: Translocates rapidly from the cytoplasm to
 CC the nuclei, and especially to the nucleoli, upon heat shock (By
 CC similarity).

CC -!- INDUCTION: Constitutively synthesized.
 CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Y00054; AAA68265.1; -;
 CC EMBL; M11942; AAA41354.1; -;
 CC EMBL; BC061547; AAH61547.1; -;
 CC PIR; S07197; S07197;
 CC PDB; 1CKR; NMR; A=385-543.
 CC PDB; 7HSC; NMR; A=385-543.
 CC RGD; 621725; Hspa8.
 CC InterPro; IPR001023; Hsp70.
 CC Pfam; PF00012; HSP70; 1.
 CC PRINTS; PR00301; HEATSHOCK70.
 CC TIGRFAMs; TIGR01991; HSCA; 1.
 CC PROSITE; PS00297; HSP70_1; 1.
 CC PROSITE; PS00329; HSP70_2; 1.
 CC PROSITE; PS01036; HSP70_3; 1.
 CC 3D-structure; ATP-binding; Chaperone; Heat shock; Multigene family;
 KW Nuclear protein.
 FT STRAND 396 397
 FT STRAND 401 405
 FT TURN 406 408
 FT STRAND 409 411
 FT TURN 416 417
 FT STRAND 418 419
 FT STRAND 422 429
 FT STRAND 438 444
 FT STRAND 454 461
 FT TURN 469 470
 FT STRAND 473 481
 FT STRAND 482 484
 FT STRAND 485 492
 FT TURN 493 496
 FT STRAND 497 503
 FT TURN 505 506
 FT HELIX 511 518
 FT TURN 519 521
 FT HELIX 522 527
 FT TURN 528 530
 FT TURN 532 534
 FT STRAND 541 541
 SQ SEQUENCE 646 AA; 70871 MW; 03A27B30B6C076ED CRC64;

Query Match 83.8%; Score 1100.5; DB 1; Length 646;
 Best Local Similarity 81.7%; Pred. No. 6.3e-60;
 Matches 215; Conservative 23; Mismatches 20; Indels 5; Gaps 3;

Qy 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNTIPTKTQTFTTYSNDQPGVLIQVY 60
 Db 384 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNTIPTKTQTFTTYSNDQPGVLIQVY 443

Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVQIETVFDIDANGILNVATDKSTGKANKITI 120
 Db 444 EGERAMTKDNNLLGKLFELTGIPPPAPRGVQIETVFDIDANGILNVATDKSTGKANKITI 503

Qy 121 TNDKGRLSKEBIERMVQEAKEYKAEDVQRRVSAKNALESYAFNMKSASVEDEGLKGGKIS 180
 Db 504 TNDKGRLSKEBIERMVQEAKEYKAEDKQDKVSKNSLESYAFNMKATVDEKLGKIN 563

Qy 181 EADKKKVLDCQEVISWLDANTLAEKDFEHRKKELEOVNCPPIISGLYQAGG-PG--PG 237
 Db 564 DEDKQKILDKCNEIISWLDKNQTAKEBEFHEQKQLEKVCNPIITKLYQSAGGMPGMPG 623

Qy 238 GF--GAQGPKGSGSGPTIEVD 258
 Db 624 GFPGGAPPSGSGSGPTIEVD 646

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Db 624 GPPGGAPPSSGASGPTIEVD 646
RESULT 26
Q75PJ4 ID Q75PJ4 PRELIMINARY; PRT; 646 AA.
AC Q75PJ4
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DN Heat shock protein.
GN Name=hsp98;
OS Numida meleagris (Helmeted guineafowl).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Numididae; Numida.
OX NCBI_TaxID=8996;
RN 1
RP SEQUENCE FROM N.A.
RA Imamoto S., Hara H., Yoshida Y., Hanzawa K., Watanabe S.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AB167744; BAD12572.1; -.
DR HSSP; P19120; IATR.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; Hsp70_1; 1.
DR PROSITE; PS00329; Hsp70_2; 1.
DR PROSITE; PS01036; Hsp70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 646 AA; 70870 MW; EDDD8CB1E52A6EFC CRC64;
Query Match 83.8%; Score 1100.5; DB 2; Length 646;
Best Local Similarity 81.7%; Pred. No. 6.3e-60;
Matches 215; Conservative 23; Mismatches 20; Indels 5; Gaps 3;
Qy 1 KSENVQDLLLDVAPLSLGLETAGVMTALIKRNTIPTKTQTFTTYSNDQPGVLIQVY 60
Db 384 KSENVQDLLLDVTPLSLGLETAGVMTVLKRWNTIPTKTQTFTTYSNDQPGVLIQVY 443
Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPQIEVTFDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTKNNLLGKFLTGTPPAPRGVPQIEVTFDANGILNVATDKSTGKANKITI 503
Qy 121 TNDKGRLSKEIERMVQEAKEYKAEDVQREVRSAKNALSYAFNMKSAVEDEGLKGKIS 180
Db 504 TNDKGRLSKEDIERMVQEAKEYKAEDKQDRKVSKNLSYAFNMKATVDEKLGKIS 563
Qy 181 EADKKVLDKQEVISWLDANTLAEKDFEHRKLEQVNCNPIISGLYQAGG-PG-PG 237
Db 564 DEDKQKLDKCNELINWLDKNQTAERDSEYHQKELEKVCNPIITKLQYQSAGGPGGMPG 623
Qy 238 GF--GAQPKGGSGGPTIEVD 258
Db 624 GPPGGAPPSSGASGPTIEVD 646
RESULT 27
Q6TDUO ID Q6TDUO PRELIMINARY; PRT; 653 AA.
AC Q6TDUO
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DN Name=hsp70;
GN Dicertrarchus labrax (European sea bass).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Moronidae; Dicertrarchus.
OX NCBI_TaxID=13489;
RN 1
RP SEQUENCE FROM N.A.
RA Gornati R., Vigetti D., Saroglia M., Bernardini G.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY423555; AAR01102.2; -.
DR HSSP; P19120; IATR.
DR GO; GO:0005524; P:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; Hsp70_1; 1.
DR PROSITE; PS00329; Hsp70_2; 1.
DR PROSITE; PS01036; Hsp70_3; 1.
KW ATP-binding.
SQ SEQUENCE 653 AA; 71367 MW; 8E14197F9189E1D8 CRC64;
Query Match 83.6%; Score 1098; DB 2; Length 653;
Best Local Similarity 80.2%; Pred. No. 9.2e-60;
Matches 215; Conservative 21; Mismatches 22; Indels 10; Gaps 3;
Qy 1 KSENVQDLLLDVAPLSLGLETAGVMTALIKRNTIPTKTQTFTTYSNDQPGVLIQVY 60
Db 386 KSENVQDLLLDVTPLSLGLETAGVMTVLKRWNTIPTKTQTFTTYSNDQPGVLIQVY 445
Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPQIEVTFDANGILNVATDKSTGKANKITI 120
Db 446 EGERAMTRDNNLLGKFLTGTPPAPRGVPQIEVTFDANGIMNVSAVDKSTGKANKITI 505
Qy 121 TNDKGRLSKEIERMVQEAKEYKAEDVQREVRSAKNALSYAFNMKSAVEDEGLKGKIS 180
Db 506 TNDKGRLSKEDIERMVQEAKEYKAEDDVQDRKVSKNLSYAFNMKSTVDEDLAKGIS 565
Qy 181 EADKKVLDKQEVISWLDANTLAEKDFEHRKLEQVNCNPIISGLYQAGG-PG----- 235
Db 566 DDDKQKLDKCNELINWLDKNQTAERDSEYHQKELEKVCNPIITKLQYQSAGGPGGMPG 625
Qy 236 --PGGP---GAQPKGGSGGPTIEVD 258
Db 626 GPPGGAPPSSGASGPTIEVD 653
RESULT 28
Q96BE0 ID Q96BE0 PRELIMINARY; PRT; 269 AA.
AC Q96BE0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RA Straussberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; BC015699; AAH15699.1; -.
DR HSSP; P04475; 1Q5L.
DR GO; GO:0005524; P:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
KW ATP-binding; Hypothetical protein.
FT NON_TER 1
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SQ SEQUENCE 269 AA; 29361 MW; 4435C53CF9385475 CRC64;

Query Match      83.5%; Score 1097.5; DB 2; Length 269;
Best Local Similarity 81.4%; Pred. No. 3.4e-60;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

Qy 1 KSENVQDILLDVLAPSLGLETAGVMTALIKRNTSTPTKTQTQITFTTYSNQPGVLIQVY 60
    |||||
Db 7 KSENVQDILLDVLAPSLGLETAGVMTALIKRNTSTPTKTQTQITFTTYSNQPGVLIQVY 66
    |||||
Qy 61 EGERAMTKONNLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
    |||||
Db 67 EGERAMTKONNLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 126
    |||||
Qy 121 TNDKGRLSKEEIERMVQAEKYKAEDVQERVSANNALESYAFNMKSADVEGLKCKIS 180
    |||||
Db 127 TNDKGRLSKEEIERMVQAEKYKAEDVQERVSANNALESYAFNMKSADVEGLKCKIS 186
    |||||
Qy 181 EADKKVLDKCOEIVSWLDANTLAEKDFEHKRELEQVNCNPIISGLYQAGG-PG--PG 237
    |||||
Db 187 EADKKVLDKCOEIVSWLDANTLAEKDFEHKRELEQVNCNPIISGLYQAGG-PG--PG 246
    |||||
Qy 238 GF--GAQPGKGGSGGPTIEVD 258
    |||||
Db 247 GFPGGGAPPSGGSGGPTIEVD 269

RESULT 29
Q961S6 PRELIMINARY; PRT; 586 AA.
AC Q961S6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE HSPA8 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
    and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RA Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DE EMBL: BC007276; AA07276.1; --
DR HSP70, P19120, 3HSC
DR GO: 0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
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DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
SQ SEQUENCE 586 AA; 64602 MW; 8640B210CABE3475 CRC64;

Query Match      83.5%; Score 1097.5; DB 2; Length 586;
Best Local Similarity 81.4%; Pred. No. 8.7e-60;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

Qy 1 KSENVQDILLDVLAPSLGLETAGVMTALIKRNTSTPTKTQTQITFTTYSNQPGVLIQVY 60
    |||||
Db 324 KSENVQDILLDVLAPSLGLETAGVMTALIKRNTSTPTKTQTQITFTTYSNQPGVLIQVY 383
    |||||
Qy 61 EGERAMTKONNLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
    |||||
Db 384 EGERAMTKONNLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 443
    |||||
Qy 121 TNDKGRLSKEEIERMVQAEKYKAEDVQERVSANNALESYAFNMKSADVEGLKCKIS 180
    |||||
Db 444 TNDKGRLSKEEIERMVQAEKYKAEDVQERVSANNALESYAFNMKSADVEGLKCKIS 503
    |||||
Qy 181 EADKKVLDKCOEIVSWLDANTLAEKDFEHKRELEQVNCNPIISGLYQAGG-PG--PG 237
    |||||
Db 504 EADKKVLDKCOEIVSWLDANTLAEKDFEHKRELEQVNCNPIISGLYQAGG-PG--PG 563
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Qy 238 GF--GAQPGKGGSGGPTIEVD 258
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Db 564 GFPGGGAPPSGGSGGPTIEVD 586

RESULT 30
HS7C HUMAN STANDARD; PRT; 646 AA.
AC P11142; Q9H3R6;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Heat shock cognate 71 kDa protein.
GN Name=HSPA8; Synonyms=HSC70, HSP73, HSPA10;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=87259994; PubMed=3037489;
RA Dworniczak B.P., Mirault M.-E.;
RT "Structure and expression of a human gene coding for a 71 kd heat
    shock 'cognate' protein."
RL Nucleic Acids Res. 15:5181-5197(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=20545701; PubMed=11093761;
RA Tsukahara F., Yoshioka T., Muraki T.;
RT "Molecular and functional characterization of HSC54, a novel variant
    of human heat shock cognate protein 70."
RL Mol. Pharmacol. 58:1257-1263(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Niswonger M.L., Berk L.R., Srivastava P.K.;
RT "Complete coding sequence of human HSC70."
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Placenta, and Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanches A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krywinski M.T., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [5]
 RP SEQUENCE OF 50-55; 103-107 AND 580-596.
 RX MEDLINE=93162043; PubMed=1286667;
 RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
 RA Vandekerckhove J.;
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel
 RT protein database of normal human epidermal keratinocytes.";
 RL Electrophoresis 13:960-969 (1992).
 RN [6]
 RP SEQUENCE OF 77-86; 221-236 AND 302-311.
 RX MEDLINE=96311348; PubMed=8713105; DOI=10.1006/bbr.1996.1082;
 RA Egerton M., Moritz R.L., Drucker B., Kelsa A., Simpson R.J.;
 RT "Identification of the 70kd heat shock cognate protein (Hsc70) and
 RT alpha-actinin-1 as novel phosphorylation-containing proteins in T
 RT lymphocytes.";
 RL Biochem. Biophys. Res. Commun. 224:666-674 (1996).
 RN [7]
 RP SUBCELLULAR LOCATION.
 RX PubMed=1586970;
 RA Hattori H., Liu Y.-C., Tohrai I., Ueda M., Kaneda T., Kobayashi T.,
 RA Tanabe K., Ohtsuka K.;
 RT "Intracellular localization and partial amino acid sequence of a
 RT stress-inducible 40-kDa protein in HeLa cells.";
 RL Cell Struct. Funct. 17:77-86 (1992).
 CC -!- FUNCTION: Chaperone. Isoform 2 may function as an endogenous
 CC inhibitory regulator of HSC70 by competing the cochaperones.
 CC -!- SUBCELLULAR LOCATION: Translocates rapidly from the cytoplasm to
 CC the nuclei, and especially to the nucleoli, upon heat shock.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P11142-1; Sequence=Displayed;
 CC Name=2; Synonyms=HSC54;
 CC IsoId=P11142-2; Sequence=VSP_002427;
 CC -!- TISSUE SPECIFICITY: Ubiquitous.
 CC -!- INDUCTION: Constitutively synthesized.
 CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC -----
 CC EMBL; Y00371; CAA68445.1; --
 CC EMBL; AB034951; BAB18615.1; --
 CC EMBL; AF352832; AAK17898.1; --
 CC EMBL; BC016179; AAH16179.1; --
 CC EMBL; BC016660; AAH16660.1; --
 CC EMBL; BC019816; AAH19816.1; --
 CC PIR; A27077; A27077.
 CC HSP; P19120; 1A7R.
 CC SWISS-2DPAGE; P11142; HUMAN.
 CC Aarhus/Ghent-2DPAGE; 6504; IEF.
 CC HSC-2DPAGE; P11142; HUMAN.

DR OGP; P11142; --
 DR PHC1-2DPAGE; P11142; --
 DR Genew; HGNC:5241; HSPA8.
 DR H-InvdB; HIX0010213; --
 DR MIM; 600816; --
 DR GO; GO:0005622; C:intracellular; NAS.
 DR GO; GO:0042823; F:ATPase activity; coupled; NAS.
 DR GO; GO:0006457; F:protein folding; NAS.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR TIGRFAMs; TIGR01991; HscA; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW Alternative splicing; ATP-binding; Chaperone;
 KW Direct protein sequencing; Heat shock; Multigene family;
 KW Nuclear protein.
 KW VAKSPDIC 464 616 Missing (in isoform 2).
 FT VAKSPDIC 464 616
 SQ SEQUENCE 646 AA; 70898 MW; 9AA27B210730670C CRC64;
 /FTID=VSP_002427.
 Query Match 83.5%; Score 1097.5; DB 1; Length 646;
 Best Local Similarity 81.4%; Pred. No. 9.7e-60;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVQDLLLLLDVAPLSGLTETAGGVMTALIKRNTSTPTKTQTQITFTYSDNQPGVLIQVY 60
 DB 384 KSENVQDLLLLLDVTPLSGLTETAGGVMTALIKRNTSTPTKTQTQITFTYSDNQPGVLIQVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVQIETVDFDANGILNVATDKSTGKANKITI 120
 DB 444 EGERAMTKNNLLGKFLTGTIPAPRGVQIETVDFDANGILNVATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEIERMVQAEKYAEDEVQREVSNAKNALESYAFNMKSAVEDGLKGGKIS 180
 DB 504 TNDKGRLSKEDIERMVQAEKYAEDEVQREVSNAKNALESYAFNMKSAVEDGLKGGKIN 563
 QY 181 EADKKKVLDCQEVISWLDANTLAEDKDFEHRKELEQVCNPIISGLYQAGG-PG--PG 237
 DB 564 DEDKQKILDKCNELIINWLDKNQTAKEFEFEHQKELEKVCNPIITKLYQSAGMGPMGP 623
 QY 238 GF--GAQGPKGSGSGPTIEVD 258
 DB 624 GFQGGGAPPSSGSGSGPTIEVD 646
 RESULT 31
 HS7C SAGOE
 ID HS7C SAGOE STANDARD; PRT; 646 AA.
 AC Q71UJ34;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DE Heat shock cognate 71 kDa protein (intracellular vitamin D binding
 DE protein 1).
 GN Name=HSPA8; Synonyms=IDBP1;
 OS *Saguinus oedipus* (Cotton-top tamarin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; *Saguinus*.
 ON NCBI_TaxID=9490;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wu S., Ren S., Chen H., Chien R., Gacad M.A., Adams J.S.;
 RT "Cloning and expression of two novel cDNAs for hsp-70-related
 RT intracellular vitamin D binding proteins.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Chaperone. Isoform 2 may function as an endogenous
 CC inhibitory regulator of HSC70 by competing the cochaperones (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Translocates rapidly from the cytoplasm to
 CC the nuclei, and especially to the nucleoli, upon heat shock (By

CC similarity).
 CC -I- INDUCTION: Constitutively synthesized.
 CC -I- SIMILARITY: Belongs to the heat shock protein 70 family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF142571; AAF66593.1; -
 CC InterPro: IPR001023; Hsp70.
 CC Pfam: PF00012; HSP70; 1.
 CC PRINTS: PR00301; HEATSHOCK70.
 CC PRODOM: PD000089; Hsp70; 1.
 CC PROSITE: PS00297; HSP70_1; 1.
 CC PROSITE: PS00329; HSP70_2; 1.
 CC PROSITE: PS01036; HSP70_3; 1.
 CC ATP-binding; Chaperone; Multigene family; Nuclear protein.
 KW SEQUENCE 646 AA; 70898 MW; 9AA27B210730670C CRC64;
 SQ
 Query Match 83.5%; Score 1097.5; DB 1; Length 646;
 Best Local Similarity 81.4%; Pred. No. 9.7e-60;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 Qy 1 KSENVQDLLLLLDVAPLSLGLETAGGVTALIKRNTIPTKTQTFTTYSNQPGLVQVY 60
 Db 384 KSENVQDLLLLLDVTPLSLGLETAGGVTALIKRNTIPTKTQTFTTYSNQPGLVQVY 443
 Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 Db 444 EGERAMTKNNLLGKLFELTGIPLPPAPRGVPOIEVTFDIDANGILNVSADVSTGKANKITI 503
 Qy 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQREVRSYAKNALESYAFNMKSASVEDEGLKGIS 180
 Db 504 TNDKGRLSKEDIERMVOEAEKYKAEDKQDKVSKNSLESYAFNMKATVEDEKLQKIN 563
 Qy 181 EADKKVLDKQCVISWLDANTLAEDKDEFEHKKRLEQVCNPIISGLYQAGG-PG--PG 237
 Db 564 DEDQKILDKCNEVINLWLDKNTAEKFEFHQKELEKVCNPIITKLYQSAGGMPGMPG 623
 Qy 238 GF--GAQGPKGSGSGPTIEVD 258
 Db 624 GFPGGAPPFGSGSGSGPTIEVD 646
 RESULT 32
 Q7ZVJ1 ID Q7ZVJ1 PRELIMINARY; PRT; 649 AA.
 AC Q7ZVJ1
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hsp88 protein.
 GN Name=hsp88;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=Whole body;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blackley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=Whole body;
 RA Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: Belongs to the heat shock protein 70 family.
 CC EMBL: BC045841; AAH45841.1; -
 CC HSP; P19120; IATR.
 CC ZFIN: ZDB-GENE-990415-92; hsp88.
 CC GO: GO:0005524; F:ATP binding; IEA.
 CC InterPro: IPR001023; Hsp70.
 CC Pfam: PF00012; HSP70; 1.
 CC PRINTS: PR00301; HEATSHOCK70.
 CC PRODOM: PD000089; Hsp70; 1.
 CC PROSITE: PS00297; HSP70_1; 1.
 CC PROSITE: PS00329; HSP70_2; 1.
 CC PROSITE: PS01036; HSP70_3; 1.
 CC ATP-binding.
 KW SEQUENCE 649 AA; 71198 MW; 9C006B74724919B CRC64;
 SQ
 Query Match 83.5%; Score 1097; DB 2; Length 649;
 Best Local Similarity 81.2%; Pred. No. 1e-59;
 Matches 216; Conservative 19; Mismatches 23; Indels 8; Gaps 3;
 Qy 1 KSENVQDLLLLLDVAPLSLGLETAGGVTALIKRNTIPTKTQTFTTYSNQPGLVQVY 60
 Db 384 KSENVQDLLLLLDVTPLSLGLETAGGVTALIKRNTIPTKTQTFTTYSNQPGLVQVY 443
 Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 Db 444 EGERAMTKNNLLGKLFELTGIPLPPAPRGVPOIEVTFDIDANGIMNVSADVSTGKANKITI 503
 Qy 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQREVRSYAKNALESYAFNMKSASVEDEGLKGIS 180
 Db 504 TNDKGRLSKEDIERMVOEAEKYKAEDDQDKVSKNSLESYAFNMKSTVEDEKLKGIS 563
 Qy 181 EADKKVLDKQCVISWLDANTLAEDKDEFEHKKRLEQVCNPIISGLYQAGG-PG---- 235
 Db 564 DEDQKILDKCNEVINLWLDKNTAEKFEFHQKELEKVCNPIITKLYQSAGGMPGMPG 623
 Qy 236 --PGGP-GAQPKGSGSGPTIEVD 258
 Db 624 GMPGGPPGAGAPGGSGSGPTIEVD 649
 RESULT 33
 Q6NZD0 ID Q6NZD0 PRELIMINARY; PRT; 646 AA.
 AC Q6NZD0
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Heat shock protein 8.
 GN Name=hsp8;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

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RC STRAIN=CS7BL/6J; TISSUE=Embryonic Germ Cell;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=Embryonic Germ Cell;
RA Strausberg R.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; BC066191; AAH66191.1; -.
DR HSP; P19120; IATR.
DR GO; GO:0042623; F:ATPase activity, coupled; IDA.
DR GO; GO:0003754; F:chaperone activity; IDA.
DR GO; GO:0005155; F:protein binding; IPI.
DR GO; GO:0051085; P:chaperone cofactor dependent protein folding; IGI.
DR GO; GO:0006457; P:protein folding; IDA.
DR GO; GO:0000074; P:regulation of cell cycle; IDA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR KW ATP-binding; Heat shock.
SQ SEQUENCE 646 AA; 70871 MW; 03AC7530B8CE76ED CRC64;

Query Match 83.4%; Score 1096.5; DB 2; Length 646;
Best Local Similarity 81.3%; Pred. No. 1.1e-59;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

Qy 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTYSDNQPGVLIQVY 60
Db 384 KSENVQDLLLDVTPLSGLGTAGVMTVLKRNITPTKTQITFTYSDNQPGVLIQVY 443

Qy 61 EGERAMTKDNNLGRFELSGIPPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKDNNLGRFELSGIPPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 503

Qy 121 TNDKGRLSKKEIERMVOAEAKYKAEDEQVQERVSQAKNALESYAFNMKSAVEDEGLKGGKIS 180
Db 504 TNDKGRLSKEDIERMVOAEAKYKAEDEKQQRDSKNSLESYAFNMKATVEDEKLQKIN 563

Qy 181 EADKKVKLDKQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGG-PG--PG 237
Db 564 DEDQKILDKNEIISWLDKNOTAEFEHQKELEKVCNPIITKLQYQAGGPGGMPG 623

Qy 238 GF--GAQGPKGSGSGPTIEVD 258
Db 624 GFPGGGAPPSSGGASGPTIEVD 646

RESULT 34
Q8AVE2

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ID Q8AVE2 PRELIMINARY; PRT; 650 AA.
AC 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hsc70-prov protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; BC041201; AAH41201.1; -.
DR HSP; P19120; IATR.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR KW ATP-binding.
SQ SEQUENCE 650 AA; 71188 MW; CAE53D1D3275E6B5 CRC64;

Query Match 83.4%; Score 1096.5; DB 2; Length 650;
Best Local Similarity 81.3%; Pred. No. 1.1e-59;
Matches 217; Conservative 23; Mismatches 18; Indels 9; Gaps 4;

Qy 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTYSDNQPGVLIQVY 60
Db 384 KSENVQDLLLDVTPLSGLGTAGVMTVLKRNITPTKTQITFTYSDNQPGVLIQVY 443

Qy 61 EGERAMTKDNNLGRFELSGIPPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120

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Db 444 EGERAMTKDNNLLGKFLGTGIPAPRGVPOIEVTFDIDANGILNVSADVSTGKKNKITI 503
Qy 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAAKNALSYAFNMKSAVEDGLGKGIS 180
Db 504 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAAKNALSYAFNMKSAVEDGLGKGIS 563
Qy 181 EADKKVLDKCOEIVSWLDANTLAEDKDFEHRKELEQVNCNPIISGLYQAGG---PG 235
Db 564 DEDQKLEKNEVIAWLDKQNTAKDFEHRKELEQVNCNPIISGLYQAGGMPG 623
Qy 236 --PGP-CAQG-PKGGSGGPTIEVD 258
Db 624 GMPGFCGAGPTGGASSGPTIEVD 650

RESULT 35

Q8NE72 PRELIMINARY; PRT; 641 AA.
AC Q8NE72; 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
GN Heat shock 70kDa protein i-like.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wozney K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bonfield G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX Strausberg R.;
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR HSP; P08107; I1H0.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70; 1.
DR PROSITE; PS00329; HSP70; 1.
DR PROSITE; PS01036; HSP70; 3; 1.
KW ATP-binding; Heat shock.
FT NON TER 1.
SQ SEQUENCE 641 AA; 70393 MW; E4417F62C6D86ACA CRC64;

Query Match 83.3%; Score 1095; DB 2; Length 641;
Best Local Similarity 81.5%; Pred. No. 1.4e-59;
Matches 216; Conservative 19; Mismatches 16; Indels 16; Gaps 2;
Qy 1 KSENVQDILLDVLAPLSGLTAGGVMTALIKENSTIPTKTQTFITTSYSDNQPGVLIQVY 60
Db 386 KSENVQDILLDVLAPLSGLTAGGVMTALMKRNTIPTKTQTFITTSYSDNQPGVLIQVY 445
Qy 61 EGERAMTKDNNLLGRFELSIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKKNKITI 120
Db 446 EGERAMTKDNNLLGRFELTGIPTAPRGVPOIEVTFDIDANGILNVTAMDKSTGKKNKITI 505
Qy 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAAKNALSYAFNMKSAVEDGLGKGIS 180
Db 506 ANDKGRLSKEEIERMVOEAEKYKAEDVQERVSAAKNALSYAFNMKSAVEDGLGKGIS 565
Qy 181 EADKKVLDKCOEIVSWLDANTLAEDKDFEHRKELEQVNCNPIISGLYQAGGPGGFG 240
Db 566 ESDKNKILDKCNELLWLVNQLAEDKDFHKKLEQVNCNPIITKLYQG-----G 616
Qy 241 AQPKGGSG-----SGPTIEVD 258
Db 617 CTGPACGTGYVGRPATGPTIEVD 641

RESULT 36

Q801X8 PRELIMINARY; PRT; 631 AA.
AC Q801X8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heat shock cognate 70 kDa (Fragment).
GN Name=HSC70;
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC Watabe S., Kondo H., Hashimoto S.;
RA Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AB092840; BAC67185.1; -
DR HSP; P19120; 3HSC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00329; HSP70; 2; 1.
DR PROSITE; PS01036; HSP70; 3; 1.
KW ATP-binding; Heat shock.
FT NON TER 1.
SQ SEQUENCE 631 AA; 69436 MW; 6CA60C8E66DDDBIA CRC64;

Query Match 83.3%; Score 1094; DB 2; Length 631;
Best Local Similarity 81.2%; Pred. No. 1.6e-59;
Matches 216; Conservative 19; Mismatches 23; Indels 8; Gaps 3;
Qy 1 KSENVQDILLDVLAPLSGLTAGGVMTALIKENSTIPTKTQTFITTSYSDNQPGVLIQVY 60
Db 366 KSENVQDILLDVLAPLSGLTAGGVMTALIKRNTIPTKTQTFITTSYSDNQPGVLIQVY 425
Qy 61 EGERAMTKDNNLLGRFELSIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKKNKITI 120
Db 426 EGERAMTKDNNLLGKFLGTGIPAPRGVPOIEVTFDIDANGILNVSADSTGKKNKITI 485
Qy 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAAKNALSYAFNMKSAVEDGLGKGIS 180

DR 486 TYDKRLSKEDIERMVHEAEKYSDEDDVQREKVSXKNGLESYAFNMKSTVEDEKLKGKIS 545
DR PFam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
KW ATP-binding; Heat shock.
FT NON TER 1
SQ SEQUENCE 282 AA; 30884 MW; D8177623CF106307 CRC64;
Query Match 83.1%; Score 1092; DB 2; Length 282;
Best Local Similarity 84.5%; Pred. No. 7.9e-60;
Matches 218; Conservative 17; Mismatches 21; Indels 2; Gaps 2;
Qy 1 KSENVQDLILLDVAPLSGLGTAGVMTALIKRSTIPTKQTQITFTTYSNDQPGVLIQVY 60
Db 27 KSEKVDLLLDVAPLSGLGTAGVMTLVLIKRNSTIPTKQTQITFTTYSNDQPGVLIQVY 86
Qy 61 EGERAMTKDNLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 87 EGERAMTRDNLGRFELTGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 146
Qy 121 TNDKRLSKKEIERMVQEAERYKAEDQREKIAAKNALESYAFNMKSAVDEGLKGKIS 180
Db 147 TNDKRLSKKEIERMVQEAERYKAEDQREKIAAKNALESYAFNMKSAVDEGLKGKIS 206
Qy 181 EADKKVLDKQEVISWLDANTLAEKDFEHRKELEQVNCPIISGLYQAGGPGGFG 240
Db 207 ESDKKKILDKCNVLSWLEANQLAEKDFEHRKELENCNPIITKLYQ-SGCTGPTCTP 265
Qy 241 AQGPKGGSGGPTIEVD 258
Db 266 GYTP-GRATYGTPTIEVD 282
RESULT 38
Q91ZU4 PRELIMINARY; PRT; 461 AA.
ID Q91ZU4
AC Q91ZU4, 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Heat shock protein Hsc70t (Fragment).
GN Name=Hsc70t;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B10.A;
RX MEDLINE=9216447; PubMed=10199925; DOI=10.1007/s002510050522;
RA Snoek M., van Vugt H.;
RT "The sequence and organization of the mouse valyl-tRNA synthetase gene
G7a/Bat6 located in the MHC class III region.";
RL Immunogenetics 49:468-470 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=B10.A;
RX MEDLINE=97124840; PubMed=8954773; DOI=10.1006/geno.1996.0585;
RA Snoek M., van Dinten L., van Vugt H.;
RT "A novel gene, G7e, resembling a viral envelope gene, is located at
the recombinational hot spot in the class III region of the mouse
Genomics 38:5-12 (1996)."
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=B10.A;
RX MEDLINE=94299288; PubMed=8026864;
RA Snoek M., Olavsen M.G., van Vugt H., Milner C.M., Teuscher C.,
Campbell R.D.;
RT "Coding sequences and levels of expression of Hsc70t are identical in
mice with different Orch-1 alleles.";
RL Immunogenetics 40:159-162 (1994).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=B10.A;
RX MEDLINE=98211706; PubMed=9551980;
RA Snoek M., Teuscher C., van Vugt H.;
RT "Molecular analysis of the major MHC recombinational hot spot located
within the G7c gene of the murine class III region that is involved in
disease susceptibility";
RL J. Immunol. 160:266-272 (1998).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=B10.A;
RX MEDLINE=21655112; PubMed=11797099; DOI=10.1007/s00251-001-0381-0;
RA van Kooij M., de Groot K., van Vugt H., Aten J., Snoek M.;
RT "Genotype versus phenotype: conflicting results in mapping a lung
tumor susceptibility locus to the G7c recombinational interval in the
mouse MHC class III region.";
RL Immunogenetics 53:656-661 (2001).
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AF397035; AAL1448.1; --
DR HSP; P04475; I05L.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.

DR 486 TYDKRLSKEDIERMVHEAEKYSDEDDVQREKVSXKNGLESYAFNMKSTVEDEKLKGKIS 545
DR PFam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
KW ATP-binding; Heat shock.
FT NON TER 1
SQ SEQUENCE 282 AA; 30884 MW; D8177623CF106307 CRC64;
Query Match 83.1%; Score 1092; DB 2; Length 282;
Best Local Similarity 84.5%; Pred. No. 7.9e-60;
Matches 218; Conservative 17; Mismatches 21; Indels 2; Gaps 2;
Qy 1 KSENVQDLILLDVAPLSGLGTAGVMTALIKRSTIPTKQTQITFTTYSNDQPGVLIQVY 60
Db 27 KSEKVDLLLDVAPLSGLGTAGVMTLVLIKRNSTIPTKQTQITFTTYSNDQPGVLIQVY 86
Qy 61 EGERAMTKDNLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 87 EGERAMTRDNLGRFELTGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 146
Qy 121 TNDKRLSKKEIERMVQEAERYKAEDQREKIAAKNALESYAFNMKSAVDEGLKGKIS 180
Db 147 TNDKRLSKKEIERMVQEAERYKAEDQREKIAAKNALESYAFNMKSAVDEGLKGKIS 206
Qy 181 EADKKVLDKQEVISWLDANTLAEKDFEHRKELEQVNCPIISGLYQAGGPGGFG 240
Db 207 ESDKKKILDKCNVLSWLEANQLAEKDFEHRKELENCNPIITKLYQ-SGCTGPTCTP 265
Qy 241 AQGPKGGSGGPTIEVD 258
Db 266 GYTP-GRATYGTPTIEVD 282
RESULT 38
Q91ZU4 PRELIMINARY; PRT; 461 AA.
ID Q91ZU4
AC Q91ZU4, 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Heat shock protein Hsc70t (Fragment).
GN Name=Hsc70t;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B10.A;
RX MEDLINE=9216447; PubMed=10199925; DOI=10.1007/s002510050522;
RA Snoek M., van Vugt H.;
RT "The sequence and organization of the mouse valyl-tRNA synthetase gene
G7a/Bat6 located in the MHC class III region.";
RL Immunogenetics 49:468-470 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=B10.A;
RX MEDLINE=97124840; PubMed=8954773; DOI=10.1006/geno.1996.0585;
RA Snoek M., van Dinten L., van Vugt H.;
RT "A novel gene, G7e, resembling a viral envelope gene, is located at
the recombinational hot spot in the class III region of the mouse
Genomics 38:5-12 (1996)."
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=B10.A;
RX MEDLINE=94299288; PubMed=8026864;
RA Snoek M., Olavsen M.G., van Vugt H., Milner C.M., Teuscher C.,
Campbell R.D.;
RT "Coding sequences and levels of expression of Hsc70t are identical in
mice with different Orch-1 alleles.";
RL Immunogenetics 40:159-162 (1994).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=B10.A;
RX MEDLINE=98211706; PubMed=9551980;
RA Snoek M., Teuscher C., van Vugt H.;
RT "Molecular analysis of the major MHC recombinational hot spot located
within the G7c gene of the murine class III region that is involved in
disease susceptibility";
RL J. Immunol. 160:266-272 (1998).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=B10.A;
RX MEDLINE=21655112; PubMed=11797099; DOI=10.1007/s00251-001-0381-0;
RA van Kooij M., de Groot K., van Vugt H., Aten J., Snoek M.;
RT "Genotype versus phenotype: conflicting results in mapping a lung
tumor susceptibility locus to the G7c recombinational interval in the
mouse MHC class III region.";
RL Immunogenetics 53:656-661 (2001).
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AF397035; AAL1448.1; --
DR HSP; P04475; I05L.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.

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RC STRAIN=B10.A;
RX MEDLINE=98211706; PubMed=9551980;
RA Snoek M., Teuscher C., van Vugt H.;
RT "Molecular analysis of the major MHC recombinational hot spot located
RT within the G7c gene of the murine class III region that is involved in
RT disease susceptibility."
RL J. Immunol. 160:266-272(1998).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=B10.A;
RX MEDLINE=21655112; PubMed=11797099; DOI=10.1007/s00251-001-0381-0;
RA van Kooij M., de Groot K., van Vugt H., Aten J., Snoek M.;
RT "Genotype versus phenotype: conflicting results in mapping a lung
RT tumor susceptibility locus to the G7c recombination interval in the
RT mouse MHC class III region."
RL Immunogenetics 53:656-661(2001).
CC -I- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AF397036; AAL14456.1; -.
DR HSP; P08107; I53X.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
FT NON TER 1
SQ SEQUENCE 461 AA; 50982 MW; C08082B37DB90C75 CRC64;
Query Match 83.1%; Score 1092; DB 2; Length 461;
Best Local Similarity 84.5%; Pred. No. 1.4e-59;
Matches 218; Conservative 17; Mismatches 21; Indels 2; Gaps 2;
Qy 1 KSENVQDLLLDVAPLSGLGLETAGGVMTALIKRNSTIPTKTQTOIFTTYSNQPGLVQVY 60
Db 206 KSEKVDLLLDVAPLSGLGLETAGGVMTALIKRNSTIPTKTQTOIFTTYSNQPGLVQV 265
Qy 61 EGERAMTKNNLLGRFELSGTIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
Db 266 EGERAMTRDNNLLGRFDLTGTIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 325
Qy 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSNAKNALESYAFNMKSASVDEGLKDKIS 180
Db 326 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSNAKNALESYAFNMKSASVDEGLKDKIS 385
Qy 181 EADKKVKLDKQCVISWLDANTLAEKDFEHRKLEFOVNCNPIISGLYQAGGPGGFG 240
Db 386 ESDKKKILDKCNELVSLWLANQLAEKDFEHRKLENCNPNITIKLYQ-SGCTGPTCTP 444
Qy 241 AQGPKGGSGSGPTIEVD 258
Db 445 GYTP-GRAATGPTIEVD 461
RESULT 39
Q9QWU1 PRELIMINARY; PRT; 552 AA.
AC Q9QWU1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hsc70t (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX PubMed=14656967; DOI=10.1101/gr.1736803;
RA Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,
RA Campbell R.D., Hood L.;
```

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RT "Analysis of the gene-dense major histocompatibility complex class III
RT region and its comparison to mouse."
RL Genome Res. 13:2621-2636(2003).
CC -I- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AF109905; AAC84149.1; -.
DR HSP; P08107; I53X.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
FT NON TER 1
SQ SEQUENCE 552 AA; 61020 MW; AB81C1BA1F55DCAC CRC64;
Query Match 83.1%; Score 1092; DB 2; Length 552;
Best Local Similarity 84.5%; Pred. No. 1.8e-59;
Matches 218; Conservative 17; Mismatches 21; Indels 2; Gaps 2;
Qy 1 KSENVQDLLLDVAPLSGLGLETAGGVMTALIKRNSTIPTKTQTOIFTTYSNQPGLVQVY 60
Db 297 KSEKVDLLLDVAPLSGLGLETAGGVMTALIKRNSTIPTKTQTOIFTTYSNQPGLVQV 356
Qy 61 EGERAMTKNNLLGRFELSGTIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
Db 357 EGERAMTRDNNLLGRFDLTGTIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 416
Qy 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSNAKNALESYAFNMKSASVDEGLKDKIS 180
Db 417 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSNAKNALESYAFNMKSASVDEGLKDKIS 476
Qy 181 EADKKVKLDKQCVISWLDANTLAEKDFEHRKLEFOVNCNPIISGLYQAGGPGGFG 240
Db 477 ESDKKKILDKCNELVSLWLANQLAEKDFEHRKLENCNPNITIKLYQ-SGCTGPTCTP 535
Qy 241 AQGPKGGSGSGPTIEVD 258
Db 536 GYTP-GRAATGPTIEVD 552
RESULT 40
HS7C BOVIN
ID HS7C BOVIN STANDARD; PRT; 650 AA.
AC P19120;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Heat shock cognate 71 kDa protein.
GN Name=HSPA8; Synonyms=HSC70;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
CX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=91016866; PubMed=2216746;
RA Deluca-Flaherty C., McKay D.B.;
RT "Nucleotide sequence of the cDNA of a bovine 70 kilodalton heat shock
RT cognate protein."
RL Nucleic Acids Res. 18:5569-5569(1990).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 1-385.
RX MEDLINE=90348961; PubMed=2143562; DOI=10.1038/346623a0;
RA Flaherty K.M., de Luca-Flaherty C., McKay D.B.;
RT "Three-dimensional structure of the ATPase fragment of a 70K heat-
RT shock cognate protein."
RL Nature 346:623-628(1990).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 1-385.
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EX MEDLINE=94230372; PubMed=8175707;
RA Flaherty K.M., Wilbanks S.M., Deluca-Flaherty C., McKay D.B.;
RT "Structural basis of the 70-kilodalton heat shock cognate protein ATP
RT hydrolytic activity. II. Structure of the active site with ADP or ATP
RT bound to wild type and mutant ATPase fragment.";
RN J. Biol. Chem. 269:12899-12907(1994).
RL [4]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-385.
RX MEDLINE=98254532; PubMed=9585559; DOI=10.1021/bi973046m;
RA Wilbanks S.M., McKay D.B.;
RT "Structural replacement of active site monovalent cations by the
RT epsilon-amino group of lysine in the ATPase fragment of bovine
RT Hsc70.";
RL Biochemistry 37:7456-7462(1998).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 1-381.
RX MEDLINE=99017893; PubMed=9799500; DOI=10.1021/bi981510x;
RA Sousa M.C., McKay D.B.;
RT "The hydroxyl of threonine 13 of the bovine 70-kDa heat shock cognate
RT protein is essential for transducing the ATP-induced conformational
RT change.";
RL Biochemistry 37:15392-15399(1998).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-381 OF MUTANTS.
RX MEDLINE=99379828; PubMed=10451379; DOI=10.1021/bi990816g;
RA Johnson E.R., McKay D.B.;
RT "Mapping the role of active site residues for transducing an ATP-
RT induced conformational change in the bovine 70-kDa heat shock cognate
RT protein.";
RL Biochemistry 38:10823-10830(1999).
CC -1- FUNCTION: Chaperone.
CC -1- SUBCELLULAR LOCATION: Translocates rapidly from the cytoplasm to
CC the nuclei, and especially to the nucleoli, upon heat shock (By
CC similarity).
CC -1- TISSUE SPECIFICITY: Ubiquitous.
CC -1- INDUCTION: Constitutively synthesized.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL; X53827; CAA37823.1; -;
CC EMBL; X53335; CAA37422.1; -;
CC PIR; S11456; S11456.
CC PDB; 1ATR; X-ray; @=1-386.
CC PDB; 1ATS; X-ray; @=1-386.
CC PDB; 1BA0; X-ray; @=1-386.
CC PDB; 1BA1; X-ray; @=1-386.
CC PDB; 1BUP; X-ray; @=1-386.
CC PDB; 1HPW; X-ray; @=1-386.
CC PDB; 1HX1; X-ray; @=1-381.
CC PDB; 1KAX; X-ray; @=1-381.
CC PDB; 1KAY; X-ray; @=1-381.
CC PDB; 1KAZ; X-ray; @=1-381.
CC PDB; 1NGA; X-ray; @=1-386.
CC PDB; 1NGB; X-ray; @=1-386.
CC PDB; 1NGC; X-ray; @=1-386.
CC PDB; 1NGD; X-ray; @=1-386.
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CC PDB; 1NGF; X-ray; @=1-386.
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CC PDB; 1NGI; X-ray; @=1-386.
CC PDB; 1NGJ; X-ray; @=1-386.
CC PDB; 1LOM; X-ray; @=1-386.
CC PDB; 1LOO; X-ray; @=1-381.
CC PDB; 1QOO; X-ray; @=1-381.
CC PDB; 2BUP; X-ray; @=1-381.

DR PDB; 3HSC; X-ray; @=1-386.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR TIGRFAMs; TIGR01991; Hsca; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR 3D-structure; ATP-binding; Chaperone; Heat shock; Multigene family;
KW Nuclear protein.
FT STRAND 7 10
FT STRAND 15 22
FT TURN 23 24
FT STRAND 25 28
FT TURN 32 33
FT STRAND 38 39
FT STRAND 42 44
FT STRAND 49 51
FT TURN 52 52
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FT HELIX 368 380
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Query Match 83.1%; Score 1091.5; DB 1; Length 650;
Best Local Similarity 79.8%; Pred. No. 2.3e-59;
Matches 213; Conservative 25; Mismatches 20; Indels 9; Gaps 3;


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Qy 1 KSENVQDILLDVLAPLSIGLETAGGVTALIKRNSTIPTKTQTFTTYSNQPGLVQVY 60
Db 384 KSENVQDILLDVLAPLSIGLETAGGVTALIKRNSTIPTKTQTFTTYSNQPGLVQVY 443
Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 503
Qy 121 TNDKGRLSKEIERMVOEAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDEGLKKGKIS 180
Db 504 TNDKGRLSKEDIERMVOEAEKYKAEDVQRRVSAKNALESYAFNMKSTVEDEKLKKGKIS 563
Qy 181 EADKKKVLDCQOEVI SWLDANTLAEKDFEHKRELEOVNCNPIISGLYQAGG-----PG 235
Db 564 DEDKQKILDKCNEVIGWLDKKNQTAKEFEHQQKELEKVCNPIITKLYQSAGGPGGMPG 623
Qy 236 --PGGF--GAQPGKGGSGGPTIEVD 258
Db 624 GMPGGFGGAGAPGGSSGPTIEVD 650
RESULT 41
Q6TEQ5 PRELIMINARY; PRT; 649 AA.
AC Q6TEQ5;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Heat shock 70kDa protein 8.
GN Name=hsp8; Synonyms=hsp8;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney marrow;
RA Song H.D., Wu X.Y., Sun X.J., Zhou Y., Liu T.X., Deng M., Zhang G.W.,
RA Sheng Y., Chen Y., Ruan Z., Jiang C.L., Fan H.Y., Zou L.I.,
RA Kanki J.P., Look A.T., Chen Z.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY422994; AAQ97970.1; --
DR HSP; P19120; IATR.
DR ZFIN; ZDB-GENE-990415-92; hsp8.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR01023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock.
KW SEQUENCE 649 AA; 71228 MW; AB7AB34156B817EE CRC64;
Query Match 83.0%; Score 1091; DB 2; Length 649;
Best Local Similarity 80.8%; Pred. No. 2.5e-59;
Matches 215; Conservative 19; Mismatches 24; Indels 8; Gaps 3;
Qy 1 KSENVQDILLDVLAPLSIGLETAGGVTALIKRNSTIPTKTQTFTTYSNQPGLVQVY 60
Db 384 KSENVQDILLDVLAPLSIGLETAGGVTALIKRNSTIPTKTQTFTTYSNQPGLVQVY 443
Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 503
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Qy 181 EADKKKVLDCQOEVI SWLDANTLAEKDFEHKRELEOVNCNPIISGLYQAGG-PG----- 235
Db 564 DEDKQKILDKCNEVIGWLDKKNQTAKEFEHQQKELEKVCNPIITKLYQSAGGPGGMPG 623
Qy 236 --PGGF--GAQPGKGGSGGPTIEVD 258
Db 624 GMPGGFGGAGAPGGSSGPTIEVD 649
RESULT 42
Q6XVG4 PRELIMINARY; PRT; 655 AA.
AC Q6XVG4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Heat shock protein 70.
GN Name=hsp70;
OS Chlamys farreri.
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;
OC Pectinoidea; Pectinidae; Chlamys.
OX NCBI_TaxID=202578;
RN [1]
RP SEQUENCE FROM N.A.
RC Wu L., Song L., Xu W., Li H., Guo X., Xiang J.;
RA "Identification and Cloning of Heat Shock Protein 70 Gene from Scallop
RA Chlamys farreri.";
RL GaoJishu Tongxun 13:75-79(2003).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY206871; AA038780.1; --
DR HSP; P19120; IATR.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR01023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock.
KW SEQUENCE 655 AA; 71261 MW; PF8A456694F7E078 CRC64;
Query Match 83.0%; Score 1090.5; DB 2; Length 655;
Best Local Similarity 79.7%; Pred. No. 2.7e-59;
Matches 216; Conservative 16; Mismatches 26; Indels 13; Gaps 3;
Qy 1 KSENVQDILLDVLAPLSIGLETAGGVTALIKRNSTIPTKTQTFTTYSNQPGLVQVY 60
Db 385 KSENVQDILLDVLAPLSIGLETAGGVTALIKRNSTIPTKTQTFTTYSNQPGLVQVY 444
Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 445 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 504
Qy 121 TNDKGRLSKEIERMVOEAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDEGLKKGKIS 180
Db 505 TNDKGRLSKEDIERMVNDNAEYKAEDVQRRVSAKNALESYAFNMKSTAEDEDLKDKKIS 564
Qy 181 EADKKKVLDCQOEVI SWLDANTLAEKDFEHKRELEOVNCNPIISGLYQAGG----- 233
Db 565 EEDKKTITDKCSEVISWLDANQLAKEFEHQQKELEAVCNPIITKLYQAGGAGGMPG 624
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ID Q76N60 PRELIMINARY; PRT; 650 AA.
AC Q76N60;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hsc71
GN Name=HSC71;
OS Parolichthys olivaceus (Japanese flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidei; Parolichthyidae; Parolichthys.
OX NCBI_TaxID=8255;
[1]
RP SEQUENCE FROM N.A.
RA Yokoyama Y., Hashimoto H., Kubota S., Kinoshita M., Toyohara H.,
RA Sakaguchi M., Kanamori M.;
RT "Complementary DNA cloning of HSC71, a 71 kDa heat shock cognate
RL protein, in Japanese flounder Parolichthys olivaceus.";
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AB006814; BAD05136.1; -.
DR HSP; P19120; IATR.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR PRINTS; PR00301; HEATSHOCK70.
DR Pfam; PF00012; HSP70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding.
KW ATP-binding.
SQ SEQUENCE 650 AA; 71158 MW; 9F6A4A573342EBA5 CRC64;

Query Match 82.9%; Score 1089.5; DB 2; Length 650;
Best Local Similarity 80.1%; Pred. No. 3.1e-59;
Matches 214; Conservative 20; Mismatches 24; Indels 9; Gaps 3;

QY 1 KSENVQDLILLDVAPLSGLTAGVMTALIKRNTTPTKTQITFTTYSNQPGLVQVY 60
DB 384 KSENVQDLILLDVAPLSGLTAGVMTALIKRNTTPTKTQITFTTYSNQPGLVQVY 443
QY 61 EGERAMTKDNNLGRFELSGIPAPRGVPOEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKDNNLGRFELSGIPAPRGVPOEVTFDIDANGILNVTATDKSTGKANKITI 503
QY 121 TNDKGRLSKEIEIEMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDEGLGKIS 180
DB 504 TNDKGRLSKEIEIEMVQAEKYKTEDDQVRDKVSAKNGVESYAFNMKSTVEDEKLAKGIS 563
QY 181 EADKKVLDKQEVISWLDANTLAEDKDFEHRKKELEQVNCNPIISGLYQAGG-PG- 235
DB 564 DEDKQKLDKCNVVISWLDNKNQTAKEDEYHQKELEKVCNPIITKLYQSAGGPGGMPGE 623
QY 236 --PGGFGAAG--PRKGGSGSGPTIEVD 258
DB 624 GMPGFGGAGGAGPAGSGSGPTIEVD 650

RESULT 44
Q6MG67 PRELIMINARY; PRT; 641 AA.
AC Q6MG67;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Heat shock 70kD protein 1L.
GN Name=Hspall;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN
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RP SEQUENCE FROM N.A.
RC STRAIN=Brown Norway;
RX PubMed=15060004; DOI=10.1101/gr.1987704;
RA Hurt P., Walter L., Sudbrak R., Klages S., Mueller I., Shiina T.,
RA Inoko H., Lehrach H., Guenther E., Reinhardt R., Himmelbauer H.;
RT "The genomic sequence and comparative analysis of the rat major
RT histocompatibility complex.";
RL Genome Res. 14:631-639(2004).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Brown Norway;
RA Boehm S., Borzym K., Gelling S., Gimmel V., Heitmann K., Kosiura A.,
RA Lang N., Lehrach S., Thiel J., Sontag M., Hurt P., Himmelbauer H.,
RA Sudbrak R., Reinhardt R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; BX883045; CAE83979.1; -.
DR HSP; P19120; IBA1.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 641 AA; 70549 MW; C9FAE59B4685DD51 CRC64;

Query Match 82.9%; Score 1089; DB 2; Length 641;
Best Local Similarity 83.5%; Pred. No. 3.2e-59;
Matches 218; Conservative 17; Mismatches 18; Indels 8; Gaps 3;

QY 1 KSENVQDLILLDVAPLSGLTAGVMTALIKRNTTPTKTQITFTTYSNQPGLVQVY 60
DB 386 KSENVQDLILLDVAPLSGLTAGVMTALIKRNTTPTKTQITFTTYSNQPGLVQVY 445
QY 61 EGERAMTKDNNLGRFELSGIPAPRGVPOEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 446 EGERAMTKDNNLGRFELSGIPAPRGVPOEVTFDIDANGILNVTATDKSTGKANKITI 505
QY 121 TNDKGRLSKEIEIEMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDEGLGKIS 180
DB 506 TNDKGRLSKEIEIEMVQAEKYKAEDGQREKIAAKNALESYAFNMKSAVDEGLDKIS 565
QY 181 EADKKVLDKQEVISWLDANTLAEDKDFEHRKKELEQVNCNPIISGLYQ-GAGGP--GP 237
DB 566 ESDKKKLDKCEVLSWLEANLAKEEFDRKKELENMNCNPIITKLYQSGCTGTCAPG 625
QY 238 GFGAGQPKGSGSGPTIEVD 258
DB 626 -----YTPGRAATGPTIEVD 641

RESULT 45
HS7C_ICTPU STANDARD; PRT; 649 AA.
AC P47773;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock cognate 71 kDa protein.
GN Name=HSC70;
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=97090143; PubMed=8936051; DOI=10.1016/0305-0491(95)02022-5;
RX
```

RA Luft J.C., Wilson M.R., Bly J.E., Miller N.W., Clem L.W.;
RT "Identification and characterization of a heat shock protein 70 family
RT member in channel catfish (Ictalurus punctatus).";
RL Comp. Biochem. Physiol. 113B:169-174 (1996).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; U22460; AAA64872.1; -;
DR HSSP; P08109; 1CKR.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR TIGRFAMs; TIGR01991; Hsca; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock; Multigene family.
SQ SEQUENCE 649 AA; 71340 MW; D31B8D348D7583CB CRC64;

Query Match 82.8%; Score 1088; DB 1; Length 649;
Best Local Similarity 80.8%; Pred. No. 3.8e-59;
Matches 215; Conservative 19; Mismatches 24; Indels 8; Gaps 3;

QY 1 KSENVQDLLLDVAPLSLGLETAGGVTALIKRNTIPTKTQTQTFITYSDNQPGVLIQVY 60
DB 384 KSENVQDLLLDVTPLSLGIETAGGVTALIKRNTIPTKTQTQTFITYSDNQPGVLIQVY 443

QY 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
DB 444 EGERAMTKNNLLGKFFELTGIPPPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503

QY 121 TNDKGRLSKEIEIRWVQAEKYKAEDVQRRVSAKNALSYAFNMKSAVEDEGLKGKIS 180
DB 504 TNDKGRLSKEDIERWVQAEKYKVEDKQDKVSSKNSLSYAFNMKATVEDEKLGKIS 563

QY 181 EADKKVLDKQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGG-PG---- 235
DB 564 DEDKHKLKCNVEISWLDKNTAKDEYEHQKLEKVCNPIITKLYQSDGGMGMPD 623

QY 236 --PGGFGAQQ-PKGSGSGPTIEVD 258
DB 624 GMPGGFQELGAAPGGSGSGPTIEVD 649

RESULT 46
Q8UV14 PRELIMINARY; PRT; 651 AA.
ID Q8UV14
AC Q8UV14;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heat shock protein 70.
DE Name=HSP70;
GN Ambystoma mexicanum (Axolotl).
OS Ambystoma mexicanum; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
OC Ambystoma.
OX NCBI_TaxID=8296;
RN [1]
RP SEQUENCE FROM N.A.
RA Ordenez M.R., Pichon L.L., Laurens V.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY029210; AAK31583.1; -;
DR HSSP; P19120; 1ATR.

DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 651 AA; 71055 MW; 86C75FA0DCEFCB9D CRC64;

Query Match 82.8%; Score 1088; DB 2; Length 651;
Best Local Similarity 80.6%; Pred. No. 3.8e-59;
Matches 216; Conservative 22; Mismatches 20; Indels 10; Gaps 4;

QY 1 KSENVQDLLLDVAPLSLGLETAGGVTALIKRNTIPTKTQTQTFITYSDNQPGVLIQVY 60
DB 384 KSENVQDLLLDVTPLSLGIETAGGVTALIKRNTIPTKTQTQTFITYSDNQPGVLIQVY 443

QY 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
DB 444 EGERAMTKNNLLGKFFELTGIPPPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503

QY 121 TNDKGRLSKEIEIRWVQAEKYKAEDVQRRVSAKNALSYAFNMKSAVEDEGLKGKIS 180
DB 504 TNDKGRLSKEDIERWVQAEKYKVEDKQDKVSSKNSLSYAFNMKATVEDEKLGKIS 563

QY 181 EADKKVLDKQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGG-----PG 235
DB 564 DDDTKTKLEKCNRIIAWLDKNTAKDEEYEHQKLEKVCNPIITKLYQSDGGMGMPG 623

QY 236 --PGGP- GAQGPKGSGG--SGPTIEVD 258
DB 624 GMPGGFQELGAAPGGSGSGPTIEVD 651

RESULT 47
HS1A RAT STANDARD; PRT; 641 AA.
ID HS1A RAT
AC P55063;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock protein 1A (Heat shock 70 kDa protein 3) (HSP70.3).
DE Name=Hsp1A; Synonyms=Hsp70-3;
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LEW.1W/GUN;
RX MEDLINE=95012453; PubMed=7927536;
RA Walter L., Rauh F., Guenther E.;
RT "Comparative analysis of the three major histocompatibility complex-
RT linked heat shock protein 70 (Hsp70) genes of the rat.";
RL Immunogenetics 40:325-330(1994).
CC -!- FUNCTION: In cooperation with other chaperones, Hsp70s stabilize
CC preexistent proteins against aggregation and mediate the folding
CC of newly translated polypeptides in the cytosol as well as within
CC organelles. These chaperones participate in all these processes
CC through their ability to recognize nonnative conformations of
CC other proteins. They bind extended peptide segments with a net
CC hydrophobic character exposed by polypeptides during translation
CC and membrane translocation, or following stress-induced damage.
CC -!- INDUCTION: By heat shock.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC -----
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CC -----
 DR EMBL; X77209; CAA54424.1; -.
 DR PIR; S41415; S41415.
 DR HSR; P08107; LHJO.

DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR TIGRFAMs; TIGR01991; HscA; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 DR PROSITE; PS01036; HSP70_4; 1.
 KW ATP-binding; Chaperone; Heat shock; Multigene family.
 SQ SEQUENCE 641 AA; 70549 MW; 8C77AA9FD98B9252 CRC64;

Query Match 82.7%; Score 1087; DB 1; Length 641;
 Best Local Similarity 83.5%; Pred. No. 4.3e-59;
 Matches 218; Conservative 17; Mismatches 18; Indels 8; Gaps 3;

Qy 1 KSENVQDILLDVAPLSLGLETAGVMTALIKRNSTIPTKTQTFTTYSNDQPGVLIQVY 60
 |||||
 Db 386 KSEKVDLLLDVAPLSGLTAGVMTVLKRNSTIPTKTQTFTTYSNDQPGVLIQVY 445

Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVQPEVTFDIDANGILNVTATDKSTGKANKITI 120
 |||||
 Db 446 EGERAMTRDNNLLGRFDLTGIPAPRGVQPEVTFDIDANGILNVTATDKSTGKANKITI 505

Qy 121 TNDKGRLSKEEIERMVQEAERYKAEDVQREVSQNALESYAFNMKSAVEDGLGKIS 180
 |||||
 Db 506 TNDKGRLSKEEIERMVQEAERYKAEDVQREVSQNALESYAFNMKSAVEDGLGKIS 565

Qy 181 EADKKVLDKQCVISWLDANTLAEKDFEHRKELEOVNCPNIIISGLYQ-GAGGP--GPG 237
 |||||
 Db 566 ESDKKKILDKCEVLSWLEANQLAEKDFEHRKELENCNPIITKLYQ-SGCTGPTCAPG 625

Qy 238 GFAGQPGKGGSGGPTIEVD 258
 |||||
 Db 626 -----YTPGRARTGPTIEVD 641

RESULT 48

ID O88686 PRELIMINARY; PRT; 641 AA.
 AC O88686;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Spermatid-specific heat shock protein 70.
 GN Name=Hspall; Synonyms=Hsc70t;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Balb/c; TISSUE=Testis;
 RX MEDLINE=98351992; PubMed=9685725;

RA Ito Y., Ando A., Ando H., Ando J., Saijoh Y., Inoko H., Fujimoto H.;
 RT "Genomic structure of the spermatid-specific hsp70 homolog gene
 RT located in the class III region of the major histocompatibility
 RT complex of mouse and man.";
 RL J. Biochem. 124:347-353(1998).

CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
 DR EMBL; D85732; BAA32522.1; -.

DR HSSP; P08107; 183X.
 DR MGD; MGI:96231; Hspall.

DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.

DR GO; GO:0006986; P:response to unfolded protein; IEA.
 DR InterPro; IPR001023; Hsp70.

DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 DR PROSITE; PS01036; HSP70_4; 1.
 KW ATP-binding; Heat shock.
 SQ SEQUENCE 641 AA; 70623 MW; D19B11742A03BC2F CRC64;

Query Match 82.7%; Score 1087; DB 2; Length 641;
 Best Local Similarity 84.1%; Pred. No. 4.3e-59;
 Matches 217; Conservative 17; Mismatches 22; Indels 2; Gaps 2;

Qy 1 KSENVQDILLDVAPLSLGLETAGVMTALIKRNSTIPTKTQTFTTYSNDQPGVLIQVY 60
 |||||
 Db 386 KSEKVDLLLDVAPLSGLTAGVMTVLKRNSTIPTKTQTFTTYSNDQPGVLIQVY 445

Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVQPEVTFDIDANGILNVTATDKSTGKANKITI 120
 |||||
 Db 446 EGERAMTRDNNLLGRFDLTGIPAPRGVQPEVTFDIDANGILNVTATDKSTGKANKITI 505

Qy 121 TNDKGRLSKEEIERMVQEAERYKAEDVQREVSQNALESYAFNMKSAVEDGLGKIS 180
 |||||
 Db 506 TNDKGRLSKEEIERMVQEAERYKAEDVQREVSQNALESYAFNMKSAVEDGLGKIS 565

Qy 181 EADKKVLDKQCVISWLDANTLAEKDFEHRKELEOVNCPNIIISGLYQAGGPGGFG 240
 |||||
 Db 566 ESDKKKILDKCEVLSWLEANQLAEKDFEHRKELENCNPIITKLYQ-SGCTGPTCTP 624

Qy 241 AOGPKGGSGGPTIEVD 258
 |||||
 Db 625 GYTP-GRAATGPTIEVD 641

RESULT 49

ID Q7SZM7 PRELIMINARY; PRT; 644 AA.
 AC Q7SZM7;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Constitutive heat shock protein HSC70-2 (Fragment).
 GN Name=hsc70-2;
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 OX NCBI_TaxID=7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RX MEDLINE=22774674; PubMed=12893250; DOI=10.1016/S0006-291X(03)01206-3;
 RA Ali K.S., Dorgai L., Abraham M., Hermesz E.;
 RT "Tissue- and stressor-specific differential expression of two hsc70
 RT genes in carp.";
 RL Biochem. Biophys. Res. Commun. 307:503-509(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RX Khaled S.A., Hermesz E.;
 RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
 DR EMBL; AY219845; AAP51388.1; -.

DR HSSP; P19120; IATR.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR GO; GO:0006986; P:response to unfolded protein; IEA.
 DR InterPro; IPR001023; Hsp70.

DR Pfam; PF00012; HSP70; 1.
 DR ProDom; PD000089; Hsp70; 1.

DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.

DR PROSITE; PS01036; HSP70_3; 1.
 DR PROSITE; PS01036; HSP70_4; 1.

DR	Pfam; PF00012; HSP70; 1.
DR	PRINTS; PR00301; HEATSHOCK70.
DR	ProDom; PD000089; Hsp70; 1.
DR	TIGRFAMS; TIGR01991; HscA; 1.
DR	PROSITE; PS00297; HSP70_1; 1.
DR	PROSITE; PS00329; HSP70_2; 1.
DR	PROSITE; PS01036; HSP70_3; 1.
KW	ATP-binding; Heat shock.
FT	CONFLICT 182 183
SEQ	SEQUENCE 651 AA; 71283 MW; 8701630ACBC4BE0 CRC64;
Query Match 82.5%; Score 1084; DB 1; Length 651;	
Best Local Similarity 79.5%; Pred. No. 6.7e-59;	
Matches 213; Conservative 21; Mismatches 24; Indels 10; Gaps 3	
QY	1 KSENVQDLLLLDVAPLSLGLETAGGVTALIKRNSTIPKTKQTQITPTTSDNPGVLIOVY 60
DB	384 KSENVQDLLLLDVTFLSLGIETAGGVTMLIKRNITTPKTKQTQITPTTSDNPGVLIOVY 443
QY	61 EGERAMTKNNLGRFELSGIIPPAPRGVPQIEVTFDIANGILNVATDKSTGKANKITI 120
DB	444 EGERAMTKNNLCKFELTGIPAPRGVPQIEVTFDIANGIMNVSAADKSTGENKITI 503
QY	121 TNDKGRLSKEEIERMVQEAKEYKAEDVEQRERVSAAKNALSYAFNMKSASVEDGLKGKIS 180
DB	504 TNDKGRLSKEDIERMVQEAKEYKCDDVQRDKVSSKNSLESYAFNMKSATVEDEKLQGKIS 563
QY	181 EADKKLVLDKCOEVISWLDTANTLAEBDFEHKRKELEVNCNPITISGLYQGAGG-PG---- 235
DB	564 DEBTKILEKCNVEVIGWLDKDNRAKREGEYHGHQLEKVCVNPITIKLYQGAGMPCGGHPE 623
QY	236 --PGGF---GAQGPKGGSGSGPTTIEVD 258
DB	624 GMAGGPPGAGGAAPGGGSGSGPTTIEVD 651
RESULT 53	
ID	073885 PRELIMINARY; PRT; 646 AA.
OC	AC
OT	01-AUG-1998 (TrEMBLrel. 07, Created)
DT	01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DE	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Heat shock cognate 70.
GN	Name=hsc70;
OS	Gallus gallus (Chicken).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC	Gallus.
ON	NCB1_TaxID=9031;
RX	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=White Leghorn; TISSUE=Whole embryo;
RX	MEDLINE=98374286; Pubmed=9707581; DOI=10.1073/pnas.95.17.9950;
RA	de la Rosa E.J.; Vega-Nunez E., Morales A.V., Serna J., Rubio E.,
RA	de Pablo F.;
RT	"Modulation of the chaperone heat shock cognate 70 by embryonic
RT	(pro)insulin correlates with prevention of apoptosis.";
RL	Proc. Natl. Acad. Sci. U.S.A. 95:9950-9955(1998).
CC	-/- SIMILARITY: Belong to the heat shock protein 70 family.
DR	ENBL; AJ004940; CAA06233.1; -
DR	HSP; P19120; IATR.
DR	GO; GO:0005524; F:ATP binding; IEA.
DR	GO; GO:0006457; P:protein folding; IEA.
DR	GO; GO:0006986; P:response to unfolded protein; IEA.
DR	InterPro; IPR001023; Hsp70.
DR	Pfam; PF00012; HSP70; 1.
DR	PRINTS; PR00301; HEATSHOCK70.
DR	ProDom; PD000089; Hsp70; 1.
DR	PROSITE; PS00297; HSP70_1; 1.
DR	PROSITE; PS00329; HSP70_2; 1.
DR	PROSITE; PS01036; HSP70_3; 1.
KW	ATP-binding; Heat shock.

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SQ SEQUENCE 646 AA; 70826 MW; 2151332ED42C5B9B CRC64;
Query Match 82.1%; Score 1078.5; DB 2; Length 646;
Best Local Similarity 80.2%; Pred. No. 1.5e-58;
Matches 211; Conservative 23; Mismatches 24; Indels 5; Gaps 3;

QY 1 KSENVQDILLDVLAPLSGLTAGGVTALIKRNSTIPTKTQTFTTYSNQPGLVLIQVY 60
DB 384 KSENVQDILLDVLAPLSGLTAGGVTALIKRNSTIPTKTQTFTTYSNQPGLVLIQVY 443

QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
DB 444 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 503

QY 121 TNDKGRLSKEIEIRWVQAEYKAEDVQERVSAAKNALSYAFNMKSASVEDEGLKDKIS 180
DB 504 TNDKGRLSKEIEIRWVQAEYKAEDVQERVSAAKNALSYAFNMKSATVEDEKLPGKIL 563

QY 181 EADKKVKLDKQCEVISWLDANTLAEDKFEHKELEQVNCNPIISGLYQAGG-PG--PG 237
DB 564 DEDHQNLIDKCNELIINWLDKNTAEKEFEHKELEQVNCNPIITKLQYQAGGMPGMPG 623

QY 238 GF--GAQPGKGGSGGPTIEVD 258
DB 624 GFPGGAPPSSGSGGPTIEVD 646

RESULT 54
Q9XZJ2 PRELIMINARY; PRT; 659 AA.
AC Q9XZJ2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heat shock protein 70 (71kDa heat shock connate protein).
GN Name=hsp70; Synonyms=HSC71;
OS Crassostrea gigas (Pacific oyster).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
OC Ostreoida; Ostreidae; Crassostrea.
OX NCBI_taxid=29159;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20541285; PubMed=11092738;
RX Gourdine I., Gricourt L., Kellner K., Roch P., Escoubas J.-M.;
RT "Characterization of a cDNA encoding a 72 kDa heat shock cognate
RT protein (Hsc72) from the Pacific oyster, Crassostrea gigas.";
RL DNA Seq. 11:265-270(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Yokoyama Y.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AF144646; AAD31042.1; -.
DR EMBL; AB122084; BADI5287.1; -.
DR HSSP; P19120; 3HSC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock.
KW ATP-binding; Heat shock.
SQ SEQUENCE 659 AA; 72042 MW; 907C52AB780AD3F8 CRC64;
Query Match 82.0%; Score 1077; DB 2; Length 659;
Best Local Similarity 79.3%; Pred. No. 1.8e-58;
Matches 214; Conservative 19; Mismatches 25; Indels 12; Gaps 4;

QY 1 KSENVQDILLDVLAPLSGLTAGGVTALIKRNSTIPTKTQTFTTYSNQPGLVLIQVY 60
DB 384 KSENVQDILLDVLAPLSGLTAGGVTALIKRNSTIPTKTQTFTTYSNQPGLVLIQVY 443

QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
DB 444 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 503

QY 121 TNDKGRLSKEIEIRWVQAEYKAEDVQERVSAAKNALSYAFNMKSASVEDEGLKDKIS 180
DB 504 TNDKGRLSKEIEIRWVQAEYKAEDVQERVSAAKNALSYAFNMKSATVEDEKLPGKIL 563

QY 181 EADKKVKLDKQCEVISWLDANTLAEDKFEHKELEQVNCNPIISGLYQAGG-PG--PG 237
DB 564 DEDHQNLIDKCNELIINWLDKNTAEKEFEHKELEQVNCNPIITKLQYQAGGMPGMPG 623

QY 238 GF--GAQPGKGGSGGPTIEVD 258
DB 624 GFPGGAPPSSGSGGPTIEVD 646

RESULT 55
Q23954 PRELIMINARY; PRT; 345 AA.
AC Q23954;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Heat shock protein 70 (Fragment).
OS Dirofilaria immitis (Canine heartworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Dirofilaria.
OX NCBI_taxid=6287;
RN [1]
RP SEQUENCE FROM N.A.
RA Culpepper J.A., Friedman L., Dale B.;
RL Submitted (AUG-1992) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; M95648; AAA28298.1; -.
DR HSSP; P19120; 3HSC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock.
KW ATP-binding; Heat shock.
FT NON TER 345
SQ SEQUENCE 345 AA; 37497 MW; 42963D21A7585F09 CRC64;
Query Match 81.7%; Score 1074; DB 2; Length 345;
Best Local Similarity 80.9%; Pred. No. 1.3e-58;
Matches 212; Conservative 18; Mismatches 28; Indels 4; Gaps 3;

QY 1 KSENVQDILLDVLAPLSGLTAGGVTALIKRNSTIPTKTQTFTTYSNQPGLVLIQVY 60
DB 84 KSENVQDILLDVLAPLSGLTAGGVTALIKRNSTIPTKTQTFTTYSNQPGLVLIQVY 143

QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
DB 144 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 203

QY 121 TNDKGRLSKEIEIRWVQAEYKAEDVQERVSAAKNALSYAFNMKSASVEDEGLKDKIS 180
DB 204 TNDKGRLSKEIEIRWVQAEYKAEDVQERVSAAKNALSYAFNMKSATVEDEKLKDKIS 263

QY 181 EADKKVKLDKQCEVISWLDANTLAEDKFEHKELEQVNCNPIISGLYQAGG-PG--PG 237
DB 264 EDDKKKTQEKDETVRWLDGNQTAEDKFEHKELEQVNCNPIITKLQYQAGGMPGMPG 323

QY 238 GFAGQPGKGGSGGPTIEVD 258
DB 324 GFPGGAPPSSGSGGPTIEVD 345
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RESULT 56
O73788
ID O73788 PRELIMINARY; PRT; 650 AA.
AC O73788;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Heat shock protein 70.
GN Name=HSP70;
OS Paralicthys olivaceus (Japanese flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Pleuronectiformes;
OC Pleuronectoidei; Paralicthidae; Paralicthys.
OC NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim W.J., Lee J.H., Kim K.K., Lee S.J., Kang H.S., Kim H.D.;
RT "Molecular cloning and characterization of a heat shock protein 70-
related cDNA from olive flounder (Paralicthys olivaceus).";
RL Han-gug yangig Hag-hoiji 12:91-100(1999).
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AF053059; AAC33859.1; -.
DR HSP; P19120; IATR.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 650 AA; 71115 MW; 6B24E7D409FC76EA CRC64;

Query Match 81.7%; Score 1073.5; DB 2; Length 650;
Best Local Similarity 79.0%; Pred. No. 3e-58;
Matches 211; Conservative 22; Mismatches 25; Indels 9; Gaps 3;

Qy 1 KSENVQDLLLLDVAPLSGLTAGVMTALIKRNTIPTKTQTFTTYSNDNQPVLIQVY 60
Db 384 KSENVQDLLLLDVTPLSGIETAGVMTLVIKRNTIPTKTQTFTTYSNDNQPVLIQVY 443

Qy 61 EGERAMTKDNNLGRFELSGIPAPRGVQPIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTRDNNLLGKFLTGIPAPRGVQPIEVTFDIDANGIMNVSAADKSTGKANKITI 503

Qy 121 TNDKGRLSKEIERMVQEAERYKAEDVQERVSANAKLESYAFNMKSAVEDEGLKGKIS 180
Db 504 TNDKGRLSKEDIERMVQEAERYKTEDDQVRDKVSAKNGVESYAFNMKSTVEDEKLAKGIS 563

Qy 181 EADKKVKLDKQEVISWLDANTLAEKDFEHRKELSOVCNPIISGLYQAGGPG- 235
Db 564 DEDKQKILDKCNEVISWLNKNTAEKDEYHQKLEKVCNPIITKLYQSAGGMPGGMPE 623

Qy 236 --PGGFGAQQ--PKGSSGSGPTIEVD 258
Db 624 GMPGGFGAGGAPAGSSGPTIEVD 650

RESULT 57
O6AZH8
ID O6AZH8 PRELIMINARY; PRT; 652 AA.
AC O6AZH8;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Heart;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=Heart;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Jordan B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Iqbalano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA TISSUE=Heart;
RX Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; BC077998; AAH77998.1; -.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Hypothetical protein.
SQ SEQUENCE 652 AA; 71379 MW; F5B8A6ABCF1FDCHA CRC64;

Query Match 81.7%; Score 1073.5; DB 2; Length 652;
Best Local Similarity 77.3%; Pred. No. 3e-58;
Matches 208; Conservative 25; Mismatches 25; Indels 11; Gaps 2;

Qy 1 KSENVQDLLLLDVAPLSGLTAGVMTALIKRNTIPTKTQTFTTYSNDNQPVLIQVY 60
Db 384 KSENVQDLLLLDVTPLSGIETAGVMTLVIKRNTIPTKTQTFTTYSNDNQPVLIQVY 443

Qy 61 EGERAMTKDNNLGRFELSGIPAPRGVQPIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKDNNLGRFELSGIPAPRGVQPIEVTFDIDANGIMNVSAVDKSTGKANKITI 503

Qy 121 TNDKGRLSKEIERMVQEAERYKAEDVQERVSANAKLESYAFNMKSAVEDEGLKGKIS 180
Db 504 TNDKGRLSKEDIERMVQEAERYKTEDDQVRDKVSAKNGVESYAFNMKSTVEDEKLAKGIS 563

Qy 181 EADKKVKLDKQEVISWLDANTLAEKDFEHRKELSOVCNPIISGLYQAGGPG- 235
Db 564 QEDKQKILDKCNEVISWLDNRQMAKEEYHQKELQNLNPIITKLYQAGGAGMPGGM 623

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Qy 236 ----PGGF--GAQPKGSGSGPTIEVD 258
Db 624 PGMPGGPGAGAGAGGSGSGPTIEVD 652

RESULT 58
Q86QW8
ID Q86QW8 PRELIMINARY; PRT; 654 AA.
AC Q86QW8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hsp70 family member (Fragment).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE FROM N.A.
RA Qin W., Tyshenko M.G., Wu B.S., Walker V.K., Robertson M.R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY178988; AA021473.1; -.
DR HSSP; P19120; 3HSC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD00089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
FT NON TER 654
SQ SEQUENCE 654 AA; 71408 MW; 3389F746D03B2F4B CRC64;

Query Match 81.4%; Score 1070; DB 2; Length 654;
Best Local Similarity 78.5%; Pred. No. 5e-58;
Matches 212; Conservative 19; Mismatches 27; Indels 12; Gaps 3;

Qy 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTTYSNDQPGVLIQVY 60
Db 385 KSEEVQDLLLDVTPLSGLGTAGVMTTLIKRNTTIPTKTQITFTTYSNDQPGVLIQVY 444
Qy 61 EGERAMTKDNNLLGPFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 445 EGERAMTKDNNLLGKFELTGIPAPRGVPQIEVTFDIDANGILNVTAVEKSTGKENKITI 504
Qy 121 TNDKGRLSKEIERMVQAEKYKAEDVQERVSAAKNALSYAFNMKSAVEDEGLKGKIS 180
Db 505 TNDKGRLSKEIERMVQAEKYKAEDVQERVSAAKNALSYAFNMKSTVDEKLKDKIS 564
Qy 181 EADKKVLDKCOEVIWLDANTLAEKDFEHKREKLEQVNCNPIISGLYQAGG-----PG 235
Db 565 DSDKQTILDKCNVIRWLDANQLAEKFEKQKATIAAKNGLESYCFNMKSTVDEKLKDKIS 624
Qy 236 --PGGF-----GAQPKGSGSGPTIEVD 258
Db 625 GFPGGFPAGAGGAGGAGGAGPTIEVD 654

RESULT 59
Q6WAW3
ID Q6WAW3 PRELIMINARY; PRT; 655 AA.
AC Q6WAW3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heat shock protein 70.
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE FROM N.A.
RA Qin W., Tyshenko M.G., Wu B.S., Walker V.K., Robertson M.R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY178988; AA021473.1; -.
DR HSSP; P19120; 3HSC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD00089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
FT NON TER 654
SQ SEQUENCE 654 AA; 71408 MW; 3389F746D03B2F4B CRC64;

Query Match 81.4%; Score 1070; DB 2; Length 654;
Best Local Similarity 78.5%; Pred. No. 5e-58;
Matches 212; Conservative 19; Mismatches 27; Indels 12; Gaps 3;

Qy 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTTYSNDQPGVLIQVY 60
Db 385 KSEEVQDLLLDVTPLSGLGTAGVMTTLIKRNTTIPTKTQITFTTYSNDQPGVLIQVY 444
Qy 61 EGERAMTKDNNLLGPFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 445 EGERAMTKDNNLLGKFELTGIPAPRGVPQIEVTFDIDANGILNVTAVEKSTGKENKITI 504
Qy 121 TNDKGRLSKEIERMVQAEKYKAEDVQERVSAAKNALSYAFNMKSAVEDEGLKGKIS 180
Db 505 TNDKGRLSKEIERMVQAEKYKAEDVQERVSAAKNALSYAFNMKSTVDEKLKDKIS 564
Qy 181 EADKKVLDKCOEVIWLDANTLAEKDFEHKREKLEQVNCNPIISGLYQAGG-----PG 235
Db 565 DSDKQTILDKCNVIRWLDANQLAEKFEKQKATIAAKNGLESYCFNMKSTVDEKLKDKIS 624
Qy 236 --PGGF-----GAQPKGSGSGPTIEVD 258
Db 625 GFPGGFPAGAGGAGGAGGAGPTIEVD 654

RESULT 59
Q6WAW3
ID Q6WAW3 PRELIMINARY; PRT; 655 AA.
AC Q6WAW3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heat shock protein 70.
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE FROM N.A.
RA Qin W., Tyshenko M.G., Wu B.S., Walker V.K., Robertson M.R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY178988; AA021473.1; -.
DR HSSP; P19120; 3HSC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD00089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
FT NON TER 654
SQ SEQUENCE 654 AA; 71408 MW; 3389F746D03B2F4B CRC64;

Query Match 81.4%; Score 1070; DB 2; Length 655;
Best Local Similarity 78.5%; Pred. No. 5e-58;
Matches 212; Conservative 19; Mismatches 27; Indels 12; Gaps 3;

Qy 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTTYSNDQPGVLIQVY 60
Db 386 KSEEVQDLLLDVTPLSGLGTAGVMTTLIKRNTTIPTKTQITFTTYSNDQPGVLIQVY 445
Qy 61 EGERAMTKDNNLLGPFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 446 EGERAMTKDNNLLGKFELTGIPAPRGVPQIEVTFDIDANGILNVTAVEKSTGKENKITI 505
Qy 121 TNDKGRLSKEIERMVQAEKYKAEDVQERVSAAKNALSYAFNMKSAVEDEGLKGKIS 180
Db 506 TNDKGRLSKEIERMVQAEKYKAEDVQERVSAAKNALSYAFNMKSTVDEKLKDKIS 565
Qy 181 EADKKVLDKCOEVIWLDANTLAEKDFEHKREKLEQVNCNPIISGLYQAGG-----PG 235
Db 566 DSDKQTILDKCNVIRWLDANQLAEKFEKQKATIAAKNGLESYCFNMKSTVDEKLKDKIS 625
Qy 236 --PGGF-----GAQPKGSGSGPTIEVD 258
Db 626 GFPGGFPAGAGGAGGAGGAGPTIEVD 655

RESULT 60
Q6PH56
ID Q6PH56 PRELIMINARY; PRT; 643 AA.
AC Q6PH56;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hsp70 protein.
GN Name=hsp70;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
 RA Villalon D.K., Muzny K.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus J., Schnerch D.E., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Strausberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
 DR EMBL; BC056709; AAH56709.1; -.
 DR HSSP; F19120; IATR.
 DR ZFIN; ZDB-GENE-990415-91; hsp70.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR InterPro; IPR001023; Hsp70.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00297; Hsp70; 1.
 DR PROSITE; PS00329; Hsp70; 2; 1.
 DR PROSITE; PS01036; Hsp70; 3; 1.
 KW ATP-binding.
 SQ SEQUENCE 643 AA; 70469 MW; EBC67C8CAD366161 CRC64;
 Query Match 81.4%; Score 1069; DB 2; Length 643;
 Best Local Similarity 80.3%; Pred. No. 5.6e-58;
 Matches 208; Conservative 26; Mismatches 21; Indels 4; Gaps 2;
 QY 2 SENVDLLLDVAPLSGLTAGGVTALIKRNTSTPTKQTQFTTYSNDQPGVLIQVY 61
 DB 387 SGNVDLLLDVAPLSGLTAGGVTALIKRNTTPTKQTQFTTYSNDQPGVLIQVFE 446
 QY 62 GERAMTKNNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVATDKSTGKANKITI 121
 DB 447 GERAMTKNNLLGKLFELTGIPAPRGVQIEVTFDIDANGILNVSAADKSTGKANKITI 506
 QY 122 NDKGRLSKEEIERMVQEAKEYKAEDVQRRVSAKNALESYAFNMKSAVEDSLGKISE 181
 DB 507 NDKGRLSKEEIERMVQEAKEYKAEDDLQREKISAKNSLESYAFNMKNSVEDDNLGKISE 566
 QY 182 ADKKVLDKQCEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGGPGGFGA 241
 DB 567 EDKRVIEKCNKAVSWLENQNLADKEEYHQLKELEKVCNPIISGLYQ--GGMPAGGCGA 624
 QY 242 Q--GPKGGSGSGPTIEVD 258
 DB 625 QARGASGASAGPTIEVD 643
 RESULT 61
 Q7Z1W9 PRELIMINARY; PRT; 658 AA.
 ID Q7Z1W9
 AC Q7Z1W9
 DT 01-OCT-2003 (TRENBLrel. 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Heat shock protein 70.
 OS Crassostrea ariakensis.
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
 OC Ostreoidae; Ostreidae; Crassostrea.
 OX NCBI_TaxID=94323;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Q.-Z., Wu X.-Z., Pan J.-P., Gao J.-S., Zhang G.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
 DR EMBL; AY172024; AAO41703.1; -.
 DR HSSP; P19120; IATR.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR GO; GO:0006986; P:response to unfolded protein; IEA.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; Hsp70; 1.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00297; Hsp70; 1; 1.
 DR PROSITE; PS00329; Hsp70; 2; 1.
 DR PROSITE; PS01036; Hsp70; 3; 1.
 KW ATP-binding; Heat shock.
 SQ SEQUENCE 658 AA; 71933 MW; 39C1DEF29A71F0E1 CRC64;
 Query Match 81.2%; Score 1067; DB 2; Length 658;
 Best Local Similarity 78.5%; Pred. No. 7.7e-58;
 Matches 212; Conservative 20; Mismatches 26; Indels 12; Gaps 4;
 QY 1 KSENVQDLLLDVAPLSGLTAGGVTALIKRNTSTPTKQTQFTTYSNDQPGVLIQVY 60
 DB 389 KSEEVQDLLLDVAPLSGLTAGGVTALIKRNTTPTKQTQFTTYSNDQPGVLIQVY 448
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 449 EGERAMTKNNLLGKLFELTGIPAPRGVQIEVTFDIDANGILNVSAVDKSTGKANKITI 508
 QY 121 TNDKGRLSKEEIERMVQEAKEYKAEDVQRRVSAKNALESYAFNMKSAVEDSLGKISE 180
 DB 509 TNDKGRLSKEEIERMVQEAKEYKAEDVQRRVSAKNALESYAFNMKSTVDDEKLKDKIS 568
 QY 181 EADKKVLDKQCEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGG--PG 236
 DB 569 EGDKKTLLDKCEEIKWMDQNLADKEEYHQLKELEKVCNPIITKLYQASGGAPGGMP 628
 QY 237 GGP-----GAG-----PKGGSGSGPTIEVD 258
 DB 629 GGMPNFGGAPGGAPGGSGGSGPTIEVD 658
 RESULT 62
 Q6QAN5 PRELIMINARY; PRT; 490 AA.
 ID Q6QAN5
 AC Q6QAN5
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE 70 kDa heat shock protein (Fragment).
 GN Name=HSP70;
 OS Megachile rotundata (alfalfa leafcutting bee).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
 OC Megachilidae; Megachilinae; Megachile.
 OX NCBI_TaxID=143995;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yocum G.D., Kemp W.P.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
 DR EMBL; AY550115; AAS57864.1; -.
 DR HSSP; P19120; IATR.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR GO; GO:0006986; P:response to unfolded protein; IEA.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; Hsp70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00329; Hsp70; 2; 1.
 DR PROSITE; PS01036; Hsp70; 3; 1.
 KW ATP-binding; Heat shock.
 FT NON_TER 1
 SQ SEQUENCE 490 AA; 53882 MW; 09D2DF0F038CEDBD CRC64;

Query Match 81.1%; Score 1066; DB 2; Length 490;
 Best Local Similarity 79.5%; Pred. No. 6.2e-58;
 Matches 205; Conservative 21; Mismatches 33; Indels 0; Gaps 0;

QY 1 KSENVQDILLDVLPLSLGSLTAGVMTALIKRSTIPTKTQITFTTYSNDQPGVLIQVY 60
 DB 233 KSEAVQDILLDVLPLSLGSLTAGVMTALIKRSTIPTKTQITFTTYSNDQPGVLIQVY 292

QY 61 EGERAMTKDNNILGRFELSGIPPPAPRGVPOLEVFDDIDANGILNVATDKSTGKANKITI 120
 DB 293 EGERAMTKDNNILGRFELSGIPPPAPRGVPOLEVFDDIDANGILNVATDKSTGKANKITI 352

QY 121 TNDKGRLSKEBIERVMQAEYKAEDEVRQERVSANNALESYAFNMKSAVDEGLKKGKIS 180
 DB 353 TNDKGRLSKEDIERVMQAEYKAEDEVRQERVSANNALESYAFNMKSTMEDEKVKDKID 412

QY 181 EADKKVLDKCOEIVSWLDANTLAEKDFEHRKELEOVNPIISGLYQAGGPGGFG 240
 DB 413 PSDKDKVLNKCNEIVSWLDNRQLAEKEEFVDKQELSVNPIVTKLYQAGGAGGPGGFP 472

QY 241 AQGPKGGSGGPTIEVD 258
 DB 473 GSAPGGGAGGPTIEVD 490

RESULT 63

Q6PGX4 PRELIMINARY; PRT; 647 AA.

ID Q6PGX4
 AC Q6PGX4
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Hypothetical protein zgc:63663.
 GN ORFNames=zgc:63663;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole body;
 RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heilef K.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole body;
 RA Strausberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: Belongs to the heat shock protein 70 family.
 DR EMBL; BC056797; AAHS6797.1; -.
 DR HSP; P19120; IATR.
 DR ZFIN; ZDB-GENE-040426-1221; zgc:63663.

DR GO; GO:0005524; F:ATP binding; IEA.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00297; Hsp70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Hypothetical protein.
 SQ SEQUENCE 647 AA; 70946 MW; 2D956FB5F0FC6D65 CRC64;

Query Match 81.1%; Score 1066; DB 2; Length 647;
 Best Local Similarity 80.8%; Pred. No. 8.6e-58;
 Matches 212; Conservative 21; Mismatches 22; Indels 10; Gaps 4;

QY 2 SENVQDILLDVLPLSLGSLTAGVMTALIKRSTIPTKTQITFTTYSNDQPGVLIQVY 61
 DB 385 SENVQDILLDVLPLSLGSLTAGVMTALIKRSTIPTKTQITFTTYSNDQPGVLIQVY 444

QY 62 GERAMTKDNNILGRFELSGIPPPAPRGVPOLEVFDDIDANGILNVATDKSTGKANKITI 121
 DB 445 GERAMTKDNNILGRFELSGIPPPAPRGVPOLEVFDDIDANGILNVATDKSTGKANKITI 504

QY 122 NDKGRLSKEBIERVMQAEYKAEDEVRQERVSANNALESYAFNMKSAVDEGLKKGKIS 181
 DB 505 NDKGRLSKEDIERVMQAEYKAEDEVRQERVSANNALESYAFNMKSTMEDEKVKDKID 564

QY 182 ADKKVLDKCOEIVSWLDANTLAEKDFEHRKELEOVNPIISGLYQAGGPGG 235
 DB 565 EDKRTITDKCNEIVSWLDNRQLAEKEEFVDKQELSVNPIVTKLYQAGGAGGPGG 624

QY 236 -PGGF-GAQPCKGGSGGPTIEVD 258
 DB 625 MPGGYPGQG--SGSSSGPTIEVD 647

RESULT 64

Q8IS62 PRELIMINARY; PRT; 656 AA.

ID Q8IS62
 AC Q8IS62
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Heat-shock protein 70.
 DE Cotesia rubecula.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidea;
 OC Braconidae; Microgasterinae; Cotesia.
 OX NCBI_TaxID=32392;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22578532; PubMed=12692281; DOI=10.1099/vir.0.19026-0;
 RA Agari S., Zhang G., Schmidt O.;
 RT "Polydnavirus particle proteins with similarities to molecular
 chaperones, heat-shock protein 70 and calreticulin.";
 RL J. Gen. Virol. 84:1165-1171(2003).
 CC -I- SIMILARITY: Belongs to the heat shock protein 70 family.
 DR EMBL; AY150371; AA7310.1; -.
 DR HSP; P19120; IATR.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR InterPro; IPR001023; Hsp70.
 DR InterPro; IPR00169; Pept_cys_acsite.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
 KW ATP-binding.
 SQ SEQUENCE 656 AA; 71486 MW; 49D46612B84AB020 CRC64;

Query Match 81.0%; Score 1064.5; DB 2; Length 656;
 Best Local Similarity 76.9%; Pred. No. 1.1e-57;
 Matches 210; Conservative 20; Mismatches 28; Indels 15; Gaps 2;

KW	ATP-binding; Heat shock.
SQ	SEQUENCE 634 AA; AB5CDCC13D134OC8 CRC64;
Query Match	81.0%; Score 1064; DB 2; Length 634;
Best Local Similarity	79.5%; Pred.No. 1.le-57;
Matches	205; Conservative 23; Mismatches 20; Indels 10; Gaps 1;
Qy	1 KSNVQDLLLLDVAPLSGLGLETAGGVMTALIKNSNIPYKQTQIFTTYSNQPGVLIOVY 60 ::: ::: ::: ::: ::: ::: ::: ::
Dd	387 KSENVQDLLLDDVTPLSLGIETAGGVMTALIKENTTIPTKTQTFTTYSNQSSVLVOVV 446 ::: ::: ::: ::: ::: ::: ::: ::
Qy	61 EGRAMTKNNLAGRELSGIPPARGVPQIEVEDIDANGIILNTATDKSTCKANKITI 120 ::: ::: ::: ::: ::: ::: ::: ::
Dd	447 EGRAMTKNNLGKFDLTGPPARGVPQIEVFIDANGIILNVSAVDKSTGENKITI 506 ::: ::: ::: ::: ::: ::: ::: ::
Qy	121 TNDKGRLSKEEIERMWOAEKYKAEDVEQRERVSAKNALESYAFNMKSAYEDELKGKIS 180 ::: ::: ::: ::: ::: ::: ::: ::
Dd	507 TNDKGRLSKDDIRMWQOAEKYKAEDANRDRVGAKNSLESYTNNMQTVDEKLKGKIS 566 ::: ::: ::: ::: ::: ::: ::: ::
Qy	181 EADKKVKLDKCQEIVSWLDANTLAEKDFEPHKRKELBQCNPILSIGLYQGAGPGPGCGFG 240 ::: ::: ::: ::: ::: ::: ::: ::
Dd	567 DQDKQKVLDRCQEVISWLDRNQMAEEYEHHQKELEKLCNPITVKLYQGAGGAGGGSG 626 ::: ::: ::: ::: ::: ::: ::: ::
Qy	241 AQPKGGSNGSPTEEVD 258
Dd	627 -----GPTEEVD 634
RESULT 66	
Q9NGK9	PRELIMINARY; PRT; 645 AA.
ID Q9NGK9	AC Q9NGK9; AC Q9NGK9;
DT 01-OCT-2000	(TrEMBLrel. 15, Created)
DT 01-OCT-2000	(TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004	(TrEMBLrel. 26, Last annotation update)
De	Heat shock protein 70.
OS	"Wuchereria bancrofti."
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC	Onchocercidae; Wuchereria.
NX NCBI_TaxId=6293;	[1]
RN SEQUENCE FROM N.A.	
RX PubMed=15013783; DOI=10.1016/j.exppara.2004.01.001;	
RA Ravi V., Kubofcik J., Bandopathaya S., Geetha M., Narayanan R.B.,	
RA Nutman T.B., Kaliraj P.;	
RT "Wuchereria bancrofti": cloning and characterization of heat shock	
RL protein 70 from the human lymphatic filarial parasite.";	
RE Exp. Parasitol. 106:1-10(2004).	
RN [2]	
RN SEQUENCE FROM N.A.	
RP Varadarajan V., Kubofcik J., Vijayalakshmi P., Narayanan R.,	
RP Kaliraj P., Kunthala J., Nutman T.;	
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases	
CC -1- SIMILARITY:	Belongs to the heat shock protein 70 family.
DR EMBL; AF250996; AAP6987.1; .	
DR HSPSP; P19120; 3HSC.	
DR GO; GO:0005524; F:ATP binding; IEA.	
DR GO; GO:0006457; P:protein folding; IEA.	
DR GO; GO:0006986; P:response to unfolded protein; IEA.	
DR InterPro; IPR001023; Hsp70.	
DR Pfam; PF00012; HSP70; 1.	
DR PRINTS; PR00301; HEATSHOCK70.	
DR DR PROSITE; PS00297; HSP70_1; 1.	
DR DR PROSITE; PS00329; HSP70_2; 1.	
DR DR PROSITE; PS01036; HSP70_3; 1.	
KW ATP-binding; Heat shock.	
SQ SEQUENCE 645 AA; 70415 MW; BDE9F3A6D8EACS9D9 CRC64;	
Query Match	81.0%; Score 1064; DB 2; Length 645;
Best Local Similarity	79.8%; Pred.No. 1.le-57;
Matches	209; Conservative 21; Mismatches 28; Indels 4; Gaps 3;
Oy	1 KSENVQDLLLLDVAPLSGLGLETAGGVMTALIKNSNIPYKQTQIFTTYSNQPGVLIOVY 60 ::: ::: ::: ::: ::: ::: ::: ::

Db 384 KSEAVQDLLLLDVAPLSLGIEGTAGVMTALIKRNTTPTKTSQTSPTTYSNQPGLVQVY 443
 Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 Db 444 EGERALTNDKNNLLGKFLSGIPPPAPRGVPOIEVTFDIDANGILNVSAQDKSTGKQNKITI 503
 Qy 121 TNDKGRLSKEEIERMWQAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGGKIS 180
 Db 504 TNDKGRLSKEEIERMWQAEKYKAEDVQERVSNAKNALESYAFNMKQTIIEDEKFKKIS 563
 Qy 181 EADKKVKLDKQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGG--PG 237
 Db 564 BEDKKKIPKCDTETWLDGNTQAEKDFEHRKKELEQVNCNPIITKLYQSAGMFGMPG 623
 Qy 238 GFAGQPKGGS--GSQPTTIEVD 258
 Db 624 GMPGAPGAGSTGGGPTTIEVD 645

RESULT 67

P79984 PRELIMINARY; PRT; 649 AA.
 AC P79984;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE HSC70 protein.
 GN Name=hsp8; Synonyms=hsc70;
 OS Brachydanio rerio (zebrafish)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98059927; PubMed=9397538;
 RX DOI=10.1002/(SICI)1520-6408(1997)21:3<223::AID-DVGS>3.3.CO;2-5;
 RA Santacruz H., Vriz S., Angelier N.;
 RT "Molecular characterization of a heat shock cognate cDNA of zebrafish,
 RT hsc70, and developmental expression of the corresponding
 RT transcripts.";
 RL Dev. Genet. 21:223-233(1997).
 CC -I- SIMILARITY: Belongs to the heat shock protein 70 family.
 DR EMBL; Y11413; CAA72216.1; -;
 DR HSP; P19120; 3HSC.
 DR ZFIN; ZDB-GENE-990415-92; hsp8.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding.
 SQ SEQUENCE 649 AA; 71175 MW; 775FPA28B3DF444 CRC64;

Query Match 81.0%; Score 1064; DB 2; Length 649;
 Best Local Similarity 79.8%; Pred. No. 1.2e-57;
 Matches 213; Conservative 20; Mismatches 24; Indels 10; Gaps 4;

Qy 1 KSENVQDLLLLDVAPLSLGIEGTAGVMTALIKRNTTPTKTSQTSPTTYSNQPGLVQVY 60
 Db 384 KSENVQDLLLLDVAPLSLGIEGTAGVMTALIKRNTTPTKTSQTSPTTYSNQPGLVQVY 443
 Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 Db 444 EGERAMTKDNNLLGKFLSGIPPPAPRGVPOIEVTFDIDANGILNVSAVDSKSTGKANKITI 503
 Qy 121 TNDKGRLSKEEIERMWQAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGGKIS 180
 Db 504 TNDKGRLSKEEIERMWQAEKYKAEDVQERVSNAKNALESYAFNMKSTVEDEKFKKIS 563

Qy 181 EADKKVKLDKQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGG-----PG 235
 Db 564 DEDKQKLDKCNKNEVIGWLDKNQTAERBEFHQOK-LEKVCNCPITTKLYQSAGACLVECPN 622
 Qy 236 -PGGF--GAQGPKGSGSGPTTIEVD 258
 Db 623 VPGGPPGAGAAPAGGSSSGPTTIEVD 649

RESULT 68

Q6GUAB PRELIMINARY; PRT; 652 AA.
 AC Q6GUAB;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Heat shock protein 70.
 OS Penaeus vannamei (Penaeid shrimp) (European white shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 OC Penaeidae; Litopenaeus.
 OX NCBI_TaxID=6689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Xie S.T.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: Belongs to the heat shock protein 70 family.
 DR EMBL; AY645906; AAT46566.1; -;
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0006986; P:response to unfolded protein; IEA.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Heat shock.
 SQ SEQUENCE 652 AA; 71522 MW; 956F88CD06C04B4 CRC64;

Query Match 80.9%; Score 1063.5; DB 2; Length 652;
 Best Local Similarity 78.1%; Pred. No. 1.2e-57;
 Matches 210; Conservative 18; Mismatches 30; Indels 11; Gaps 3;

Qy 1 KSENVQDLLLLDVAPLSLGIEGTAGVMTALIKRNTTPTKTSQTSPTTYSNQPGLVQVY 60
 Db 384 KSENVQDLLLLDVAPLSLGIEGTAGVMTALIKRNTTPTKTSQTSPTTYSNQPGLVQVY 443
 Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 Db 444 EGERAMTKDNNLLGKFLSGIPPPAPRGVPOIEVTFDIDANGILNVSAVDSKSTGKANKITI 503
 Qy 121 TNDKGRLSKEEIERMWQAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGGKIS 180
 Db 504 TNDKGRLSKEEIERMWQAEKYKADDEKQDRISAKNSLESYCFNMKSTVEDEKFKKIS 563
 Qy 181 EADKKVKLDKQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGG--PG--P 236
 Db 564 EEDRNKILETCNETIKWLDNMNQLGEKEEYEHQKEIBQVCNPIITTKMYAAGGAPPGMP 623
 Qy 237 GGF-----GAQGPKGSGSGPTTIEVD 258
 Db 624 GGFPGGAPGAGAAPAGGSSSGPTTIEVD 652

RESULT 69

Q71KW5 PRELIMINARY; PRT; 652 AA.
 ID Q71KW5
 AC Q71KW5;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heat shock protein 70.
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE FROM N.A.
RA Lo W.-Y., Song Y.-L.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AF474375; AAQ05768.1; -.
DR HSSP; P19120; IBA1.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; Hsp70_1; 1.
DR PROSITE; PS00329; Hsp70_2; 1.
DR PROSITE; PS01036; Hsp70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 652 AA; 71481 MW; FDFADA929ECF6413 CRC64;

Query Match 80.9%; Score 1063.5; DB 2; Length 652;
Best Local Similarity 78.1%; Pred. No. 1.2e-57;
Matches 210; Conservative 18; Mismatches 30; Indels 11; Gaps 3;

QY 1 KSENVQDLLLLDVAPLSGLTAGVMTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVY 60
Db KSEAQVQDLLLLDVAPLSGLTAGVMTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVY 443

QY 61 EGERAMTKONLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db EGERAMTKONLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 503

QY 121 TNDKGRLSKEELRMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDGLKGKIS 180
Db TNDKGRLSKEELRMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDGLKGKIS 563

QY 181 EADKKKVLKCOEIVSWLDANTLAEKDFEHRKELEQVNCNPIISGLYQGAGG--PG--P 236
Db EEDRNKILETCNETIKWLDNQLGEKEEYEHKQIEQVNCNPIITKMYAAGGAPPGGMP 623

QY 237 GGF-----GAQGPKGSGSGPTIEVD 258
Db GGFPGGAPGAGGAPGAGSGSGPTIEVD 652

RESULT 70
Q17267 PRELIMINARY; PRT; 335 AA.
AC Q17267;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Heat shock protein 70, hsp70A2 (Fragment).
GN Name=hsc70;
OS Brugia pahangi (Filarial nematode worm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Brugia.
OX NCBI_TaxID=6280;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=89278663; PubMed=2659668;
RA Selkirk M.E., Denham D.A., Partono F., Maizels R.M.;
RT "Heat shock cognate 70 is a prominent immunogen in Brugian filariasis."
RL J. Immunol. 143:299-308 (1989).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.

DR EMBL; M27191; AAA27857.1; -.
DR PIR; A45805; A45805.
DR HSSP; P19120; 3HSC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS01036; Hsp70_3; 1.
KW ATP-binding; Heat shock.
FT NON_TER 1
SQ SEQUENCE 335 AA; 36241 MW; B4717A8B99D80C0B CRC64;

Query Match 80.9%; Score 1063; DB 2; Length 335;
Best Local Similarity 79.8%; Pred. No. 6.1e-58;
Matches 209; Conservative 20; Mismatches 29; Indels 4; Gaps 3;

QY 1 KSENVQDLLLLDVAPLSGLTAGVMTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVY 60
Db KSEAQVQDLLLLDVAPLSGLTAGVMTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVY 133

QY 61 EGERAMTKONLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db EGERAMTKONLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 193

QY 121 TNDKGRLSKEELRMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDGLKGKIS 180
Db TNDKGRLSKEELRMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDGLKGKIS 253

QY 181 EADKKKVLKCOEIVSWLDANTLAEKDFEHRKELEQVNCNPIISGLYQGAGG--PG--P 237
Db EEDKKIQEKCDQETRWLDGNQTAEKDEFEHRKELEQVNCNPIITKLYQSAGMGPGMPG 313

QY 238 GFGAGQPKGGS--GSGPTIEVD 258
Db GMPGAPGAGSGSGPTIEVD 335

RESULT 71
HS70_BRUMA STANDARD; PRT; 644 AA.
ID HS70_BRUMA
AC P27541;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock 70 kDa protein.
GN Name=Hsp70;
OS Brugia malayi (Filarial nematode worm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Brugia.
OX NCBI_TaxID=6279;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92131059; PubMed=1775166; DOI=10.1016/0166-6851(91)90066-F;
RA Rothstein N., Rajan T.V.;
RT "Characterization of an hsp70 gene from the human filarial parasite, Brugia malayi (Nematoda)."
RL Mol. Biochem. Parasitol. 49:229-238 (1991).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
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CC -----
DR EMBL; M68933; AAC17926.1; -.
DR PIR; A45635; A45635.
DR HSSP; P19120; 3HSC.
DR InterPro; IPR001023; Hsp70.

DR Pfam: PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR PRODOM; PD000089; Hsp70; 1.
 DR TIGRFAMs; TIGR01991; HscA; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Heat shock.
 SQ SEQUENCE 644 AA; 70220 MW; DE07774C9CAB2925 CRC64;

Query Match 80.9%; Score 1063; DB 1; Length 644;
 Best Local Similarity 79.8%; Pred. No. 1.3e-57;
 Matches 209; Conservative 20; Mismatches 29; Indels 4; Gaps 3;

Qy 1 KSENVQDLLLLDVAPLSGLTAGGVTALIKRNTIPTKTQTQITFTTYSNQPGVLIQVY 60
 |||||
 Db 316 KSEVQDLLLLDVPLSLGIELTAGGVTALIKNTIPTKTQTFTTYADNQPGVLIQVY 375
 |||||

Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
 |||||
 Db 376 EGERAMTKDNNLLGKGFELSGIPAPRGVPQIEVTFDIDANGILNVSAVDKSTGKANKITI 435
 |||||

Qy 121 TNDKGRLSKEIERMVQEAERYKAEDVQERVSNAKNALESYAFNMKSASVEDEGLKGKIS 180
 |||||
 Db 436 TNDKGRLSKEDIERMVNEAEKYSDEKQETAAKNSLESYCFNMKSTVEDEKLKDKIS 495
 |||||

Qy 181 EADKKVLDKQEVISWLDANTLAEDFEHFKRKELEQVNCNPIISGLYQAGG-PG---- 235
 |||||
 Db 496 ASDKQVLDKNDIILKWDANQLADKEEYEHKQKLESIENPIVTKLYQGTGGMPGMP 555
 |||||

Qy 236 --PGFGAQ--GPKGGSGGPTIEVD 258
 |||||
 Db 556 GFGAGGAAPGGAGPGGGSGPTIEVD 583
 |||||

RESULT 73
 HS72 HUMAN
 ID HS72 HUMAN STANDARD; PRT; 639 AA.
 AC PS4652; Q15508; Q9UE78;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Heat shock-related 70 kDa protein 2 (Heat shock 70 kDa protein 2).
 GN Name=HSPA2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Goralski T.J., Krensky A.M.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Brain, and Eye;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins S.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.H.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF 1-126 FROM N.A.
 RX MEDLINE=95152505; PubMed=7849706;

Qy 1 KSENVQDLLLLDVAPLSGLTAGGVTALIKRNTIPTKTQTQITFTTYSNQPGVLIQVY 60
 |||||
 Db 383 KSEAVQDLLLLDVAPLSGLTAGGVTALIKRNTIPTKTSETFTTYSNQPGVLIQVY 442
 |||||

Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
 |||||
 Db 443 EGERALTKDNNLLGKGFELSGIPAPRGVPQIEVTFDIDANGILNVSAQDKSTGKANKITI 502
 |||||

Qy 121 TNDKGRLSKEIERMVQEAERYKAEDVQERVSNAKNALESYAFNMKSASVEDEGLKGKIS 180
 |||||
 Db 503 TNDKGRLSKEDIERMVQEAERYKADDEAQKRIAANKNALESYAFNMKQTIEDKDKIS 562
 |||||

Qy 181 EADKKVLDKQEVISWLDANTLAEDFEHFKRKELEQVNCNPIISGLYQAGG-PG--PG 237
 |||||
 Db 563 EEDKKIKQEKDETWRWDGNQTAEDFEHFKRKELESCVNCNPIITKLYQSGAGMPGMP 622
 |||||

Qy 238 GFGAGQPKGS--GSGPTIEVD 258
 |||||
 Db 623 GMPGAPGAGSGTGGPTIEVD 644
 |||||

RESULT 72
 Q6QAN4
 ID Q6QAN4 PRELIMINARY; PRT; 583 AA.
 AC Q6QAN4;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE 70 kDa heat shock cognate protein (Fragment).
 GN Name=HSC70;
 OS Megachile rotundata (alfalfa leafcutting bee).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
 OC Megachilidae; Megachilinae; Megachile.
 OX NCBI_TaxID=143995;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yocum G.D., Kemp W.P.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
 DR EMBL; AY550116; AAS57865.1; -
 DR HSP; P19120; 1ATF.
 DR GO; GO:0005524; P:ATP binding; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR GO; GO:0006986; P:response to unfolded protein; IEA.
 DR InterPro; IPR001023; HSP70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR PRODOM; PD000089; Hsp70; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Heat shock.
 FT NON_TER 1
 SQ SEQUENCE 583 AA; 64023 MW; 3EDB8051BEC5F88 CRC64;

Query Match 80.7%; Score 1060; DB 2; Length 583;
 Best Local Similarity 77.6%; Pred. No. 1.8e-57;
 Matches 208; Conservative 23; Mismatches 27; Indels 10; Gaps 3;

RA Roux A.-F., Nguyen V.T.T., Squire J.A., Cox D.W.;
 RL "A heat shock gene at 14q22: mapping and expression";
 Hum. Mol. Genet. 3:1819-1822(1994).
 CC -!- FUNCTION: In cooperation with other chaperones, Hsp70s stabilize
 CC preexistent proteins against aggregation and mediate the folding
 CC of newly translated polypeptides in the cytosol as well as within
 CC organelles. These chaperones participate in all these processes
 CC through their ability to recognize nonnative conformations of
 CC other proteins. They bind extended peptide segments with a net
 CC hydrophobic character exposed by polypeptides during translation
 CC and membrane translocation, or following stress-induced damage.
 CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
 CC
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 CC
 CC EMBL; L26336; AAA52698.1; -;
 CC EMBL; U56725; AAD11466.1; -;
 CC EMBL; BC001752; AAH01752.1; -;
 CC EMBL; BC036107; AAH36107.1; -;
 CC EMBL; U10149; AAC50076.1; -;
 CC PIR; A55719; A55719.
 CC HSSP; P19120; 3HSC.
 CC Genew; HGNC:5235; HSPA2.
 CC H-InvDB; HIX0011736; -;
 CC MIM; 140560; -;
 CC GO; GO:0003773; P:heat shock protein activity; TAS.
 CC GO; GO:0007140; P:male meiosis; TAS.
 CC GO; GO:0007286; P:spermatid development; TAS.
 CC InterPro; IPR001023; Hsp70.
 CC Pfam; PF00012; HSP70; 1.
 CC PRINTS; PR00301; HEATSHOCK70.
 CC ProDom; PD000089; Hsp70; 1.
 CC TIGRFAMs; TIGR01991; Hsca; 1.
 CC PROSITE; PS00297; HSP70_1; 1.
 CC PROSITE; PS00329; HSP70_2; 1.
 CC PROSITE; PS01036; HSP70_3; 1.
 CC ATP-binding; Chaperone; Heat shock; Multigene family.
 FT CONFLICT 14 14 T -> P (in Ref. 3; AAH36107).
 FT CONFLICT 54 54 Missing (in Ref. 3).
 FT CONFLICT 80 80 E -> G (in Ref. 3; AAH36107).
 FT CONFLICT 266 266 L -> S (in Ref. 2).
 FT CONFLICT 639 639 AA; 70021 MW; 3851755494E7B729 CRC64;
 SQ SEQUENCE 639 AA; 70021 MW; 3851755494E7B729 CRC64;
 Query Match 80.6%; Score 1059.5; DB 1; Length 639;
 Best Local Similarity 79.1%; Pred. No. 2.2e-57;
 Matches 204; Conservative 24; Mismatches 25; Indels 5; Gaps 1;
 QY 1 KSENVQDLLLLDVAPLSGLTAGVMTALIKRNTIPTKTQTFTTYSNDQPGVLIQVY 60
 DB 387 KSENVQDLLLLDVAPLSGLTAGVMTPLIKRNTIPTKTQTFTTYSNDQSVLVQVY 446
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 447 EGERAMTKNNLLGKFDLTGIPAPRGVPQIEVTFDIDANGILNVTADKSTGKANKITI 506
 QY 121 TNDKGRLSKEIERMVOBAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDGLGKIS 180
 DB 507 TNDKGRLSKDDIDRMVQEAERKSEDEANRVAKNALESYTYNIKQTVDEKLGKIS 566
 QY 181 EADKKVLDKQEVISWLDANTLAKDEFEHKKRKELEQVNCPIISGLYQAGGPGGFG 240
 DB 567 EQDKNKILDKQEVINWLDNRQMAEKDEYEHKQELERVCNPIISKLYQGGPGGGSGGG 626
 QY 241 AQGPKGSGSGPTIEVD 258
 DB 627 S-----GASGGPTIEVD 639

RESULT 74

Q27121 PRELIMINARY; PRT; 658 AA.
 AC Q27121;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Heat shock cognate protein.
 OS Urechis caupo (Innkeeper worm) (Spoonworm).
 OC Eukaryota; Metazoa; Echiura; Xenopneusta; Urechidae; Urechis.
 OC NCBI_TaxID=6431;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94155469; PubMed=8111976;
 RA Rosenthal E.;
 RT "Sequence analysis of translationally controlled maternal mRNAs from
 RT Urechis caupo";
 RL Dev. Genet. 14:485-491(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Rosenthal E.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
 CC EMBL; U30456; AAA74394.1; -;
 CC HSSP; P19120; 3HSC.
 CC GO; GO:0005524; P:ATP binding; IEA.
 CC GO; GO:0006457; P:protein folding; IEA.
 CC GO; GO:0006986; P:response to unfolded protein; IEA.
 CC InterPro; IPR001023; Hsp70.
 CC Pfam; PF00012; HSP70; 1.
 CC PRINTS; PR00301; HEATSHOCK70.
 CC ProDom; PD000089; Hsp70; 1.
 CC PROSITE; PS00297; HSP70_1; 1.
 CC PROSITE; PS00329; HSP70_2; 1.
 CC PROSITE; PS01036; HSP70_3; 1.
 CC ATP-binding; Heat shock.
 KW ATP-binding; Heat shock.
 SQ SEQUENCE 658 AA; 71698 MW; DB54FB2425F3357B CRC64;
 Query Match 80.6%; Score 1059.5; DB 2; Length 658;
 Best Local Similarity 75.0%; Pred. No. 2.2e-57;
 Matches 207; Conservative 24; Mismatches 26; Indels 19; Gaps 2;
 QY 1 KSENVQDLLLLDVAPLSGLTAGVMTALIKRNTIPTKTQTFTTYSNDQPGVLIQVY 60
 DB 384 KSEEVQDLLLLDVAPLSGLTAGVMTSLIKRNTTPTKTQTFTTVDNQPGVLIQVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 444 EGERAMTKNNLLGKFLSGIPAPRGVPQIEVTFDIDANGILNVSAYDKSTGKANKITI 503
 QY 121 TNDKGRLSKEIERMVOBAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDGLGKIS 180
 DB 504 TNDKGRLSKEDIERMVKEAEQYKGEDEAQRPIITAKNSLESYAFNMKSTVEDEKVKIS 563
 QY 181 EADKKVLDKQEVISWLDANTLAKDEFEHKKRKELEQVNCPIISGLYQAGGPGG----- 235
 DB 564 DEDTKIIDKCNVITWLDANQLAKDEFAHQKELEGVCFVMTKLYOAGGAPGMPGG 623
 QY 236 -----PGGGAQPGKSGSGPTIEVD 258
 DB 624 MPGGMPGMPGMPGGAGAPPGGSG-GPTIEVD 658
 RESULT 75
 HS70_PLEWA
 ID HS70_PLEWA STANDARD; PRT; 645 AA.
 AC Q91291;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Heat shock 70 kDa protein (HSP70).
 GN Name=HSP70;

GO: GO:0000723; P:telomere maintenance; IMP.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR KEGG; K01691; HSP70; 1.
FT NON TER 1
SQ SEQUENCE 228 AA; 24872 MW; BD7A09314CE0FEDC CRC64;
Query Match 80.4%; Score 1056; DB 2; Length 228;
Best Local Similarity 91.6%; Pred. No. 1e-57;
Matches 207; Conservative 11; Mismatches 6; Indels 2; Gaps 2;
QY 34 NSTIPTKQTQFTTYSNDQGVLIQVYEGERAMTKNNLLGRFELSGLPPAPRGVQIEV 93
DB 4 NSTIPTKQTQFTTYSNDQGVLIQVYEGERAMTRDNNLLGRFELS-IPAPRGVQIEV 62
QY 94 TFDIDANGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQAEKKADEVRERV 153
DB 63 TFDIDANGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQAEKKADEVRERV 122
QY 154 SAKNALESYAFNMKSAVEDGLKGISEADKKKVLDDKQEVISWLDANTLAEKDFEHR 213
DB 123 AKNALESYAFNMKSAVEDGLKGISEADKKKVLDDKQEVISWLDNTLADKEFVHR 182
QY 214 KELEQVNCPIISGLYQAGGPGGGAQG-PKGGSGSGPTIEVD 258
DB 183 EEELRVCSPIISGLYQAGGPGGGAQAPPKGAGSGSGPTIEVD 228
RESULT 78
O96541 PRELIMINARY; PRT; 645 AA.
ID O96541
AC O96541
DT 01-MAY-1999 (T-EMBLrel. 10, Created)
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DR Heat shock protein 70.
OS Setaria digitata.
OC Eukaryota; Metazoa; Chromadorea; Spirurida; Filarioidea;
OC Setariidae; Setaria.
OX NCBI_TaxID=48799;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99314887; PubMed=10428634; DOI=10.1016/S0020-7519(99)00002-8;
RA Jayasena S.M., Chandrasekharan N.V., Karunanayake E.H.;
RT "Molecular characterisation of a hsp70 gene from the filarial parasite
Setaria digitata";
RL Int. J. Parasitol. 29:581-591(1999).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AF079360; AAD13154.1; -;
DR HSP; P19120; 3HSC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 645 AA; 70292 MW; 4D0E39AB64540366 CRC64;
Query Match 80.4%; Score 1056; DB 2; Length 645;
Best Local Similarity 79.4%; Pred. No. 3.6e-57;
Matches 208; Conservative 21; Mismatches 29; Indels 4; Gaps 3;
QY 1 KSENVQDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQTQFTTYSNDQGVLIQV 60
DB 384 KSEAVQDLLLDVAPLSLGLTAGGVTALIKRNTIPTKQTQFTTYSNDQGVLIQV 443
QY 61 EGERAMTKNNLLGRFELSGLPPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKNNLLGRFELSGLPPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVQAEKKADEVRERVSAKNALESYAFNMKSAVEDGLKGI 180
DB 504 TNDKGRLSKEEIERMVQAEKKADEVRERVAACKNALESYAFNMKSTVEDDKPKDKVP 563
Query Match 80.4%; Score 1056; DB 2; Length 645;
Best Local Similarity 79.4%; Pred. No. 3.6e-57;
Matches 208; Conservative 21; Mismatches 29; Indels 4; Gaps 3;
QY 1 KSENVQDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQTQFTTYSNDQGVLIQV 60
DB 384 KSEAVQDLLLDVAPLSLGLTAGGVTALIKRNTIPTKQTQFTTYSNDQGVLIQV 443
QY 61 EGERAMTKNNLLGRFELSGLPPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKNNLLGRFELSGLPPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVQAEKKADEVRERVSAKNALESYAFNMKSAVEDGLKGI 180
DB 504 TNDKGRLSKEEIERMVQAEKKADEVRERVAACKNALESYAFNMKSTVEDDKPKDKVP 563
Query Match 80.3%; Score 1055; DB 2; Length 649;
Best Local Similarity 77.8%; Pred. No. 4.2e-57;
Matches 207; Conservative 23; Mismatches 28; Indels 8; Gaps 4;
QY 1 KSENVQDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQTQFTTYSNDQGVLIQV 60
DB 384 KSEAVQDLLLDVAPLSLGLTAGGVTALIKRNTIPTKQTQFTTYSNDQGVLIQV 443
QY 61 EGERAMTKNNLLGRFELSGLPPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKNNLLGRFELSGLPPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVQAEKKADEVRERVSAKNALESYAFNMKSAVEDGLKGI 180
DB 504 TNDKGRLSKEEIERMVQAEKKADEVRERVAACKNALESYAFNMKSTVEDDKPKDKVP 563
Query Match 80.4%; Score 1056; DB 2; Length 645;
Best Local Similarity 79.4%; Pred. No. 3.6e-57;
Matches 208; Conservative 21; Mismatches 29; Indels 4; Gaps 3;
QY 1 KSENVQDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQTQFTTYSNDQGVLIQV 60
DB 384 KSEAVQDLLLDVAPLSLGLTAGGVTALIKRNTIPTKQTQFTTYSNDQGVLIQV 443
QY 61 EGERAMTKNNLLGRFELSGLPPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKNNLLGRFELSGLPPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVQAEKKADEVRERVSAKNALESYAFNMKSAVEDGLKGI 180
DB 504 TNDKGRLSKEEIERMVQAEKKADEVRERVAACKNALESYAFNMKSTVEDDKPKDKVP 563
Query Match 80.4%; Score 1056; DB 2; Length 645;
Best Local Similarity 79.4%; Pred. No. 3.6e-57;
Matches 208; Conservative 21; Mismatches 29; Indels 4; Gaps 3;
QY 1 KSENVQDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQTQFTTYSNDQGVLIQV 60
DB 384 KSEAVQDLLLDVAPLSLGLTAGGVTALIKRNTIPTKQTQFTTYSNDQGVLIQV 443
QY 61 EGERAMTKNNLLGRFELSGLPPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKNNLLGRFELSGLPPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVQAEKKADEVRERVSAKNALESYAFNMKSAVEDGLKGI 180
DB 504 TNDKGRLSKEEIERMVQAEKKADEVRERVAACKNALESYAFNMKSTVEDDKPKDKVP 563
Query Match 80.4%; Score 1056; DB 2; Length 645;
Best Local Similarity 79.4%; Pred. No. 3.6e-57;
Matches 208; Conservative 21; Mismatches 29; Indels 4; Gaps 3;
QY 1 KSENVQDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQTQFTTYSNDQGVLIQV 60
DB 384 KSEAVQDLLLDVAPLSLGLTAGGVTALIKRNTIPTKQTQFTTYSNDQGVLIQV 443
QY 61 EGERAMTKNNLLGRFELSGLPPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKNNLLGRFELSGLPPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVQAEKKADEVRERVSAKNALESYAFNMKSAVEDGLKGI 180
DB 504 TNDKGRLSKEEIERMVQAEKKADEVRERVAACKNALESYAFNMKSTVEDDKPKDKVP 563
Query Match 80.4%; Score 1056; DB 2; Length 645;
Best Local Similarity 79.4%; Pred. No. 3.6e-57;
Matches 208; Conservative 21; Mismatches 29; Indels 4; Gaps 3;
QY 1 KSENVQDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQTQFTTYSNDQGVLIQV 60
DB 384 KSEAVQDLLLDVAPLSLGLTAGGVTALIKRNTIPTKQTQFTTYSNDQGVLIQV 443
QY 61 EGERAMTKNNLLGRFELSGLPPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKNNLLGRFELSGLPPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVQAEKKADEVRERVSAKNALESYAFNMKSAVEDGLKGI 180
DB 504 TNDKGRLSKEEIERMVQAEKKADEVRERVAACKNALESYAFNMKSTVEDDKPKDKVP 563
Query Match 80.4%; Score 1056; DB 2; Length 645;
Best Local Similarity 79.4%; Pred. No. 3.6e-57;
Matches 208; Conservative 21; Mismatches 29; Indels 4; Gaps 3;
QY 1 KSENVQDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQTQFTTYSNDQGVLIQV 60
DB 384 KSEAVQDLLLDVAPLSLGLTAGGVTALIKRNTIPTKQTQFTTYSNDQGVLIQV 443
QY 61 EGERAMTKNNLLGRFELSGLPPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKNNLLGRFELSGLPPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVQAEKKADEVRERVSAKNALESYAFNMKSAVEDGLKGI 180
DB 504 TNDKGRLSKEEIERMVQAEKKADEVRERVAACKNALESYAFNMKSTVEDDKPKDKVP 563
Query Match 80.4%; Score 1056; DB 2; Length 645;
Best Local Similarity 79.4%; Pred. No. 3.6e-57;
Matches 208; Conservative 21; Mismatches 29; Indels 4; Gaps 3;
QY 1 KSENVQDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQTQ

```
RESULT 80
HS72 MOUSE
ID HS72 MOUSE STANDARD; PRT; 633 AA.
AC P1V156;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock-related 70 kDa protein 2 (Heat shock protein 70.2).
GN Name=Hsp72; Synonyms=Hsp70.2, Hsp70-2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88302212; PubMed=3405224;
RA Zakari Z.F., Wolgemuth D.J., Hunt C.R.;
RT "Identification and sequence analysis of a new member of the mouse
RT HSP70 gene family and characterization of its unique cellular and
RT developmental pattern of expression in the male germ line.";
RL Mol. Cell. Biol. 8:2925-2932(1988).
CC -!- FUNCTION: In cooperation with other chaperones, Hsp70s stabilize
CC preexistent proteins against aggregation and mediate the folding
CC of newly translated polypeptides in the cytosol as well as within
CC organelles. These chaperones participate in all these processes
CC through their ability to recognize nonnative conformations of
CC other proteins. They bind extended polypeptide segments with a net
CC hydrophobic character exposed by polypeptides during translation
CC and membrane translocation, or following stress-induced damage.
CC -!- DEVELOPMENTAL STAGE: Specifically expressed in prophage stage of
CC melioidosis.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M20567; AAA37859.1; -
CC HSP; P19120; IATV.
CC MGD; MGI:96243; Hspa2.
CC GO; GO:0005515; F:protein binding; IPI.
CC InterPro; IPR001023; Hsp70.
CC Pfam; PF00012; Hsp70; 1.
CC ProDom; PD000089; Hsp70; 1.
CC TIGRFAMs; TIGR01991; HscA; 1.
CC PROSITE; PS00297; Hsp70_1; 1.
CC PROSITE; PS00329; Hsp70_2; 1.
CC PROSITE; PS01036; Hsp70_3; 1.
CC ATP-binding; Chaperone; Heat shock; Multigene family.
CC KW ATP-binding; Chaperone; Heat shock;
CC SEQUENCE 633 AA; 69740 MW; E7F9040F2AB138DD CRC64;

Query Match 80.3%; Score 1054.5; DB 1; Length 633;
Best Local Similarity 79.1%; Pred. No. 4.3e-57;
Matches 204; Conservative 23; Mismatches 20; Indels 11; Gaps 2;

QY 1 KSENVQDILLDLVAPLSGLETAGVMTALIKRNSTIPTKTQIFFTYSDNQPGVLIQVY 60
DB 387 KSENVQDILLDLVTPLSGLIETAGGVMTPLIKRNTIPTKTQITFTYSDNQSSVLVQVY 446
QY 61 EGERAMTKDNLLGLRFLSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 447 EGERAMTKDNLLGLRFLSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 506
QY 121 TNDKRLSKETTERVQAEKTKAEQVQRRVRSNAKLESYAFNMKSAVDEGLKGLKIS 180
DB 507 TNDKRLSKDDIDRWVQAEKTKAEQVQRRVRSNAKLESYAFNMKSAVDEGLKGLKIS 566
QY 181 EADKKKVLDKQEVISWLDANTLAEBKDFEHRKELEQVNCNPIISGLYQGAGPGPGGFG 240
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Db 567 EQDKNKILDKQEVINWLDNRQMAEKDEYHKKQLERVCNFIISKLYQG-----GPGG-- 620
QY 241 AQGPKGSGSGPTTIEVD 258
DB 621 -----GGSGGSGPTTIEVD 633

RESULT 81
Q99KD7 PRELIMINARY; PRT; 633 AA.
ID Q99KD7;
AC Q99KD7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Heat shock protein 2.
GN Name=Hspa2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N; TISSUE=Mammary tumor. C3, and Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.B., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Testis;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC EMBL; BC004714; AA04714.1; -
CC EMBL; BC052350; AAH52350.1; -
CC HSP; P19120; 3HSC.
CC MGD; MGI:96243; Hspa2.
CC GO; GO:0005739; C:mitochondrion; IDA.
CC GO; GO:0005515; F:protein binding; IPI.
CC InterPro; IPR001023; Hsp70.
CC Pfam; PF00012; Hsp70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC ProDom; PD000089; Hsp70; 1.
CC PROSITE; PS00297; Hsp70_1; 1.
CC PROSITE; PS00329; Hsp70_2; 1.
CC PROSITE; PS01036; Hsp70_3; 1.
CC ATP-binding; Heat shock;
CC SEQUENCE 633 AA; 69641 MW; 6F65773C7EFA69F CRC64;

Query Match 80.3%; Score 1054.5; DB 2; Length 633;
```

```
Best Local Similarity 79.1%; Pred. No. 4.3e-57;
Matches 204; Conservative 23; Mismatches 20; Indels 11; Gaps 2;

QY 1 KSENVQDLLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQIFTTYSNQPGLVQVY 60
DB KSENVQDLLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQIFTTYSNQPGLVQVY 446
QY 61 EGERAMTKDNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATADKSTGKANKITI 120
DB EGERAMTKDNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATADKSTGKANKITI 506
QY 121 TNDKRLSKKEIERMVQEAERYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKKGKIS 180
DB TNDKRLSKKDDIDRMVQEAERYKSEDEANRDRVAANKNAVESYTNIKQTVDEKURGKIS 566
QY 181 EADKKKVLDKCOEVIWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQGAGGPGPGFG 240
DB EODKNKILDKCOEVIWLDNRQMAEKDEYEHKQELERVCNPIISKLYQG---GPGG-- 620
QY 241 AQGPKGGSGGPTIEVD 258
DB -----GGSSGGPTIEVD 633

RESULT 82
Q66HL1 PRELIMINARY; PRT; 633 AA.
AC Q66HL1;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE Testis-specific heat shock protein-related gene hat70.
GN Name=Hsp70;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP TISSUE=Testis;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP TISSUE=Testis;
RC Director MGC Project;
RA Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; BC081803; AAH81803.1; --
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; Hsp70_1; 1.
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DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 633 AA; 69641 MW; 6F65773C7E9FA69F CRC64;

Query Match 80.3%; Score 1054.5; DB 2; Length 633;
Best Local Similarity 79.1%; Pred. No. 4.3e-57;
Matches 204; Conservative 23; Mismatches 20; Indels 11; Gaps 2;

QY 1 KSENVQDLLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQIFTTYSNQPGLVQVY 60
DB KSENVQDLLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQIFTTYSNQPGLVQVY 446
QY 61 EGERAMTKDNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATADKSTGKANKITI 120
DB EGERAMTKDNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATADKSTGKANKITI 506
QY 121 TNDKRLSKKEIERMVQEAERYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKKGKIS 180
DB TNDKRLSKKDDIDRMVQEAERYKSEDEANRDRVAANKNAVESYTNIKQTVDEKURGKIS 566
QY 181 EADKKKVLDKCOEVIWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQGAGGPGPGFG 240
DB EODKNKILDKCOEVIWLDNRQMAEKDEYEHKQELERVCNPIISKLYQG---GPGG-- 620
QY 241 AQGPKGGSGGPTIEVD 258
DB -----GGSSGGPTIEVD 633

RESULT 83
Q9NJB7 PRELIMINARY; PRT; 645 AA.
AC Q9NJB7;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Heat shock protein 70.
OS Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Wuchereria.
OX NCBI_TaxID=6293;
RN [1]
RP SEQUENCE FROM N.A.
RA Wijesundera S.W., Pathiratne B.N., Perera R., Karunanayake E.H.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AF167352; AAF32254.1; --
DR HSRP; P19120; 3HSC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 645 AA; 70304 MW; CBD4BE39E35B69D0 CRC64;

Query Match 80.2%; Score 1054; DB 2; Length 645;
Best Local Similarity 79.4%; Pred. No. 4.8e-57;
Matches 208; Conservative 20; Mismatches 30; Indels 4; Gaps 3;

QY 1 KSENVQDLLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQIFTTYSNQPGLVQVY 60
DB KSENVQDLLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQIFTTYSNQPGLVQVY 443
QY 61 EGERAMTKDNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATADKSTGKANKITI 120
DB EGERAMTKDNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATADKSTGKANKITI 503
```

[illegible]

RESULT 84	
Q94614	PRELIMINARY; PRT; 646 AA.
ID AC	Q94614;
AC AC	Q94614;
DT 01-FEB-1997	(TrEMBLrel. 02, Created)
DT 01-FEB-1997	(TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2004	(TrEMBLrel. 26, Last annotation update)
DE	Heat shock 70kDa protein (Fragment).
DE	Name=hsp70;
GN	Mesocestoides corti.
OS	Mesocestoides corti.
OC	Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
OC	Cyclophyllidae; Mesocestoididae; Mesocestoides.
OX	NCBI_TaxID=53468;
RP	[1]
RP	SEQUENCE FROM N.A.
RP	MEDLINE=92366447; PubMed=1323828;
RA	Bork P., Sander C., Valencia A.;
RA	"An ATPase domain common to prokaryotic cell cycle proteins, sugar
RT	kinases, actin, and hsp70 heat shock proteins.";
RT	Proc. Natl. Acad. Sci. U.S.A. 89:7290-7294(1992).
RL	[2]
RP	SEQUENCE FROM N.A.
RP	Teale J.M., Bangs L.A.;
RA	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC	-1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR	EMBL; U70213; AAB18390.1; -.
DR	HSSP; P19120; 3HSC.
DR	GO; GO:0005524; F:ATP binding; IEA.
DR	GO; GO:0006457; P:protein folding; IEA.
DR	GO; GO:0006986; P:response to unfolded protein; IEA.
DR	InterPro; IPR001023; Hsp70.
DR	InterPro; IPR000159; Pept_cys_acsite.
DR	Pfam; PF00012; HSP70; 1.
DR	PRINTS; PR00301; HEATSHOCK70.
DR	PROSITE; PS00297; HSP70_1; 1.
DR	PROSITE; PS00329; HSP70_2; 1.
DR	PROSITE; PS01036; HSP70_3; 1.
DR	PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
KW	ATP-binding; Heat shock.
FT	NON TER 1
FT	SEQUENCE 646 AA; 70683 MW; FF2014E17FD9F940 CRC64;

Query Match	80.1%;	Score 1052.5;	DB 2;	Length 646;
Best Local Similarity	77.7%;	Pred. No. 5.9e-57;		
Matches 209;	Conservative 21;	Mismatches 28;	Indels 11;	Gaps 2
Qy	1	KGENVODLLLDVAPLSLGLETAGGVMTALIKRNSTIPTKTQTFTTYSNQGVLIIQVY	60	
Db	378	KSEAVQDLLLDVAPLSLGLETAGGVMTALIKRNTTPTKTQTFTTYSNQGVLIIQVY	437	
Qy	61	EGERAMTKDNNLLGPELSGTPPAPRGVQPLEVTFDANGILNVATDKSTCKANKITIT	120	
Db	438	EGERAMTRDNNLLGPELSGTPPAPRGVQPLEVTFDANGILSVASDKSTCKQNKITIT	497	
Qy	121	TNDKGRLSKBEETIERNVQBAEYKABDEVQREVRVSAKNALESYAFNMKSAVDEGLGKKIS	180	
Db	498	TNDKGRLSKBEETIERNVMVNDAEYKQDDQRQDVRVSAKNALESYAFNMKSTVEDSKVKKEIA	557	
Qy	181	EADKKKVLDDKCEVTSWLDANTLAEKDFEHRKLELEQVNCNPITISGLYQAGAGPG--	PGS 238	

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558  EGDRKKISKCEETIKWLDANQADKBEYEHQKLEKSVNCNPIITKTYQEBAGGCMPOG 617
239  FGAQGPFGGSG-----SGPTIEEVD 258
      |||||
      |||||
618  MPGGMPGGGSGMGGDAGSGNRPTEEVD 646

RESULT 85
Q81860
ID ID Q81860 PRELIMINARY; PRT; 650 AA.
AC Q81860;
DT DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DE Heat shock protein 70 A.
OS OC Heterodera glycines (Soybean cyst nematode).
OS OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
OC OC Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.
OX OC NCBI_TaxID=51029;
RN RN [1]
RP RP SEQUENCE FROM N.A.
RA RA Kovaleva E.S., Chitwood D.J.;
RL RL Submitted (OCT-2002) to the EMBL/GenBank/DBPJ databases.
CC CC -I- SIMILARITY: Belongs to the heat shock protein 70 family.
DR DR EMBL; AY161283; AAN78300.1; -.
DR DR HSSP; P19120; IHPM.
DR DR GO; GO:0005524; F:ATP binding; IEA.
DR DR GO; GO:0006457; P:protein folding; IEA.
DR DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR DR InterPro; IPR001023; Hsp70.
DR DR Pfam; PF00012; HSP70; 1.
DR DR PRINTS; PD00301; HEATSHOCK70.
DR DR ProDom; PD000089; Hsp70; 1.
DR DR PROSITE; PS00297; HSP70_1; 1.
DR DR PROSITE; PS00329; HSP70_2; 1.
DR DR PROSITE; PS01036; HSP70_3; 1.
DR DR ATP-binding; Heat shock.
SQ SQ SEQUENCE 650 AA; 70614 MW; 7CB8123DCBC4BF68 CRC64;

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RESULT 86
Q9GPK0
ID Q9GPK0 PRELIMINARY; PRT; 650 AA.
AC Q9GPK0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heat shock protein 70.
OS Heterodera glycines (Soybean cyst nematode) .

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DR	PRINTS; PR00301; HEATSHOCK70.
DR	ProDom; PD000089; Hsp70; 1.
DR	PROSITE; PS00297; HSP70_1; 1.
DR	PROSITE; PS00329; HSP70_2; 1.
DR	PROSITE; PS01036; HSP70_3; 1.
KW	ATP-binding; Heat shock.
SQ	SEQUENCE 636 AA; 69866 MW; 1844AC3558B7DF6 CRC64;
 Query Match 80.0%; Score 1051; DB 2; Length 636; Best Local Similarity 78.7%; Pred. No. 7.2e-57; Matches 203; Conservative	
Qy	1 KSENVQDLLLDVAPLSGLGETAGGVMTALIKRNSTIPTKQTPTTYSNDQPGLIOYV 60
Dd	387 KSENVQDLLLDVTPLSLGIETAGGVMTPLIKRNITTIPTKTQTFTTYSNQSSVLQVV 446
Qy	61 EGERAMTKNNLGRFELSGIPPAFCVGPOLEVTFDIDANGILNVTADKSTGKANKITI 120
Dd	447 EGERAMTKNNLGKFKDLTGPPAPRGVPQIEVFDDIANGILNVTAAKSTGKENKITI 506
Qy	121 TNDKGRLSKEBIERMWQEAEKYKAEDVEQRRVSAKNALESYAFNMKSASAVEDEGLKGKIS 180
Dd	507 TNDKGRLSKDDIDEMVQEAERYKSEANRDRAAKNAVESYTNYIKQTVEDEKLKGKIS 566
Qy	181 EADKKVKLVDCQEVISWLMDANTLAEKDEFPEHKRELQVCNPPIISGLYQGAGGPGGFG 240
Dd	: :
Dd	567 DQDKNKILDQCQEVINVDLRNQMAEKRDEYEHHKQLERVCNCNPIISKLYQG----GPGGGG 622
Qy	241 AQCPKGSQSGLTIEEVD 258
Dd	623 GSGSSG---GPTIEEVD 636
 RESULT 88 Q801X9 PRELIMINARY; PRT; 623 AA. ID Q801X9 PRELIMINARY; PRT; 623 AA. AC Q801X9; DT 01-JUN-2003 (TrEMBRel. 24, Created) DT 01-JUN-2003 (TrEMBRel. 24, Last sequence update) DT 01-MAR-2004 (TrEMBRel. 26, Last annotation update) DE Heat shock protein 70 kDa (Fragment). GN Name=HSP70; OS Carassius auratus (Goldfish). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; OC Cyprinidae; Carassius. OX NCBI_TaxID=7957; [!] RP SEQUENCE FROM N.A. RN Watabe S., Kondo H., Hashimoto S.; RL Submitted (Oct-2002) to the EMBL/GenBank/DDBJ databases. CC -1- SIMILARITY: Belongs to the heat shock protein 70 family. DR EWBL; AB092839; BAC67184.1; -. DR HSP; PB0107; IS3X. DR GO; GO:0005524; F:ATP binding; IEA. DR GO; GO:0006457; P:protein folding; IEA. DR GO; GO:0006986; P:response to unfolded protein; IEA. DR InterPro; IPR001023; Hsp70. DR Pfam; PF00012; HSP70; 1. DR PRINTS; PR00301; HEATSHOCK70. DR ProDom; PD000089; Hsp70; 1. DR PROSITE; PS00329; HSP70_2; 1. DR PROSITE; PS01036; HSP70_3; 1. KW ATP-binding; Heat shock. FT NON_TER 1 SQ SEQUENCE 623 AA; 68781 MW; 7A3756151749BC56 CRC64; Query Match 79.9%; Score 1050; DB 2; Length 623; Best Local Similarity 80.0%; Pred. No. 8.1e-57; Matches 208; Conservative	
Qy	2 SENVDLLLDVAPLSGLSETAGGVMTPALIKRNSTIPTKQTIFTTYSNDQPGLIOYVE 61

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Db 367 SGNVQDLLLLDVARSLSGIETAGGVMTALIKENTTIPTKQTFTSTYSDNQPVLIQVYE 426
QY 62 GERAMTKDNLLGRPELSGIPAPRGVPOIEVTFDIDANGILNVATATKSTGKANKITIT 121
Db 427 GERAMTKDNLLGKPELTGIPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITIT 486
QY 122 NDKGRLSKEETRMVQAEKYKAEDVORERVSAKNALESYAFNMKSAVEDGLKGIKISE 181
Db 487 NDKGRLSKDEITRMVQAEKYKAEDVORERVSAKNALESYAFNMKNSVEDDGLKGIKISE 546
QY 182 ADKKKVLDDKCOEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGPGFGA 241
Db 547 DDKKVIEKNEAVSLENNQLADKEEYEHHLKELEKVCNPIITKLYQ--GGMPAGGCGA 604
QY 242 QGPKGGSG---SGPTIEVD 258
Db 605 Q-TRGGSGVLRGPTIEVD 623

RESULT 89
HS70_CHICK
ID HS70_CHICK STANDARD; PRT; 634 AA.
AC P08106;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Heat shock 70 kDa protein (HSP70).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=86304452; PubMed=3017985;
RA Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.;
RT "Organization, nucleotide sequence, and transcription of the chicken
RT HSP70 gene.";
RL J. Biol. Chem. 261:12692-12699 (1986).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J02579; AAA48825.1; -.
DR PIR; A25646; A25646.
DR HSP; P08109; 1CKR.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR TIGRFAMs; TIGR01991; HscA; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock; Multigene family.
KW SEQUENCE 634 AA; 69750 MW; 4270F7F08D365AEB-CRC64;

Query Match 79.9%; Score 1050; DB 1; Length 634;
Best Local Similarity 79.1%; Pred. No. 8.2e-57;
Matches 204; Conservative 23; Mismatches 21; Indels 10; Gaps 1;

QY 1 KSENVQDLLLLDVAPLSLGLTAGGVMTALIKRNSTIPTKTQFTTYSNQPVLIQVY 60
Db 387 KSENVQDLLLLDVAPLSLGLTAGGVMTALIKRNTIPTKTQFTTYSNQSSVLVQVY 446
QY 61 EGERAMTKDNLLGRFELSGLIPAPRGVPOIEVTFDIDANGILNVATATKSTGKANKITI 120

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Db 447 EGERAMTKDNLLGKFDLTGIPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 506
QY 121 TNDKGRLSKEIERMVQAEKYKAEDVORERVSAKNALESYAFNMKSAVEDGLKGIKIS 180
Db 507 TNDKGRLSKODIDRMVQAEKYKAEDVORERVSAKNALESYAFNMKQTVTVEDEKLKGIKIS 566
QY 181 EADKKKVLDDKCOEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGPGFG 240
Db 567 DDDKQKVLDDKCOEVISSLDNRNQMAKEEYEHKKRKELEKVCNPIITKLYQAGGAGAGSG 626
QY 241 AQGPKGGSGGPTIEVD 258
Db 627 -----GPTIEVD 634

RESULT 90
O93240
ID O93240 PRELIMINARY; PRT; 640 AA.
AC O93240;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE HSP70.
OS Paralicthys olivaceus (Japanese flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidei; Paralicthyidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]_
RP SEQUENCE FROM N.A.
RA Yokoyama Y., Hashimoto H., Kubota S., Kinoshita M., Toyohara H.,
RA Sakaguchi M., Tanaka M., Seikai T., Kanamori M.;
RT "cDNA cloning of heat-inducible HSP70, a 70.6 kDa heat shock protein,
RT in Japanese flounder Paralicthys olivaceus.";
RL Fisheries Sci. 64:964-968 (1998).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AB010871; BAA31697.1; -.
DR PIR; T43724; T43724.
DR HSP; P08107; 1HJO.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding.
KW SEQUENCE 640 AA; 70608 MW; 9C8E65738F0CF705-CRC64;

Query Match 79.9%; Score 1049.5; DB 2; Length 640;
Best Local Similarity 77.8%; Pred. No. 8.9e-57;
Matches 200; Conservative 33; Mismatches 21; Indels 3; Gaps 2;

QY 2 SENVQDLLLLDVAPLSLGLTAGGVMTALIKRNSTIPTKTQFTTYSNQPVLIQVYE 61
Db 387 SENVQDLLLLDVAPLSLGLTAGGVMTALIKRNTIPTKTQFTTYSNQPVLIQVYE 446
QY 62 GERAMTKDNLLGRFELSGLIPAPRGVPOIEVTFDIDANGILNVATATKSTGKANKITIT 121
Db 447 GERAMTKDNLLGKFDLTGIPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITIT 506
QY 122 NDKGRLSKEIERMVQAEKYKAEDVORERVSAKNALESYAFNMKSAVEDGLKGIKISE 181
Db 507 NDKGRLSKQELQVQAEKYKAEDVORERVSAKNALESYAFNMKNSVEDDGLKGIKISE 566
QY 182 ADKKKVLDDKCOEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGPGFGA 241
Db 567 EDKKVIDKCNQTSISWLENNQLAEKDEYEHQKKELEKVCNPIITKLYQGA-APPPG--GS 623
QY 242 QGPKGGSGGPTIEVD 258

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Db 624 SCHAGNAOQPTIEVD 640
RESULT 91
Q8AYL6 PRELIMINARY; PRT; 634 AA.
AC Q8AYL6
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heat shock protein.
GN Name=hsp70;
OS Numida meleagris (Helmeted guinea fowl).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Numididae; Numida.
OX NCBI_TaxID=8996;
RN [1]
RP SEQUENCE FROM N.A.
RA Koike Y., Hanawa K., Hara H., Hosomichi K., Yoshida Y., Watanabe S.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AB096696; BAC24791.1; -.
DR HSP; P19120; 3HSC.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70_1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70_1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 634 AA; 69874 MW; 5D84DC80CF407F0C CRC64;

Query Match 79.8%; Score 1049; DB 2; Length 634;
Best Local Similarity 78.3%; Pred. No. 9.5e-57;
Matches 202; Conservative 25; Mismatches 21; Indels 10; Gaps 1;

QY 1 KSENVQDILLDLVAPLSGLTAGVMTALIKRNTIPTKTQITFTTSDNQPGLVQVY 60
DB 387 KSENVQDILLDLVAPLSGLTAGVMTALIKRNTIPTKTQITFTTSDNQPGLVQVY 446
QY 61 EGERAMTKDNNLGRFELSGIPPAQPGVQIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 447 EGERAMTKDNNLGRFELSGIPPAQPGVQIEVTFDIDANGILNVATDKSTGKANKITI 506
QY 121 TNDKRLSKDEIERMVQEAKEYKAEDVQERVSANNALESYAFNMKSAVEDGLKKGKIS 180
DB 507 TNDKRLSKDDIDRMVQEAKEYKAEDANRDVGAKNLSLEYNNKQTVEDDKLKGKIS 566
QY 181 EADKKKVLDKCEVTSWLDANTLAEKDFEHRKELEQVNCPIISGLYQAGGPGGFG 240
DB 567 QDQKQKVLDKCEVTSWLDNRNQMAKEEYHKKQLEKLCNPIVTKLYQAGGAGGSGG 626
QY 241 AQGPKGGSGSGPTIEVD 258
DB 627 -----GPTIEVD 634

RESULT 92
Q86MC3 PRELIMINARY; PRT; 649 AA.
AC Q86MC3
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 70kDa heat shock protein.
OS Balanus amphitrite (Barnacle).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Maxillopoda; Cirripedia;
OC Thoracica; Sessilia; Balanidae; Balanus.
OX NCBI_TaxID=32267;

Db 624 SCHAGNAOQPTIEVD 640
RESULT 91
Q8AYL6 PRELIMINARY; PRT; 634 AA.
AC Q8AYL6
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heat shock protein.
GN Name=hsp70;
OS Numida meleagris (Helmeted guinea fowl).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Numididae; Numida.
OX NCBI_TaxID=8996;
RN [1]
RP SEQUENCE FROM N.A.
RA Koike Y., Hanawa K., Hara H., Hosomichi K., Yoshida Y., Watanabe S.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AB096696; BAC24791.1; -.
DR HSP; P19120; 3HSC.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70_1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70_1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 634 AA; 69874 MW; 5D84DC80CF407F0C CRC64;

Query Match 79.8%; Score 1049; DB 2; Length 634;
Best Local Similarity 78.3%; Pred. No. 9.5e-57;
Matches 202; Conservative 25; Mismatches 21; Indels 10; Gaps 1;

QY 1 KSENVQDILLDLVAPLSGLTAGVMTALIKRNTIPTKTQITFTTSDNQPGLVQVY 60
DB 387 KSENVQDILLDLVAPLSGLTAGVMTALIKRNTIPTKTQITFTTSDNQPGLVQVY 446
QY 61 EGERAMTKDNNLGRFELSGIPPAQPGVQIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 447 EGERAMTKDNNLGRFELSGIPPAQPGVQIEVTFDIDANGILNVATDKSTGKANKITI 506
QY 121 TNDKRLSKDEIERMVQEAKEYKAEDVQERVSANNALESYAFNMKSAVEDGLKKGKIS 180
DB 507 TNDKRLSKDDIDRMVQEAKEYKAEDANRDVGAKNLSLEYNNKQTVEDDKLKGKIS 566
QY 181 EADKKKVLDKCEVTSWLDANTLAEKDFEHRKELEQVNCPIISGLYQAGGPGGFG 240
DB 567 QDQKQKVLDKCEVTSWLDNRNQMAKEEYHKKQLEKLCNPIVTKLYQAGGAGGSGG 626
QY 241 AQGPKGGSGSGPTIEVD 258
DB 627 -----GPTIEVD 634

RESULT 92
Q86MC3 PRELIMINARY; PRT; 649 AA.
AC Q86MC3
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 70kDa heat shock protein.
OS Balanus amphitrite (Barnacle).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Maxillopoda; Cirripedia;
OC Thoracica; Sessilia; Balanidae; Balanus.
OX NCBI_TaxID=32267;
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RN [1]
RP SEQUENCE FROM N.A.
RA Cheng S.H., So C.H., Chan P.K., Cheng C.W., Wu R.S.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY150182; AAN74984.1; -.
DR HSP; P19120; 3HSC.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70_1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70_1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 649 AA; 70737 MW; 4C2475790382C721 CRC64;

Query Match 79.8%; Score 1048; DB 2; Length 649;
Best Local Similarity 76.8%; Pred. No. 1.1e-56;
Matches 205; Conservative 21; Mismatches 31; Indels 10; Gaps 2;

QY 1 KSENVQDILLDLVAPLSGLTAGVMTALIKRNTIPTKTQITFTTSDNQPGLVQVY 60
DB 384 KSENVQDILLDLVAPLSGLTAGVMTALIKRNTIPTKTQITFTTSDNQPGLVQVY 443
QY 61 EGERAMTKDNNLGRFELSGIPPAQPGVQIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 444 EGERAMTKDNNLGRFELSGIPPAQPGVQIEVTFDIDANGILNVATDKSTGKANKITI 503
QY 121 TNDKRLSKDEIERMVQEAKEYKAEDVQERVSANNALESYAFNMKSAVEDGLKKGKIS 180
DB 504 TNDKRLSKDEIERMVQEAKEYKAEDVQERVSANNALESYAFNMKSAVEDGLKKGKIS 563
QY 181 EADKKKVLDKCEVTSWLDANTLAEKDFEHRKELEQVNCPIISGLYQAGGPGGFG 239
DB 564 ESDKTTIIDKNDITIKWLDGNQLAEKDFEHRKELEQVNCPIISGLYQAGGPGGFG 623
QY 240 -----GAQPKGGSGSGPTIEVD 258
DB 624 GMPGMPGGAPKGGAG-GPTIEVD 649

RESULT 93
HS72_RAT
ID HS72_RAT STANDARD; PRT; 633 AA.
AC P14659;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock-related 70 kDa protein 2 (Heat shock protein 70.2) (Testis-specific heat shock protein-related) (HST).
DE Name=Hsp2; Synonyms=Hsp70;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=90122930; PubMed=1688714; DOI=10.1016/0167-4781(90)90027-Y;
RA Wisniewski J., Kordula T., Krawczyk Z.;
RT "Isolation and nucleotide sequence analysis of the rat testis-specific major heat-shock protein (HSP70)-related gene.";
RL Biochim. Biophys. Acta 1048:93-99(1990).
CC -1- FUNCTION: In cooperation with other chaperones, Hsp70s stabilize of newly translated polypeptides in the cytosol as well as within organelles. These chaperones participate in all these processes through their ability to recognize nonnative conformations of other proteins. They bind extended peptide segments with a net
```

CC hydrophobic character exposed by polypeptides during translation
 CC and membrane translocation, or following stress-induced damage.
 CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X15705; CAA33735.1; --
 CC HSSP; P19120; 3HSC.
 CC InterPro; IPR001023; Hsp70.
 CC Pfam; PF00012; HSP70; 1.
 CC PRINTS; P00301; HEATSHOCK70.
 CC ProDom; PD000089; Hsp70; 1.
 CC TIGRFAM; TIGR01991; HsGA; 1.
 CC PROSITE; PS00297; HSP70_1; 1.
 CC PROSITE; PS00329; HSP70_2; 1.
 CC PROSITE; PS01036; HSP70_3; 1.
 CC ATP-binding; Chapterone; Heat shock; Multigene family; Spermatogenesis.
 CC KW SEQUENCE 633 AA; 69528 MW; 6878CA5C2EEBF7DA CRC64;
 CC -----
 CC Query Match 79.7%; Score 1047.5; DB 1; Length 633;
 CC Best Local Similarity 78.7%; Pred. No. 1.2e-56;
 CC Matches 203; Conservative 23; Mismatches 26; Indels 11; Gaps 2;
 CC -----
 CC QY 1 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTPTKQTQITFTYSDNQPGVLIQVY 60
 CC Db 387 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTPTKQTQITFTYSDNQSVLVQVY 446
 CC QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVTATDKSTGKANKITI 120
 CC Db 447 EGERAMTKDNNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVTATDKSTGKANKITI 506
 CC QY 121 TNDKGRLSKEETRMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDEGLKKGKIS 180
 CC Db 507 TNDKGRLSKDDIDRMVQAEADGYKSEDEANRDVAANKAVESYTNIKQTVEDEKLKGKIS 566
 CC QY 181 EADKKVLDKQEVISWLDANTLAEKDFEHRKELQVNCNPIISGLYQAGGPGGFG 240
 CC Db 567 EQDKNKLKDCQEVINWLDNRQMAEKDEYEHKQELERVCNPIISKLQYQ---GPGG-- 620
 CC QY 241 AQGPKGGSGSGPTIEVD 258
 CC Db 621 -----GGSGSGGPTIEVD 633
 CC -----
 CC RESULT 94
 CC Q7PYRS PRELIMINARY; PRT; 656 AA.
 CC ID Q7PYRS5
 CC AC Q7PYRS5
 CC DT 01-WAR-2004 (Tremblrel. 26, Created)
 CC DT 01-WAR-2004 (Tremblrel. 26, Last sequence update)
 CC DT 01-WAR-2004 (Tremblrel. 26, Last annotation update)
 CC DE AGCPL2309
 CC GN Name=agCG9697; ORFNames=ENSGANG00000017398;
 CC OS Anopheles gambiae str. PEST.
 CC OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 CC OX NCBI_TaxID=180454;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=PEST;
 CC RA Anopheles Genome Sequencing Consortium;
 CC RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC DR EMBL; AAA01008987; EAA01046.1; --

DR HSSP; P19120; LATR.
 DR GO; GO:0005524; F-ATP binding; IEA.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; P00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 DR ATP-binding.
 DR KW SEQUENCE 656 AA; 71375 MW; 0CBCFD5FC07B894A CRC64;
 DR -----
 DR Query Match 79.6%; Score 1045.5; DB 2; Length 656;
 DR Best Local Similarity 77.1%; Pred. No. 1.6e-56;
 DR Matches 209; Conservative 22; Mismatches 27; Indels 13; Gaps 4;
 DR -----
 DR QY 1 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTPTKQTQITFTYSDNQPGVLIQVY 60
 DR Db 386 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTPTKQTQITFTYSDNQPGVLIQV 445
 DR QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DR Db 446 EGERAMTKDNNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVTATDKSTGKANKITI 505
 DR QY 121 TNDKGRLSKEETRMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDEGLKKGKIS 180
 DR Db 506 TNDKGRLSKEDIERMVQAEKYRTDEKQKETISAKNALESYCFNMKATMEDDKLKKIT 565
 DR QY 181 EADKKVLDKQEVISWLDANTLAEKDFEHRKELQVNCNPIISGLYQAGG---PG 235
 DR Db 566 DSDKTLVLDKNDITKWLDAQNLADKEEYEHKQELERVCNPIISKLQYQAGGAPGMPG 625
 DR QY 236 -PGGF-GAQQPKG-----GSGSGPTIEVD 258
 DR Db 626 PFGAPGAGGAAGGAAGGAGSGSGPTIEVD 656
 DR -----
 DR RESULT 95
 DR HS7D MANSE
 DR ID HS7D MANSE STANDARD; PRT; 652 AA.
 DR AC Q90639;
 DR DT 16-OCT-2001 (Rel. 40, Created)
 DR DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DR DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DR DE Heat shock 70 kDa protein cognate 4 (Hsc 70-4).
 DR OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
 CC Sphingidae; Sphinginae; Manduca.
 CC OX NCBI_TaxID=7130;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE=Prothoracic gland;
 CC RX MEDLINE=20304587; PubMed=10844250; DOI=10.1016/S0965-1748(00)00031-X;
 CC RA Rybczynski R., Gilbert L.I.;
 CC RT "cDNA cloning and expression of a hormone-regulated heat shock protein
 CC (hsc 70) from the prothoracic gland of Manduca sexta.";
 CC RT Insect Biochem. Mol. Biol. 30:579-589(2000).
 CC RL Insect Biochem. Mol. Biol. 30:579-589(2000).
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- DEVELOPMENTAL STAGE: Heat shock cognate proteins are expressed
 CC constitutively during normal development.
 CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF194819; AAF09496.1; --
 CC HSSP; P19120; 3HSC.

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DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR TIGRFAMs; TIGR01991; Hsca; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock; Multigene family; Nuclear protein.
KW SEQUENCE 652 AA; 71431 MW; F5DBPEA4FEF76E3E CRC64;
SQ
Query Match 79.4%; Score 1043.5; DB 1; Length 652;
Best Local Similarity 76.2%; Pred. No. 2.2e-56;
Matches 205; Conservative 24; Mismatches 29; Indels 11; Gaps 3;
Qy 1 KSENVQDLLLDVAPLSGLTETAGGVMTALIKRNSTIPTKOTQITFTTYSNDQPGVLIQVY 60
Db 384 KSENVQDLLLDVAPLSGLTETAGGVMTALIKRNSTIPTKOTQITFTTYSNDQPGVLIQV 443
Qy 61 EGERAMTKDNLLGRFELSGIPPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTKDNLLGRFELSGIPPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 503
Qy 121 TNDKGRLSKEIERMVQAEKYKAEDVQRRVSAKNALSYAFNMKSAVEDEGLKGKIS 180
Db 504 TNDKGRLSKEIERMVQAEKYKAEDVQRRVSAKNALSYAFNMKSAVEDEGLKGKIS 563
Qy 181 EADKKVKLDKQCEVISWLDANTLAEKDFEHRKELEQVNCPIISGLYQAGG-PG--PG 237
Db 564 DSDKQTLKCNDRITKWLDSHQLADKEEYHKELEGICNPITIKLYQAGGPGGMPG 623
Qy 238 GF-----GAQPGKGGSGSGPTIEVD 258
Db 624 GMPFGGAPGAGGAAPGGAGPTIEVD 652
RESULT 96
ID HS73 BOVIN STANDARD; PRT; 631 AA.
AC P34933;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock 70 kDa protein 3.
GN Name=HSP70-3;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93122795; PubMed=1478667;
RT "Synthetic conservation of HSP70 genes in cattle and humans.";
RL Genomics 14:863-868(1992).
CC -1- FUNCTION: In cooperation with other chaperones, Hsp70s stabilize
CC preexistent proteins against aggregation and mediate the folding
CC of newly translated polypeptides in the cytosol as well as within
CC organelles. These chaperones participate in all these processes
CC through their ability to recognize nonnative conformations of
CC other proteins. They bind extended peptide segments with a net
CC hydrophobic character exposed by polypeptides during translation
CC and membrane translocation, or following stress-induced damage.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
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CC EMBL; L10428; AAA30569.1; -.
DR HSP; P19120; 3HSC.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR TIGRFAMs; TIGR01991; Hsca; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Chaperone; Heat shock; Multigene family.
KW SEQUENCE 631 AA; 69199 MW; 01ACA20600C9322F CRC64;
SQ
Query Match 79.4%; Score 1043; DB 1; Length 631;
Best Local Similarity 78.3%; Pred. No. 2.2e-56;
Matches 202; Conservative 24; Mismatches 24; Indels 8; Gaps 2;
Qy 1 KSENVQDLLLDVAPLSGLTETAGGVMTALIKRNSTIPTKOTQITFTTYSNDQPGVLIQVY 60
Db 382 KSENVQDLLLDVAPLSGLTETAGGVMTALIKRNSTIPTKOTQITFTTYSNDQSSVLQVY 441
Qy 61 EGERAMTKDNLLGRFELSGIPPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 442 EGERAMTKDNLLGRFELSGIPPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 501
Qy 121 TNDKGRLSKEIERMVQAEKYKAEDVQRRVSAKNALSYAFNMKSAVEDEGLKGKIS 180
Db 502 TNDKGRLSKEIERMVQAEKYKAEDVQRRVSAKNALSYAFNMKSAVEDEGLKGKIS 561
Qy 181 EADKKVKLDKQCEVISWLDANTLAEKDFEHRKELEQVNCPIISGLYQAGGPGGPGFG 240
Db 562 DQDKNKILDKQCEVINWLDNRQMAEKDEYHKELEQVNCPIISGLYQG---GPGGGG 617
Qy 241 AQPGKGGSGSGPTIEVD 258
Db 618 GSGASG----GPTIEVD 631
RESULT 97
ID O73922 PRELIMINARY; PRT; 639 AA.
AC O73922;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heat shock protein 70.
GN Name=HSP70;
OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8127;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20291068; PubMed=10828441; DOI=10.1016/S0014-5793(00)01538-6;
RT Molina A., Biemar F., Mueller F., Iyengar A., Prunet P., Maclean N.,
RA Martial J.A., Muller M.;
RT "Cloning and expression analysis of an inducible HSP70 gene from
RT tilapia fish.";
RL FEBS Lett. 474:5-10(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Molina A.I.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AJ001312; CAA04673.1; -.
DR HSP; P08107; IHJO.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
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DR Pfam: PF00012; HSP70_1.
DR PRINTS: PR00301; HEATSHOCK70.
DR ProDom: PD000089; HSP70_1.
DR PROSITE: PS00297; HSP70_1; 1.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock_
SQ SEQUENCE 639 AA; 70292 MW; B296FA98407BD4AE CRC64;

Query Match
Best Local Similarity 79.3%; Score 1042.5; DB 2; Length 639;
Matches 203; Conservative 28; Mismatches 23; Indels 3; Gaps 2;

QY 2 SENVQDLLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQITFTTYSNQPGLVLIQVY 61
DB 386 SGNVQDLLLLDVAPLSGLGLETAGGVTALIKRNTTPTKQTQITFTTYSNQPGLVLIQVY 445

QY 62 GERAMTKNNLLGRFELSGIPPPAPRGVQIEVTFDIDANGILNVATDKSTGKANKITI 121
DB 446 GERAMTKNNLLGKFLGIPPPAPRGVQIEVTFDIDANGILNVSAVDKSTGKANKITI 505

QY 122 NDKGRLSKEEIERMVOEAEKYKADEVQREVRSYAKNALESYAFNMKSAYEDELGKGI 181
DB 506 NDKGRLSKEEIERMVOEAEKYKAEDDLDQDKIAAKNSLESYAFNMKSAYEDELGKGI 565

QY 182 ADKKKVLKQCVISWLDANTLAEDFEHKKKELEQVNCNPIISGLYQAGGPGFGA 241
DB 566 EDKKKVLKQCVISWLDANTLAEDFEHKKKELEQVNCNPIISGLYQAGGPGFGA 241

QY 242 QGPKGSGSGGPTIEVD 258
DB 625 QARAG--SQGPTIEVD 639

RESULT 98
HS70 ONCTS
ID HS70 ONCTS STANDARD; PRT; 644 AA.
AC Q91233;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock 70 kDa protein (HSP70).
GN Name=HSP70;
OS Oncorhynchus tshawytscha (Chinook salmon) (King salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Procacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OC NCBI_TaxID=74940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC CRL-1681;
RA Hargis M.T., Goff H., Dauble D.D., Howard S., Candido P., Hickey E.,
RA Weber L.A.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U35064; AAA78276.1; -.
DR HSP; F08109; ICRK.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; HSP70_1.
DR TIGRFAMs; TIGR01991; HSCA; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.

DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock_
SQ SEQUENCE 639 AA; 70292 MW; B296FA98407BD4AE CRC64;

Query Match
Best Local Similarity 79.3%; Score 1042.5; DB 2; Length 639;
Matches 203; Conservative 28; Mismatches 23; Indels 3; Gaps 2;

QY 2 SENVQDLLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQITFTTYSNQPGLVLIQVY 61
DB 386 SGNVQDLLLLDVAPLSGLGLETAGGVTALIKRNTTPTKQTQITFTTYSNQPGLVLIQVY 445

QY 62 GERAMTKNNLLGRFELSGIPPPAPRGVQIEVTFDIDANGILNVATDKSTGKANKITI 121
DB 446 GERAMTKNNLLGKFLGIPPPAPRGVQIEVTFDIDANGILNVSAVDKSTGKANKITI 505

QY 122 NDKGRLSKEEIERMVOEAEKYKADEVQREVRSYAKNALESYAFNMKSAYEDELGKGI 181
DB 506 NDKGRLSKEEIERMVOEAEKYKAEDDLDQDKIAAKNSLESYAFNMKSAYEDELGKGI 565

QY 182 ADKKKVLKQCVISWLDANTLAEDFEHKKKELEQVNCNPIISGLYQAGGPGFGA 241
DB 566 EDKKKVLKQCVISWLDANTLAEDFEHKKKELEQVNCNPIISGLYQAGGPGFGA 241

QY 242 QGPKGSGSGGPTIEVD 258
DB 625 QARAG--SQGPTIEVD 639

RESULT 98
HS70 ONCTS
ID HS70 ONCTS STANDARD; PRT; 644 AA.
AC Q91233;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock 70 kDa protein (HSP70).
GN Name=HSP70;
OS Oncorhynchus tshawytscha (Chinook salmon) (King salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Procacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OC NCBI_TaxID=74940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC CRL-1681;
RA Hargis M.T., Goff H., Dauble D.D., Howard S., Candido P., Hickey E.,
RA Weber L.A.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U35064; AAA78276.1; -.
DR HSP; F08109; ICRK.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; HSP70_1.
DR TIGRFAMs; TIGR01991; HSCA; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.

DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock; Multigene family.
SQ SEQUENCE 644 AA; 70976 MW; 25DSC8AA2464B939 CRC64;

Query Match
Best Local Similarity 77.6%; Pred. No. 2.4e-56;
Matches 201; Conservative 30; Mismatches 27; Indels 1; Gaps 1;

QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQITFTTYSNQPGLVLIQVY 60
DB 386 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNTTPTKQTQITFTTYSNQPGLVLIQVY 445

QY 61 EGERAMTKNNLLGRFELSGIPPPAPRGVQIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 446 EGERAMTKNNLLGKFLGIPPPAPRGVQIEVTFDIDANGILNVSAVDKSTGKANKITI 505

QY 121 TNDKGRLSKEEIERMVOEAEKYKADEVQREVRSYAKNALESYAFNMKSAYEDELGKGI 180
DB 506 TNDKGRLSKEEIERMVOEAEKYKAEDDLDQDKIAAKNSLESYAFNMKSAYEDELGKGI 565

QY 181 EADKKKVLKQCVISWLDANTLAEDFEHKKKELEQVNCNPIISGLYQAGGPGFGA 239
DB 566 QEDKKKVLKQCVISWLDANTLAEDFEHKKKELEQVNCNPIISGLYQAGGPGFGA 239

QY 240 GAQPKGSGSGGPTIEVD 258
DB 626 QARTSSGDSGSGPTIEVD 644

RESULT 99
Q17310
ID Q17310 PRELIMINARY; PRT; 653 AA.
AC Q17310;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ceratitis capitata heat shock-like protein.
OS Ceratitis capitata (Mediterranean fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Tephritidae; Tephritidae; Ceratitis.
OC NCBI_TaxID=7213;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98119518; PubMed=9459430;
RA Thanaphum S., Haymer D.S.;
RT "A member of the hsp70 gene family from the Mediterranean fruit fly,
RT Ceratitis capitata."
RL Insect Mol. Biol. 7:63-72(1998).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC EMBL; U20256; AAC23392.1; -.
DR HSP; P19120; IBA1.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 653 AA; 71194 MW; 0745A6AC1041FAPC CRC64;

Query Match
Best Local Similarity 75.6%; Pred. No. 2.7e-56;
Matches 204; Conservative 29; Mismatches 25; Indels 12; Gaps 4;

QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQITFTTYSNQPGLVLIQVY 60
DB 384 KSQEVQDLLLLDVAPLSGLGLETAGGVTALIKRNTTPTKQTQITFTTYSNQPGLVLIQVY 443

QY 61 EGERAMTKNNLLGRFELSGIPPPAPRGVQIEVTFDIDANGILNVATDKSTGKANKITI 120
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Db 623 NFGAPGAGGPTFGAGSGSGPTIEVD 650

Search completed: April 6, 2005, 17:24:15
Job time : 205 secs

Db 444 EGERAMTKDNLLGKFEISGIPPAAPRGVPQIEVTFDIDANGILNVTALERTNKENKITI 503
QY 121 TNDKGRLSKEETIRWVQAEKYKASDEVQERVSNAKNALESYAFNMKSAVEDGLKKGKIS 180
Db 504 TNDKGRLSKEETIRWVQAEKYKASDEVQERVSNAKNALESYAFNMKSAVEDGLKKGKIS 563
QY 181 EADKKKVLDDKQOEVIISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGG-----PG 235
Db 564 ESDRTTILDKNETIKWLDANQLAEKEVEYHRQKELEQVNCNPIITKLYQAGGAGPGGMPG 623
QY 236 --PGGF-----GAQCPKG--GSGSGPTIEVD 258
Db 624 GIPGFGPAGGAGGAGGAGTGAGPTIEVD 650

RESULT 100

Q8ITL5 PRELIMINARY; PRT; 650 AA.
AC Q8ITL5
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Heat shock cognate 70
OS Chironomus tentans (Widge).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;
OC Chironomidae; Chironominae; Chironomus.
OX NCBI_TaxID=7153;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=22431718; PubMed=12542632;
RA Karouna-Renier N.K., Yang W.-J., Rao K.R.;
RT "Cloning and characterization of a 70 kDa heat shock cognate gene.
RT (HSC70) from two species of Chironomus.";
RL Insect Mol. Biol. 12:19-26(2003).
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AF448433; AAN14525.1; -.
DR HSSP; P19120; 1BA1.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 650 AA; 71340 MW; F826AAEA0228C18A CRC64;

Query Match 79.3%; Score 1041.5; DB 2; Length 650;
Best Local Similarity 76.1%; Pred No. 2.8e-56;
Matches 204; Conservative 24; Mismatches 29; Indels 11; Gaps 3;
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Db 384 KSEEVQDILLDLVAPLSGLTAGGVMITALIKRNSTIPTKTQIPTTYSNDQPGVLIQVY 443
QY 61 EGERAMTKDNLLGKFEISGIPPAAPRGVPQIEVTFDIDANGILNVTALERTNKENKITI 120
Db 444 EGERAMTKDNLLGKFEISGIPPAAPRGVPQIEVTFDIDANGILNVTALERTNKENKITI 503
QY 121 TNDKGRLSKEETIRWVQAEKYKASDEVQERVSNAKNALESYAFNMKSAVEDGLKKGKIS 180
Db 504 TNDKGRLSKEETIRWVQAEKYKASDEVQERVSNAKNALESYAFNMKSAVEDGLKKGKIS 563
QY 181 EADKKKVLDDKQOEVIISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGGAGPGGPF- 239
Db 564 ESDKKIINDKNETIKWLDANQLAEKEVEYHRQKELEQVNCNPIITKLYQAGG-APGGMP 622
QY 240 ---GAQG-----PKGSGSGPTIEVD 258

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 6, 2005, 16:55:53 ; Search time 43 Seconds
(without alignments)
577.301 Million cell updates/sec

Title: US-09-646-835-1_COPY_384_641

Perfect score: 1314

Sequence: 1 KSENVQDLLLDVAPLSGL.....FGAQPKGSGSGPTIEVD 258

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1314	100.0	641	2 A45871	dnak-type molecule
2	1298.5	98.8	640	2 A29160	dnak-type molecule
3	1295	98.6	641	2 S3357	dnak-type molecule
4	1279.5	97.4	638	2 S31766	dnak-type molecule
5	1279	97.3	641	2 S35718	dnak-type molecule
6	1258	95.7	641	2 I54542	dnak-type molecule
7	1228.5	93.5	642	2 JH0095	dnak-type molecule
8	1216	92.5	420	2 A26283	dnak-type molecule
9	1100.5	83.8	646	2 S31716	dnak-type molecule
10	1100.5	83.8	646	2 A35922	dnak-type molecule
11	1100.5	83.8	646	2 JC4853	dnak-type molecule
12	1100.5	83.8	646	2 S07197	dnak-type molecule
13	1099	83.6	641	2 B45871	dnak-type molecule
14	1097.5	83.5	646	2 A27077	dnak-type molecule
15	1094.5	83.3	646	2 A45935	dnak-type molecule
16	1092	83.1	641	2 I49761	dnak-type molecule
17	1091.5	83.1	650	2 S11456	dnak-type molecule
18	1087	82.7	641	2 S21415	dnak-type molecule
19	1084	82.5	651	2 S21175	dnak-type molecule
20	1063	80.9	335	2 A45805	dnak-type molecule
21	1063	80.9	644	2 A45635	dnak-type molecule
22	1059.5	80.6	639	2 A55719	dnak-type molecule
23	1058	80.5	645	2 I51129	dnak-type molecule
24	1054.5	80.3	633	2 S10859	dnak-type molecule
25	1050	79.9	634	2 A25646	dnak-type molecule
26	1049.5	79.9	640	2 T43724	dnak-type molecule
27	1047.5	79.7	633	2 S08211	dnak-type molecule
28	1036.5	78.9	647	1 HRL70	dnak-type molecule
29	1034	78.7	640	2 T21394	hypothetical prote

30	1023	77.9	651	2 A36333	dnak-type molecule
31	1012	77.0	643	2 S09036	dnak-type molecule
32	1009	76.8	645	2 JC5642	dnak-type molecule
33	1008	76.7	643	2 S25585	dnak-type molecule
34	1007	76.6	654	2 S27004	dnak-type molecule
35	994	75.6	640	1 HHKW7A	dnak-type molecule
36	988	75.2	637	2 A48469	dnak-type molecule
37	964	73.4	647	2 T45522	heat shock protein
38	958	72.9	641	2 JN0668	dnak-type molecule
39	955	72.7	651	2 S46302	dnak-type molecule
40	955	72.7	651	2 T48271	dnak-type molecule
41	953	72.5	653	2 T48270	dnak-type molecule
42	948.5	72.2	647	2 S44168	dnak-type molecule
43	943	71.8	651	2 JC4786	dnak-type molecule
44	943	71.8	653	2 A42582	dnak-type molecule
45	939	71.5	649	2 S53126	dnak-type molecule
46	938	71.4	651	2 T45517	heat shock protein
47	928.5	70.7	646	2 S37165	dnak-type molecule
48	928	70.6	651	2 S03250	dnak-type molecule
49	921.5	70.1	644	2 S14950	dnak-type molecule
50	921	70.1	645	2 A25089	dnak-type molecule
51	913.5	69.5	521	2 S51682	dnak-type molecule
52	911.5	69.4	649	2 J01515	dnak-type molecule
53	911	69.3	656	2 S51712	dnak-type molecule
54	910	69.3	652	2 A53163	dnak-type molecule
55	909.5	69.2	644	2 S67431	dnak-type molecule
56	909	69.2	650	2 S14949	dnak-type molecule
57	906	68.9	648	2 S53498	dnak-type molecule
58	904.5	68.8	645	2 S14992	dnak-type molecule
59	904	68.8	651	2 JC7132	heat shock protein
60	903	68.7	640	2 T43730	dnak-type molecule
61	902	68.6	647	2 T41121	heat shock protein
62	901	68.6	573	2 S18181	dnak-type molecule
63	896	68.2	646	2 B86295	hypothetical prote
64	894	68.0	650	2 D30093	heat shock protein
65	893.5	68.0	639	2 S20139	dnak-type molecule
66	893	68.0	642	1 HHBYA1	dnak-type molecule
67	891.5	67.8	642	2 B36590	dnak-type molecule
68	890	67.7	653	2 S11448	dnak-type molecule
69	883	67.2	379	2 T46588	dnak-type molecule
70	883	67.2	641	2 PC7036	heat shock protein
71	883	67.2	653	2 S52727	dnak-type molecule
72	881	67.0	641	1 HHFF72	dnak-type molecule
73	880	67.0	655	2 S18349	dnak-type molecule
74	879	66.9	649	2 S42488	dnak-type molecule
75	876	66.7	639	2 JC1391	dnak-type molecule
76	876	66.7	645	2 S41372	dnak-type molecule
77	874	66.5	649	2 S36753	dnak-type molecule
78	873	66.4	630	2 A34041	dnak-type molecule
79	868.5	66.1	636	2 A48872	dnak-type molecule
80	868.5	66.1	640	2 S37394	dnak-type molecule
81	864.5	65.8	681	2 JU0164	dnak-type molecule
82	864	65.8	686	2 A49242	dnak-type molecule
83	862.5	65.6	651	2 JC4610	dnak-type molecule
84	861	65.5	646	2 T46650	heat shock protein
85	860.5	65.5	313	2 A26485	dnak-type molecule
86	857.5	65.3	313	2 B31238	dnak-type molecule
87	853.5	65.0	465	2 T07620	dnak-type molecule
88	852	64.8	680	2 S06158	dnak-type molecule
89	842.5	64.1	643	2 S49303	dnak-type molecule
90	842	64.1	646	2 A44985	dnak-type molecule
91	839.5	63.9	661	2 A25398	dnak-type molecule
92	837	63.7	651	2 JC2215	dnak-type molecule
93	827.5	63.0	675	1 HHUM7B	dnak-type molecule
94	824	62.7	632	2 T45471	dnak-type molecule
95	823.5	62.7	261	2 S14875	dnak-type molecule
96	816.5	62.1	636	2 T45468	dnak-type molecule
97	798	60.7	656	2 A48439	dnak-type molecule
98	797.5	60.7	645	2 T22169	hypothetical prote
99	793	60.4	617	2 H96605	probable heat choc
100	785.5	59.8	643	2 T19211	hypothetical prote

ALIGNMENTS

RESULT 1

A45871
dnaK-type molecular chaperone HSP70-1 - human
N:Alternate names: heat shock protein HSP70-1
C:Species: Homo sapiens (man)
C>Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
C:Accession: A45871
R:Milner, C.M.; Campbell, R.D.
Immunogenetics 32, 242-251, 1990
A:Title: Structure and expression of the three MHC-linked HSP70 genes.
A:Reference number: A45871; MUID:91055806; PMID:1700760
A:Accession: A45871
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-641 <ML>
A:Cross-references: UNIPROT:P08107; GB:M59828; GB:M34267; NID:g188487; PIDN:AAA63226.1;
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein comp
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match	100.0%;	Score 1314;	DB 2;	Length 641;
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QY 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTTYSNQPGLIQVY 60
DB 384 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTTYSNQPGLIQVY 443

QY 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
DB 444 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 503

QY 121 TNDKGRLSKEIERMVQEAQYKAEDEVQREVRSKNALESYAFNMKSAVEDEGLKGKIS 180
DB 504 TNDKGRLSKEIERMVQEAQYKAEDEVQREVRSKNALESYAFNMKSAVEDEGLKGKIS 563

QY 181 EADKKKVLDCQEVISWLDANTLAEKDFEHKRELEQVNCNPIISGLYQAGGPGGFG 240
DB 564 EADKKKVLDCQEVISWLDANTLAEKDFEHKRELEQVNCNPIISGLYQAGGPGGFG 623

QY 241 AQQPKGSGSGPTIEVD 258
DB 624 AQQPKGSGSGPTIEVD 641

RESULT 2

A29160
dnaK-type molecular chaperone HSPALL - human
N:Alternate names: heat shock protein, 70K
C:Species: Homo sapiens (man)
C>Date: 16-Aug-1988 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: A29160; I37561; I37562
R:Hunt, C.; Morimoto, R.I.
Proc. Natl. Acad. Sci. U.S.A. 82, 6455-6459, 1985
A:Title: Conserved features of eukaryotic hsp70 genes revealed by comparison with the nu
A:Reference number: A29160; MUID:86016721; PMID:3931075
A:Accession: A29160
A:Molecule type: DNA
A:Residues: 1-640 <HUN>
A:Note: the authors mistranslated residues 463, 491, and 492
R:Drabent, B.; Genthe, A.; Benecke, B.J.
Nucleic Acids Res. 14, 8933-8948, 1986
A:Title: In vitro transcription of a human hsp 70 heat shock gene by extracts prepared f
A:Reference number: I37561; MUID:87066768; PMID:3786141
A:Accession: I37561
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-22 <RES>

A:Cross-references: EMBL:X04676; NID:g32480; PIDN:CAA28381.1; PID:g32481
A:Accession: I37562
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 616-640 <RE2>
A:Cross-references: EMBL:X04677; NID:g32482; PIDN:CAA28382.1; PID:g32483
C:Genetics:
A:Gene: GDB:HSPALL; HSP70-HOM
A:Cross-references: GDB:120058; OMIM:140559
A:Map position: 6p21.3-6p21.3
A:Introns: #status absent
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein comp
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match	98.8%;	Score 1298.5;	DB 2;	Length 640;
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DB 384 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTTYSNQPGLIQVY 443

QY 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
DB 444 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 502

QY 121 TNDKGRLSKEIERMVQEAQYKAEDEVQREVRSKNALESYAFNMKSAVEDEGLKGKIS 180
DB 503 TNDKGRLSKEIERMVQEAQYKAEDEVQREVRSKNALESYAFNMKSAVEDEGLKGKIS 562

QY 181 EADKKKVLDCQEVISWLDANTLAEKDFEHKRELEQVNCNPIISGLYQAGGPGGFG 240
DB 563 EADKKKVLDCQEVISWLDANTLAEKDFEHKRELEQVNCNPIISGLYQAGGPGGFG 622

QY 241 AQQPKGSGSGPTIEVD 258
DB 623 AQQPKGSGSGPTIEVD 640

RESULT 3

S53357
dnaK-type molecular chaperone hsp70 - bovine
N:Alternate names: 70K heat shock protein
C:Species: Bos primigenius taurus (cattle)
C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C:Accession: S53357
R:Gutierrez, J.A.; Guerriero Jr., V.
Biochem. J. 305, 197-203, 1995
A:Title: Chemical modifications of a recombinant bovine stress-inducible 70 kDa heat-sho
A:Reference number: S53357; MUID:95126904; PMID:7826329
A:Accession: S53357
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-641 <GT>
A:Cross-references: UNIPROT:Q27975; EMBL:U09861; NID:g497937; PIDN:AAA73914.1; PID:g49793
C:Genetics:
A:Gene: hsp70
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein comp
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match	98.6%;	Score 1295;	DB 2;	Length 641;
Best Local Similarity	98.8%;	Pred. No. 2.1e-76;		
Matches	255;	Conservative 1;	Mismatches 2;	Indels 0; Gaps 0;

QY 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTTYSNQPGLIQVY 60
DB 384 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTTYSNQPGLIQVY 443

QY 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120

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Db 444 EGERAMTRDNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 503
Qy 121 TNDKGRLSKEIERMVOEAKYKAEDVQRRVRSKNALESYAFNMKSADVEDEGLKGKIS 180
Db 504 TNDKGRLSKEIERMVOEAKYKAEDVQRRVRSKNALESYAFNMKSADVEDEGLKGKIS 563
Qy 181 EADKKKVLDCQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQGAGGPGGFG 240
Db 564 EADKKKVLDCQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQGAGGPGGFG 623
Qy 241 AQPKGGSGSGPTIEEVD 258
Db 624 AQPKGGSGSGPTIEEVD 641

RESULT 4
S31766
dnak-type molecular chaperone hsp70 - green monkey
N;Alternate names: heat shock protein 70
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S31766; I36927
R;Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
submitted to the EMBL Data Library, January 1993
A;Description: Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock protein
A;Reference number: S31766
A;Accession: S31766
A;Molecule type: mRNA
A;Residues: 1-638 <SAI>
A;Cross-references: UNIPROT:Q28222
R;Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
FEBS Lett. 355, 282-286, 1994
A;Title: The hsc70 gene which is slightly induced by heat is the main virus inducible me
A;Reference number: I36927; MUID:95080396; PMID:7988690
A;Accession: I36927
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-638 <RES>
A;Cross-references: EMBL:X70684; NID:g22781; PIDN:CAA50019.1; PID:g22782
A;Experimental source: kidney; cell line COS-1
C;Genetics:
A;Gene: hsp70
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein compl
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
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Best Local Similarity 98.1%; Pred. NO. 2.1e-75;
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Qy 1 KSENVQDLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQITFTTYSNDQPGVLQVY 60
Db 382 KSENVQDLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQITFTTYSNDQPGVLQVY 441
Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 442 EGERAMTKDNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 500
Qy 121 TNDKGRLSKEIERMVOEAKYKAEDVQRRVRSKNALESYAFNMKSADVEDEGLKGKIS 180
Db 501 TNDKGRLSKEIERMVOEAKYKAEDVQRRVRSKNALESYAFNMKSADVEDEGLKGKIS 560
Qy 181 EADKKKVLDCQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQGAGGPGGFG 240
Db 561 EADKKKVLDCQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQGAGGPGGFG 620
Qy 241 AQPKGGSGSGPTIEEVD 258
Db 621 AQPKGGSGSGPTIEEVD 638
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RESULT 5
S35718
dnak-type molecular chaperone hsp70 - pig
N;Alternate names: heat shock protein hsp70
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 09-Dec-1993 #sequence_revision 28-May-1995 #text_change 09-Jul-2004
C;Accession: S35718
R;Peelman, L.J.; van de Weghe, A.R.; Coppieters, W.R.; Van Zeveren, A.J.; Bouquet, Y.H.
Immunogenetics 35, 286-289, 1992
A;Title: Complete nucleotide sequence of a porcine HSP70 gene.
A;Reference number: S35718; MUID:92175874; PMID:1339404
A;Accession: S35718
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-641 <PBE>
A;Cross-references: UNIPROT:P34930; EMBL:M69100
C;Genetics:
A;Gene: hsp70
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein compl
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 97.3%; Score 1279; DB 2; Length 641;
Best Local Similarity 97.3%; Pred. NO. 2.3e-75;
Matches 251; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy 1 KSENVQDLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQITFTTYSNDQPGVLQVY 60
Db 384 KSENVQDLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQITFTTYSNDQPGVLQVY 443
Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKDNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 503
Qy 121 TNDKGRLSKEIERMVOEAKYKAEDVQRRVRSKNALESYAFNMKSADVEDEGLKGKIS 180
Db 504 TNDKGRLSKEIERMVOEAKYKAEDVQRRVRSKNALESYAFNMKSADVEDEGLKGKIS 563
Qy 181 EADKKKVLDCQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQGAGGPGGFG 240
Db 564 EADKKKVLDCQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQGAGGPGGFG 623
Qy 241 AQPKGGSGSGPTIEEVD 258
Db 624 APDLKGGSGSGPTIEEVD 641

RESULT 6
I54542
dnak-type molecular chaperone HSP70 - rat
N;Alternate names: dnak-type molecular chaperone HSP70ib; heat shock protein 70
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I54542; I68986; S43388; S47522; I56574; S35955; S38199; S41413; S41414
R;Walter, L.; Rauh, F.; Gunther, E.
Immunogenetics 40, 325-330, 1994
A;Title: Comparative analysis of the three major histocompatibility complex-linked heat
A;Reference number: I54542; MUID:95012453; PMID:7927536
A;Accession: I54542
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-641 <WAL1>
A;Cross-references: UNIPROT:Q07439; UNIPROT:Q63256; EMBL:X77207; NID:g1814000; PIDN:CAA5
A;Experimental source: HSP70.1
A;Genetics: HSP1
A;Accession: I68986
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-641 <WAL2>
A;Cross-references: EMBL:X77208; NID:g927512; PIDN:CAA54423.1; PID:g450932
A;Experimental source: HSP70.2
A;Genetics: HSP2
```

R;Mestrlil, R.; Chi, S.H.; Sayen, M.R.; Dillmann, W.H.
Biochem. J. 298, 561-569, 1994
A;Title: Isolation of a novel inducible rat heat-shock protein (HSP70) gene and its expression
A;Reference number: S43388; MUID:94190258; PMID:8141767
A;Accession: S43388
A;Molecule type: DNA
A;Residues: 1-70; NG, 73-109, 'K', 111-203, 'R', 205-261, 'P', 263, 'ADGV', 268-641 <MES>
A;Cross-references: EMBL:X75357; NID:9407163; PIDN:CAA53140.1; PID:9407164
A;Experimental source: ischaemic rat heart
R;Lisowska, K.; Widlak, W.; Krawczyk, Z.; Wolniczek, P.; Wisniewski, J.
Biochim. Biophys. Acta 1219, 64-72, 1994
A;Title: Cloning, nucleotide sequence and expression of rat heat inducible hsp70 gene.
A;Reference number: S47522; MUID:94368874; PMID:8086479
A;Accession: S47522
A;Molecule type: DNA
A;Residues: 1-70; NG, 73-407, 'A', 409-641 <LIS>
A;Cross-references: EMBL:X74271; NID:93413499; PIDN:CAA52328.1; PID:9396270
A;Note: the authors translated the codon CCG for residue 365 as Asp
R;Longo, F.M.; Wang, S.; Narasimhan, P.; Zhang, J.S.; Chen, J.; Massa, S.M.; Sharp, F.R.
J. Neurosci. Res. 36, 325-335, 1993
A;Title: cDNA cloning and expression of stress-inducible rat hsp70 in normal and injured
A;Reference number: I56574; MUID:94096443; PMID:8271311
A;Accession: I56574
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-226, 'D', 228-641 <LON>
A;Cross-references: GB:L16764; NID:9294567; PIDN:AAA17441.1; PID:9294568
C;Genetics: <HSP1>
A;Gene: hsp70.1
C;Genetics: <HSP2>
A;Gene: hsp70.2
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
A;Superfamily: heat shock protein 70
C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 95.7%; Score 1258; DB 2; Length 641;
Best Local Similarity 95.3%; Pred. No. 5.2e-74;
Matches 246; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRSTIPTKTQTQTFYTSNQPGLVQVY 60
Db 384 KSENVQDLLLDVAPLSGLGTAGVMTALIKRSTIPTKTQTQTFYTSNQPGLVQVY 443
Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVQPEVTFDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKNNLLGRFELSGIPPPAPRGVQPEVTFDANGILNVTATDKSTGKANKITI 503
Qy 121 TNDKGRLSKEIERMVQEAERYKAEDVQRRVSAKNALSYAFNMKSAVEDEGLGKGIS 180
Db 504 TNDKGRLSKEIERMVQEAERYKAEDVQRRVSAKNALSYAFNMKSAVEDEGLGKGIS 563
Qy 181 EADKKKVLDCQEVISWLDANTLAKEDEFHKKELQVNCNPIISGLYQAGGPGGFG 240
Db 564 EADKKKVLDCQEVISWLDANTLAKEDEFHKKELQVNCNPIISGLYQAGGPGGFG 623
Qy 241 AQPCKGSGSGPTIEVD 258
Db 624 AQPCKGSGSGPTIEVD 641

RESULT 7
JH0095
dnak-type molecular chaperone hsp70 - mouse
N;Alternate names: heat shock protein 70
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 20-Aug-1999
C;Accession: JH0095
R;Hunt, C.; Calderwood, S.
Gene 87, 199-204, 1990
A;Title: Characterization and sequence of a mouse hsp70 gene and its expression in mouse
A;Reference number: JH0095; MUID:90236310; PMID:2332169
A;Accession: JH0095

A;Molecule type: DNA
A;Residues: 1-642 <HUN>
A;Cross-references: GB:M35021; NID:9194022; PIDN:AAA37864.1; PID:9387211
A;Experimental source: strain A7
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
A;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 93.5%; Score 1228.5; DB 2; Length 642;
Best Local Similarity 93.1%; Pred. No. 4.2e-72;
Matches 241; Conservative 11; Mismatches 6; Indels 1; Gaps 1;

Qy 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRSTIPTKTQTQTFYTSNQPGLVQVY 60
Db 384 KSENVQDLLLDVAPLSGLGTAGVMTALIKRSTIPTKTQTQTFYTSNQPGLVQVY 443
Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVQPEVTFDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKNNLLGRFELSGIPPPAPRGVQPEVTFDANGILNVTATDKSTGKANKITI 503
Qy 121 TNDKGRLSKEIERMVQEAERYKAEDVQRRVSAKNALSYAFNMKSAVEDEGLGKGIS 180
Db 504 TNDKGRLSKEIERMVQEAERYKAEDVQRRVSAKNALSYAFNMKSAVEDEGLGKGIS 563
Qy 181 EADKKKVLDCQEVISWLDANTLAKEDEFHKKELQVNCNPIISGLYQAGGPGGFG 240
Db 564 EADKKKVLDCQEVISWLDANTLAKEDEFHKKELQVNCNPIISGLYQAGGPGGFG 623
Qy 241 AQPCKGSGSGPTIEVD 258
Db 624 AQPCKGSGSGPTIEVD 642

RESULT 8
A26283
dnak-type molecular chaperone - mouse (fragment)
N;Alternate names: heat shock protein 68
C;Species: Mus musculus (house mouse)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C;Accession: A26283
R;Lowie, D.G.; Moran, L.A.
J. Biol. Chem. 261, 2102-2112, 1986
A;Title: Molecular cloning and analysis of DNA complementary to three mouse Mr=68,000 he
A;Reference number: A26283; MUID:86111900; PMID:2868009
A;Accession: A26283
A;Molecule type: mRNA
A;Residues: 1-420 <LOW>
A;Cross-references: UNIPROT:Q61696; GB:M12571; NID:9194014; PIDN:AAA57234.1; PID:9387208
A;Note: the authors translated the codon CTG for residue 173 as Val and CGC for residue
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
A;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 92.5%; Score 1216; DB 2; Length 420;
Best Local Similarity 91.9%; Pred. No. 1.6e-71;
Matches 237; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRSTIPTKTQTQTFYTSNQPGLVQVY 60
Db 163 KSENVQDLLLDVAPLSGLGTAGVMTARQANSTIPTKTQTQTFYTSNQPGLVQVY 222
Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVQPEVTFDANGILNVTATDKSTGKANKITI 120
Db 223 EGERAMTKNNLLGRFELSGIPPPAPRGVQPEVTFDANGILNVTATDKSTGKANKITI 282
Qy 121 TNDKGRLSKEIERMVQEAERYKAEDVQRRVSAKNALSYAFNMKSAVEDEGLGKGIS 180
Db 283 TNDKGRLSKEIERMVQEAERYKAEDVQRRVSAKNALSYAFNMKSAVEDEGLGKGIS 342
Qy 181 EADKKKVLDCQEVISWLDANTLAKEDEFHKKELQVNCNPIISGLYQAGGPGGFG 240
Db 624 AQPCKGSGSGPTIEVD 642

Db 624 GPPGGAPPSSGASGPTIEVD 646

RESULT 12

S07197
 dnak-type molecular chaperone hsc73 - rat
 N;Alternate names: heat shock cognate protein hsc70; heat shock cognate protein hsc73
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004
 C;Accession: S07197; I57594; S35606
 R;Singer, P.K.; Pelham, H.R.B.
 EMBO J. 6, 993-998, 1987
 A;Title: Cloning and expression of a gene encoding hsc73, the major hsp70-like protein
 A;Reference number: S07197; MUID:87246537; PMID:3595567
 A;Accession: S07197
 A;Molecule type: DNA
 A;Residues: 1-646 <SOR>
 A;Cross-references: UNIPROT:P08109; EMBL:Y00054; NID:956378; PIDN:CAA69265.1; PID:G56379
 R;O'Malley, K.; Maunon, A.; Barchas, J.D.; Kedes, L.
 Mol. Cell. Biol. 5, 3476-3483, 1985
 A;Title: Constitutively expressed rat mRNA encoding a 70-kilodalton heat-shock-like protein
 A;Reference number: I57594; MUID:86310827; PMID:3939319
 A;Accession: I57594
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-646 <RES>
 A;Cross-references: GB:M11942; NID:G204666; PIDN:AAA41354.1; PID:G204667
 R;Wang, C.; Lee, M.R.
 Biochem. J. 294, 69-77, 1993
 A;Title: High-level expression of soluble rat hsc70 in Escherichia coli: purification and
 A;Reference number: S35606; MUID:93371384; PMID:8363588
 A;Accession: S35606
 A;Molecule type: protein
 A;Residues: 2-40 <WAN>
 C;Genetics:
 A;Gene: hsc73; hsc70
 A;Introns: 137/3; 188/3; 374/1; 441/3; 508/1; 585/3
 C;Function:
 A;Description: involved in protein folding and assembling/disassembling of protein comp
 C;Superfamily: heat shock protein 70
 C;Keywords: ATP; molecular chaperone
 F;2-646/Product: dnak-type molecular chaperone hsc73 #status experimental <MAT>
 Query Match 83.8%; Score 1100.5; DB 2; Length 646;
 Best Local Similarity 81.7%; Pred. No. 8.2e-64;
 Matches 215; Conservative 23; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTIPTKTQTFTTYSNQPGLVQY 60
 DB 384 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNTTPTKTQTFTTYSNQPGLVQY 443
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 444 EGERAMTKNNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 503
 QY 121 TNDKRLSKKEIERVQAEKYKAEDEVQRRVSAKNALESYAFNMKSAVEDSLGKGIS 180
 DB 504 TNDKRLSKEDIERNVQAEKYKAEDEVQRRVSAKNSLESYAFNMKATVDEKLGKIN 563
 QY 181 EADKKKVLDCQEVISWLDANTLAERKDEFEHKELEQVCPNPIISGLYQAGGPG--PG 237
 DB 564 DEDKOKILDKCNEIISWLDKNTAEKBEFEHQKELEKVCNPIITKLYQSAGGPGGMPG 623
 QY 238 GF--GAQPKGSGSGPTIEVD 258
 DB 624 GPPGGAPPSSGASGPTIEVD 646

RESULT 13

B45871
 dnak-type molecular chaperone HSP70-Hom - human
 N;Alternate names: heat shock protein HSP70-Hom
 C;Species: Homo sapiens (man)

C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
 C;Accession: B45871
 R;Milner, C.M.; Campbell, R.D.
 Immunogenetics 32, 242-251, 1990
 A;Title: Structure and expression of the three MHC-linked HSP70 genes.
 A;Reference number: A45871; MUID:91055806; PMID:1700760
 A;Accession: B45871
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-641 <MIL>
 A;Cross-references: UNIPROT:P34931; GB:M59829; GB:M34268; NID:9188491; PIDN:AAA63228.1;
 C;Function:
 A;Description: involved in protein folding and assembling/disassembling of protein comp
 C;Superfamily: heat shock protein 70
 C;Keywords: ATP; molecular chaperone

Query Match 83.6%; Score 1099; DB 2; Length 641;
 Best Local Similarity 81.9%; Pred. No. 1e-63;
 Matches 217; Conservative 16; Mismatches 16; Indels 16; Gaps 2;
 QY 1 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTIPTKTQTFTTYSNQPGLVQY 60
 DB 386 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTIPTKTQTFTTYSNQPGLVQY 445
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 446 EGERAMTKNNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 505
 QY 121 TNDKRLSKKEIERVQAEKYKAEDEVQRRVSAKNALESYAFNMKSAVEDSLGKGIS 180
 DB 506 TNDKRLSKKEIERVQAEKYKAEDEVQRRVSAKNALESYAFNMKSVVSDSLGKGIS 565
 QY 181 EADKKKVLDCQEVISWLDANTLAERKDEFEHKELEQVCPNPIISGLYQAGGPGGFG 240
 DB 566 ESDKNKILDKCNELLSWLVNQAEKDFDHKELEQVCPNPIITKLYQG-----G 616
 QY 241 AQGPKGSG-----SGPTIEVD 258
 DB 617 CTGPACGTGYVGRPATGPTIEVD 641

RESULT 14

A27077
 dnak-type molecular chaperone - human
 N;Alternate names: heat shock cognate protein 70
 C;Species: Homo sapiens (man)
 C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
 C;Accession: A27077
 R;Dorniczak, B.; Mirault, M.E.
 Nucleic Acids Res. 15, 5181-5197, 1987
 A;Title: Structure and expression of a human gene coding for a 71 kd heat shock 'cognate
 A;Reference number: A27077; MUID:87259994; PMID:3037489
 A;Accession: A27077
 A;Molecule type: DNA
 A;Residues: 1-646 <DMO>
 A;Cross-references: UNIPROT:P11142; GB:M19141
 C;Genetics:
 A;Introns: 69/1; 137/3; 188/3; 374/1; 441/3; 508/1; 585/3
 C;Function:
 A;Description: involved in protein folding and assembling/disassembling of protein comp
 C;Superfamily: heat shock protein 70
 C;Keywords: ATP; molecular chaperone

Query Match 83.5%; Score 1097.5; DB 2; Length 646;
 Best Local Similarity 81.4%; Pred. No. 1.3e-63;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTIPTKTQTFTTYSNQPGLVQY 60
 DB 384 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNTTPTKTQTFTTYSNQPGLVQY 443
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 120

Qy	121	TNDKGRLSKEEIERMVMQEAKEYKAEDVQRERSAKNALESYAFNMKSVAVEDGLKGKIS	180
Dd	504	TNDKGRLSKEDIERMVMQEAKEYKAEDVKQDKYSSKNLSLEYAFNMKVATVEDEKLQKIN	563
Qy	181	EADKKVKLDKCQEVISWLDANTLAEKDEFHKKRKELEVCNPIISGIYQGAGG-PG--PG	237
Dd	564	DEUQKILDKNCNEIISWLDKCNQTAEKEEPHQKLEKVCNPIITKLYQSAGMGPMGP	623
Qy	238	GF--GAQGPKGSGSGPTTIEVD	258
Dd	624	GFPGGAPPSSGASSGPTTIEVD	646

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RESULT 16
I49761
dnak-type molecular chaperone Hsc70t - mouse
N;Alternate names: heat shock protein 70
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I49761
R;Snoek, M.; Olavesen, M.G.; van Vugt, H.; Milner, C.M.; Teuscher, C.; Campbell
Immunogenetics 40, 159-162, 1994
A;Title: Coding sequences and levels of expression of Hsc70t are identical in m
A;Reference number: I49761; MUID:94299288; PMID:8026864
A;Accession: I49761
A;Status: preliminary; translated from GB/EMBL/DBEY
A;Molecule type: DNA
A;Residues: 1-641 <RES>
A;Cross-references: UNIPROT:P16627; GB:L27086; NID:g457299; PIDN:AAA59362.1; PIII
C;Genetics:
A;Gene: Hsc70t
C;Function:
A;Description: involved in protein folding and assembling/disassembling of prot
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match      83.1%; Score 1092; DB 2; Length 641;
Best Local Similarity 84.5%; Pred. No. 2.9e-63;
Matches 218; Conservative 17; Mismatches 21; Indels 2; Gaps 2;

Qy      1 KSENVODLLLDVAPLSIGLETAGGVMTALIKENSTIPKQTQIFITYSDNQPGVLIOVY 60
Db      386 KSEKVDLLLDVAPLSGLGTAGGVMTVLIRKNSITPKQTQIFITYSDNQPGVLIOVY 445

Qy      61 EGERAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATATDKSTCKANKITI 120
Db      446 EGERAMTRDNLLGRFDLTGIPAPRGVPQIEVTFDIDANGILNVATAMDKSTCKANKITI 505

Qy      121 TNDKGLSKETETRMVQEAKEYKAEDVEQRRVSAAKNALESYAFNMKSAVEDGLKGKIS 180
Db      506 TNDKGLSKETETRMVQEAERYKAEDGQREKTAANKNALESYAFNMKSAVGDEGLKDKIS 565

Qy      181 EADKKVLDKCOBVISWLDANTLAEKDEPEHKRKELEQVCNPIISGLYOGAGGPGGFG 240
Db      566 ESDKKILDKCNELVSWLEANQLAEKDEFHKKRELENWCNPIITKLYQ-SGCTGTCTP 624

Qy      241 AOGPKCGSGSGPTIEVD 258
Db      625 GYTP-GRAATGPTIEVD 641

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RESULT 17
S11456
dnak-type molecular chaperone hsc70 - bovine
N;Alternate names: heat shock cognate protein, 79K
C;Species: Bos primigenius taurus (cattle)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S11456
R;DeLucca-Flaherty, C.; McKay, D.B.
Nucleic Acids Res. 18, 5569, 1990
A;Title: Nucleotide sequence of the cDNA of a bovine 70 kilodalton heat shock
A;Reference number: S11456; MUID:91016866; PMID:2216746

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A:Accession: S11456
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-650
A:Cross-references: UNIPROT:P19120; EMBL:X53827; NID:g427; PIDN:CAA37823.1; PID:g428
C:Genetics:
A:Gene: hsc70
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein complex
A:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match 83.1%; Score 1091.5; DB 2; Length 650;
Best Local Similarity 79.8%; Pred. No. 3.2e-63;
Matches 213; Conservative 25; Mismatches 20; Indels 9; Gaps 3;

Qy 1 KSENVQDLLLLDVAPLSGLTAGGVTMLIKENSTPTKQTQITFTTYSNQPGLVIOY 60
Db 384 KSENVQDLLLLDVTPLSGLTAGGVTMLIKRNTTPTKQTQITFTTYSNQPGLVIOY 443

Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTKDNNLLGKFLTGIPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503

Qy 121 TNDKGRLSKEIERMWQEAERKKAEDVQERVSAAKNALESYAFNMKSASAVEDEGLKQKIS 180
Db 504 TNDKGRLSKEDIERMWQEAERKKAEDKQDKVSKNSLSKSYAFNMKATVDEDEKLQKIN 563

Qy 181 EADKKVKLDKQCVISWLDANTLAEDFEHKKELBOVCNPIISGLYQ-QAGGP-----PG 235
Db 564 DEDKQKILDKCNEIINWLDKNQTAKEBEFHQKELEKVCNPIITKLYQSAGGMPGMPG 623

Qy 236 --PGGP--GAQPGKGGSGPTIEVD 258
Db 624 GMPGGFPGGAPPSSGASSGPTIEVD 650

RESULT 18
S41415
dnaK-type molecular chaperone Hsp70.3 - rat
N:Alternate names: heat shock protein 70
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S41415; I68987
R:Lutz, W.
submitted to the EMBL Data Library, January 1994
A:Reference number: S41413
A:Accession: S41415
A:Molecule type: DNA
A:Residues: 1-641 <LUT>
A:Cross-references: UNIPROT:P55063; EMBL:X77209; NID:g1814002; PIDN:CAA54424.1; PID:g450
R:Walter, L.; Rauh, F.; Gunther, E.
Immunogenetics 40, 325-330, 1994
A:Title: Comparative analysis of the three major histocompatibility complex-linked heat
A:Reference number: 154542; MUID:95012453; PMID:7927536
A:Accession: I68987
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-641 <RES>
A:Cross-references: EMBL:X77209; NID:g1814002; PIDN:CAA54424.1; PID:g450934
C:Genetics:
A:Gene: Hsp70-3
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein complex
A:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match 82.7%; Score 1087; DB 2; Length 641;
Best Local Similarity 83.5%; Pred. No. 6.1e-63;
Matches 218; Conservative 17; Mismatches 19; Indels 8; Gaps 3;

Qy 1 KSENVQDLLLLDVAPLSGLTAGGVTMLIKENSTPTKQTQITFTTYSNQPGLVIOY 60
Db 384 KSENVQDLLLLDVTPLSGLTAGGVTMLIKRNTTPTKQTQITFTTYSNQPGLVIOY 443

Db 386 KSEKVDLLLLDVAPLSGLTAGGVTMLIKENSTPTKQTQITFTTYSNQPGLVIOY 445

Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 446 EGERAMTRDNNLLGRFDLTGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 505

Qy 121 TNDKGRLSKEIERMWQEAERKKAEDVQERVSAAKNALESYAFNMKSASAVEDEGLKQKIS 180
Db 506 TNDKGRLSKEIERMWQEAERKKAEDGQREKTAANKNALESYAFNMKSASAVGDEGLKQKIS 565

Qy 181 EADKKVKLDKQCVISWLDANTLAEDFEHKKELBOVCNPIISGLYQ-QAGGP--GPG 237
Db 566 ESDKKILDKCSEVLWLANQAEKEEFHKKELNMCNPIITKLYQSAGGMPGMPG 625

Qy 238 GFGAQPCKGSGSGPTIEVD 258
Db 626 -----YTPGRARTGPTIEVD 641

RESULT 19
S21175
dnaK-type molecular chaperone hsc71 - rainbow trout
N:Alternate names: heat shock cognate protein 71
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S21175
R:Zafarullah, M.; Wisniewski, J.; Shworak, N.W.; Schieman, S.; Misra, S.; Gedamu, L.
Eur. J. Biochem. 204, 893-900, 1992
A:Title: Molecular cloning and characterization of a constitutively expressed heat-shock
A:Reference number: S21175; MUID:92174952; PMID:1371753
A:Accession: S21175
A:Molecule type: DNA
A:Residues: 1-651 <ZAF>
A:Cross-references: UNIPROT:P08108; EMBL:S85730; NID:g246718; PIDN:AAB21658.1; PID:g24671
C:Genetics:
A:Gene: hsc71
A:Introns: 69/1; 137/3; 188/3; 374/1; 441/3; 508/1; 585/3
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein complex
A:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match 82.5%; Score 1084; DB 2; Length 651;
Best Local Similarity 79.5%; Pred. No. 9.7e-63;
Matches 213; Conservative 21; Mismatches 24; Indels 10; Gaps 3;

Qy 1 KSENVQDLLLLDVAPLSGLTAGGVTMLIKENSTPTKQTQITFTTYSNQPGLVIOY 60
Db 384 KSENVQDLLLLDVTPLSGLTAGGVTMLIKRNTTPTKQTQITFTTYSNQPGLVIOY 443

Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTKDNNLLGKFLTGIPAPRGVPOIEVTFDIDANGIMNVSAADKSTGKANKITI 503

Qy 121 TNDKGRLSKEIERMWQEAERKKAEDVQERVSAAKNALESYAFNMKSASAVEDEGLKQKIS 180
Db 504 TNDKGRLSKEDIERMWQEAERKKAEDVDQDKVSKNSLSKSYAFNMKSTVDEDEKLQKIS 563

Qy 181 EADKKVKLDKQCVISWLDANTLAEDFEHKKELBOVCNPIISGLYQAGG--PG---- 235
Db 564 DEDKTKLEKNEIINWLDKNQTAKEEYEHQKELEKVCNPIITKLYQSAGGMPGMPG 623

Qy 236 --PGGP---GAQPGKGGSGSGPTIEVD 258
Db 624 GMAGGFPAGGAAPGGGSGSGPTIEVD 651

RESULT 20
A45805
dnaK-type molecular chaperone - nematode (Brugia pahangi) (fragment)
N:Alternate names: heat shock cognate protein 70
C:Species: Brugia pahangi
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C;Accession: A45805
J;Selkirk, M.E.; Denham, D.A.; Partono, F.; Maizels, R.M.
J. Immunol. 143, 299-308, 1989
A;Title: Heat shock cognate 70 is a prominent immunogen in brugian filariasis.
A;Reference number: A45805; MUID:89278663; PMID:2659668
A;Accession: A45805
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-335 <SEL>
A;Cross-references: UNIPROT:Q17267; GB:M26191
A;Note: the authors translated the codon CTG for residue 1 as Arg
C;Function:
A;Description: involved in protein folding and assembling/diseassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 80.9%; Score 1063; DB 2; Length 335;
Best Local Similarity 79.8%; Pred. No. 9.9e-62; Mismatches 29; Indels 4; Gaps 3;
Matches 209; Conservative 20; Mismatches 29; Indels 4; Gaps 3;

Qy 1 KSENVQDLLLDVAPLSIGLETAGGVMTALIKRNSTIPTKTQTQIFTTYSNQPGLVQVY 60
Db 74 KSEAVQDLLLDVAPLSIGLETAGGVMTALIKRNSTIPTKTQTQIFTTYSNQPGLVQVY 133

Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 134 EGERALTKNNLLGKFLSGIPPPAPRGVPEIEVTFDIDANGILNVSADKSTGKQNKITI 193

Qy 121 TNDKGRSLKKEIERMVOEAKYKAEDVQREVRSKNALESYAFNMKSAVEDEGLKGKIS 180
Db 194 TNDKGRSLKKEIERMVOEAKYKADDEAQRDIAAKNALESYAFNMKQTIIDEKLGKDKIS 253

Qy 181 EADKKVKLDKQEVISWLDANTLAEDFEHHRKELEQVNCNPIISGLYQGAGG-PG--PG 237
Db 254 EEDKKIKQEKDEIVRWLDGNQTAEDFEHHRKELESVCNPIITKLQYQAGGMPGMPG 313

Qy 238 GFAGQAGPKGGS-GSGPTIEVD 258
Db 314 GMPGAPGAGSTGGPTIEVD 335

RESULT 21
A45635
dnak-type molecular chaperone BmhsA - nematode (Brugia malayi)
N;Alternate names: heat shock protein homolog BmhsA
C;Species: Brugia malayi
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A45635
R;Rothstein, N.; Rajan, T.V.
Mol. Biochem. Parasitol. 49, 229-237, 1991
A;Title: Characterization of an hsp70 gene from the human filarial parasite, Brugia mal
A;Reference number: A45635; MUID:92131059; PMID:1775166
A;Accession: A45635
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-644 <ROT>
A;Cross-references: UNIPROT:P27541; GB:M68933; NID:g156069; PIDN:AAC17926.1; PID:g156070
A;Note: sequence extracted from NCBI backbone (NCBIN:77613, NCBI:P:77616)
C;Genetics:
A;Gene: BmhsA
C;Function:
A;Description: involved in protein folding and assembling/diseassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 80.9%; Score 1063; DB 2; Length 644;
Best Local Similarity 79.8%; Pred. No. 2.2e-61; Mismatches 29; Indels 4; Gaps 3;
Matches 209; Conservative 20; Mismatches 29; Indels 4; Gaps 3;

Qy 1 KSENVQDLLLDVAPLSIGLETAGGVMTALIKRNSTIPTKTQTQIFTTYSNQPGLVQVY 60
Db 383 KSEAVQDLLLDVAPLSIGLETAGGVMTALIKRNSTIPTKTSETFTTYSNQPGLVQVY 442

Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 443 EGERALTKNNLLGKFLSGIPPPAPRGVPOIEVTFDIDANGILNVSADKSTGKQNKITI 502

Qy 121 TNDKGRSLKKEIERMVOEAKYKAEDVQREVRSKNALESYAFNMKSAVEDEGLKGKIS 180
Db 503 TNDKGRSLKKEIERMVOEAKYKADDEAQRDIAAKNALESYAFNMKQTIIDEKLGKDKIS 562

Qy 181 EADKKVKLDKQEVISWLDANTLAEDFEHHRKELEQVNCNPIISGLYQGAGG-PG--PG 237
Db 563 EEDKKIKQEKDEIVRWLDGNQTAEDFEHHRKELESVCNPIITKLQYQAGGMPGMPG 622

Qy 238 GFAGQAGPKGGS-GSGPTIEVD 258
Db 623 GMPGAPGAGSTGGPTIEVD 644

RESULT 22
A55719
dnak-type molecular chaperone HSPA2 - human
N;Alternate names: heat shock protein A2
C;Species: Homo sapiens (man)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: A55719
R;Bonnycastle, L.L.C.; Yu, C.B.; Hunt, C.R.; Trask, B.J.; Clancy, K.P.; Weber, J.L.; Pat
Genomics 23, 85-93, 1994
A;Title: Cloning, sequencing, and mapping of the human chromosome 14 heat shock protein
A;Reference number: A55719; MUID:95130116; PMID:7829106
A;Accession: A55719
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-639 <BON>
A;Cross-references: UNIPROT:P54652; GB:L26336; NID:g476704; PIDN:AAA52698.1; PID:g476705
C;Genetics:
A;Gene: GDB:HSPA2
A;Cross-references: GDB:120059; OMIM:140560
A;Map position: 14q22-14q22
A;Introns: #status absent
C;Function:
A;Description: involved in protein folding and assembling/diseassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 80.6%; Score 1059.5; DB 2; Length 639;
Best Local Similarity 79.1%; Pred. No. 3.7e-61; Mismatches 25; Indels 5; Gaps 1;
Matches 204; Conservative 24; Mismatches 25; Indels 5; Gaps 1;

Qy 1 KSENVQDLLLDVAPLSIGLETAGGVMTALIKRNSTIPTKTQTQIFTTYSNQPGLVQVY 60
Db 387 KSENVQDLLLDVTPLSIGLETAGGVMTPLIKRNTTPTKTQTQIFTTYSNQSGLVQVY 446

Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 447 EGERAMTKNNLLGKFLDTGTIPPPAPRGVPOIEVTFDIDANGILNVTADKSTGKANKITI 506

Qy 121 TNDKGRSLKKEIERMVOEAKYKAEDVQREVRSKNALESYAFNMKSAVEDEGLKGKIS 180
Db 507 TNDKGRSLKDDIDRMVQEAERYKSEDEANRVAAKNALESYTYNIRKQTVDEKLGKIS 566

Qy 181 EADKKVKLDKQEVISWLDANTLAEDFEHHRKELEQVNCNPIISGLYQGAGGPGPG 240
Db 567 EQDKNKILDKQEVINWLDNRQNAEKDEYEHKQELERVNCNPIISKLQYQGGPGGGGG 626

Qy 241 AQGPKGSGSGPTIEVD 258
Db 627 S-----GASGPTIEVD 639

RESULT 23
I51129
dnak-type molecular chaperone hsp70 - Iberian ribbed newt
N;Alternate names: heat shock protein HSP70
C;Species: Pleurodeles waltlil (Iberian ribbed newt)

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C;Accession: I51129
 R;Billoud, B.; Rodriguez-Martin, M.L.; Berard, L.; Moreau, N.; Angelier, N.
 Development 119, 921-932, 1993
 A;Title: Constitutive expression of a somatic heat-inducible hsp70 gene during amphibian
 A;Reference number: I51129; MUID:94244484; PMID:8187647
 A;Accession: I51129
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-645 <BL>
 A;Cross-references: UNIPROT:Q91291; EMBL:X71951; NID:9431200; PIDN:CAA50749.1; PID:94312
 C;Genetics:
 A;Gene: hsp70
 C;Function:
 A;Description: involved in protein folding and assembling/disassembling of protein comp
 C;Superfamily: heat shock protein 70
 C;Keywords: ATP; molecular chaperone

Query Match 80.5%; Score 1058; DB 2; Length 645;
 Best Local Similarity 79.6%; Pred. No. 4.6e-61;
 Matches 207; Conservative 24; Mismatches 27; Indels 2; Gaps 1;

Qy 1 KSENVQDLLLDVAPLSGLGTAGGVTALIKRNTTPTKQTQTFITYSDNQPGVLQVY 60
 Db 386 KSENVQDLLLDVAPLSGLGTAGGVTALIKRNTTPTKQTQTFITYSDNQPGVLQVY 445

Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
 Db 446 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 505

Qy 121 TNDKGRLSKEIERMVQEAERYKAEDVQERVSANNALESYAFNMKSAVEDGLKGIS 180
 Db 446 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 505

Qy 506 TNDKGRLSKEIERMVQEAERYKAEDVQERVSANNALESYAFNMKSAVEDGLKGIS 565
 Db 506 TNDKGRLSKEIERMVQEAERYKAEDVQERVSANNALESYAFNMKSAVEDGLKGIS 565

Qy 181 EADKKVLDKQEVISWLDANTLAEDFPHKKELEQVNCNPIISGLYQAGGPGGFG 238
 Db 566 EDDKKIVDKQNTISWNNMAEKEEYHQKELEKVCNIIITKLYQGMPGMPGSGS 625

Qy 239 FGAQPKGGSGSGPTIEVD 258
 Db 626 SGAQARQSSSTGTIEVD 645

RESULT 24
 S10859
 dnak-type molecular chaperone HSP70.2 - mouse
 N;Alternate names: heat shock protein 70.2
 C;Species: Mus musculus (house mouse)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 30-Jan-1998
 C;Accession: S10859
 R;Zakeri, Z.F.; Wolgemuth, D.J.; Hunt, C.R.
 Mol. Cell. Biol. 8, 2925-2932, 1988
 A;Title: Identification and sequence analysis of a new member of the mouse HSP70 gene fa
 A;Reference number: S10859; MUID:88302212; PMID:3405224
 A;Accession: S10859
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-633 <ZAK>
 A;Cross-references: EMBL:M20567
 C;Genetics:
 A;Gene: HSP70.2
 C;Function:
 A;Description: involved in protein folding and assembling/disassembling of protein comp
 C;Superfamily: heat shock protein 70
 C;Keywords: ATP; molecular chaperone

Query Match 80.3%; Score 1054.5; DB 2; Length 633;
 Best Local Similarity 79.1%; Pred. NO. 7.6e-61;
 Matches 204; Conservative 23; Mismatches 20; Indels 11; Gaps 2;

Qy 1 KSENVQDLLLDVAPLSGLGTAGGVTALIKRNTTPTKQTQTFITYSDNQPGVLQVY 60

Db 387 KSENVQDLLLDVTPLSGLGTAGGVTALIKRNTTPTKQTQTFITYSDNQSVLVQVY 446
 Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
 Db 447 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 506
 Qy 121 TNDKGRLSKEIERMVQEAERYKAEDVQERVSANNALESYAFNMKSAVEDGLKGIS 180
 Db 507 TNDKGRLSKEIERMVQEAERYKAEDVQERVSANNALESYAFNMKSAVEDGLKGIS 566

Qy 181 EADKKVLDKQEVISWLDANTLAEDFPHKKELEQVNCNPIISGLYQAGGPGGFG 240
 Db 567 EDDKKIVDKQEVISWLDANTLAEDFPHKKELEQVNCNPIISGLYQAGGPGGFG 620

Qy 241 AQPCKGGSGSGPTIEVD 258
 Db 621 -----GSSGSGPTIEVD 633

RESULT 25
 A25646
 dnak-type molecular chaperone - chicken
 N;Alternate names: heat shock protein 70
 C;Species: Gallus gallus (chicken)
 C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
 C;Accession: A25646
 R;Morimoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.
 J. Biol. Chem. 261, 12692-12699, 1986
 A;Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 gene.
 A;Reference number: A25646; MUID:86304452; PMID:3017985
 A;Accession: A25646
 A;Molecule type: DNA
 A;Residues: 1-634 <MOR>
 A;Cross-references: UNIPROT:P08106; GB:J02579; NID:G211940; PIDN:AAA48825.1; PID:G211941
 A;Note: the authors translated the codon TCG for residue 583 as TTP
 C;Function:
 A;Description: involved in protein folding and assembling/disassembling of protein comp
 C;Superfamily: heat shock protein 70
 C;Keywords: ATP; molecular chaperone

Query Match 79.9%; Score 1050; DB 2; Length 634;
 Best Local Similarity 79.1%; Pred. No. 1.5e-60;
 Matches 204; Conservative 23; Mismatches 21; Indels 10; Gaps 1;

Qy 1 KSENVQDLLLDVAPLSGLGTAGGVTALIKRNTTPTKQTQTFITYSDNQPGVLQVY 60
 Db 387 KSENVQDLLLDVTPLSGLGTAGGVTALIKRNTTPTKQTQTFITYSDNQSVLVQVY 446

Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
 Db 447 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 506

Qy 121 TNDKGRLSKEIERMVQEAERYKAEDVQERVSANNALESYAFNMKSAVEDGLKGIS 180
 Db 507 TNDKGRLSKEIERMVQEAERYKAEDVQERVSANNALESYAFNMKSAVEDGLKGIS 566

Qy 181 EADKKVLDKQEVISWLDANTLAEDFPHKKELEQVNCNPIISGLYQAGGPGGFG 240
 Db 567 DODKQVLDKQEVISWLDANTLAEDFPHKKELEQVNCNPIISGLYQAGGPGGFG 626

Qy 241 AQPCKGGSGSGPTIEVD 258
 Db 627 -----GPTIEVD 634

RESULT 26
 T43724
 dnak-type molecular chaperone [imported] - Japanese flounder
 N;Alternate names: HSP70
 C;Species: Paralichthys olivaceus (Japanese flounder)
 C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
 C;Accession: T43724
 R;Yokoyama, Y.; Hashimoto, H.; Kubota, S.; Kinoshita, M.; Toyohara, H.; Sakaguchi, M.; T

submitted to the EMBL Data Library, January 1998

Original Match 70 82. Score 1049 E. PB 2. Length 640.

RESULT 27

Query Match 79 78. Score 1047 5. DB 2. Length 633.

181 EADKKKVL.DKCOEVI SWI.DANTI.AEKDFFEEHKPKELFOVCNPTTSGI.YOGAGGPRGGEG 240

A;Accession: A22175

Query Match 78 q1: score 1036 s: DB 1: Length 647:

61 ECEPAMTKNNYIJCPEEISGTPDAPDGPOTEVTEFTDANGTINVTATDKSTGKANKTTT 120

DEFICIT 20

121394

R: Basham. V.: Ainscough. R.

submitted to the EMBL Data Library, September 1996

A;Accession: T21394
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-640 <WTL>
A;Cross-references: UNIPROT:Q93601; EMBL:Z80223; PIDN:CA02319.1; GSPDB:GN00022; CESP:F2
A;Experimental source: clone F26D10
C;Genetics:
A;Gene: CESP:F26D10.3
A;Map position: 4
A;Introns: 69/1; 331/3; 558/3
C;Superfamily: heat shock protein 70

Query Match 78.7%; Score 1034; DB 2; Length 640;
Best Local Similarity 77.9%; Pred. No. 1.6e-59;
Matches 201; Conservative 21; Mismatches 34; Indels 2; Gaps 1;

QY 1 KSENVQDLLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQTFTTYSNQPQGVLIQVY 60
DB 385 KSEAVQDLLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQTFTTYSNQPQGVLIQVY 444

QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVATDSTGKANKITI 120
DB 445 EGERAMTKDNNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVATDSTGKANKITI 504

QY 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSANAKLESYAFNMKSAVEDGLGKGIS 180
DB 505 TNDKGRLSKEDIERNVNEAEKYKADDEAQRDRVAQKNSLEAHVHVHVKSLQESLRDKIP 564

QY 181 EADKKVKLDKQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGGPG 240
DB 565 PEDKKIEDKDEILKWLDSNQTAEKEFEHQKDEGLANPIISGLYQAGGAPP -A 622

QY 241 AQGPKGGSGSGPTIEVD 258
DB 623 APGGAAGAGGPTIEVD 640

RESULT 30
A36333
dnak-type molecular chaperone Hsc70-4 - fruit fly (Drosophila melanogaster)
N;Alternate names: heat shock cognate protein 70
C;Species: Drosophila melanogaster
C;Date: 25-Jan-1991 #sequence_revision 25-Jan-1991 #text_change 09-Jul-2004
C;Accession: A36333
R;Perkins, L.A.; Doctor, J.S.; Zhang, K.; Stinson, L.; Perrimon, N.; Craig, E.A.
Mol. Cell. Biol. 10, 3232-3238, 1990
A;Title: Molecular and developmental characterization of the heat shock cognate 4 gene c
A;Reference number: A36333; MUID:90258915; PMID:2111451
A;Accession: A36333
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-651 <PER>
A;Cross-references: UNIPROT:F11147; GB:M36114; NID:gl57663; PIDN:AAA28627.1; PID:gl57665
C;Genetics:
A;Gene: FlyBase:Hsc70-4
A;Cross-references: FlyBase:FBgn0001219
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone; nucleus

Query Match 77.9%; Score 1023; DB 2; Length 651;
Best Local Similarity 73.5%; Pred. No. 8.7e-59;
Matches 197; Conservative 28; Mismatches 33; Indels 10; Gaps 1;

QY 1 KSENVQDLLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQTFTTYSNQPQGVLIQVY 60
DB 384 KSEAVQDLLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQTFTTYSNQPQGVLIQVY 443

QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVATDSTGKANKITI 120
DB 444 EGERAMTKDNNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVATDSTGKANKITI 503

QY 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSANAKLESYAFNMKSAVEDGLGKGIS 180
DB 504 TNDKGRLSKEDIERNVNEAEKYKADDEAQRDRVAQKNSLEAHVHVHVKSLQESLRDKIP 563

QY 181 EADKKVKLDKQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGGPG----- 235
DB 564 DSDRTTILDKCNETIKWLDANQLADKEVEYHRKELEGVNCNPIITKLYQAGGPPGMPG 623

QY 236 -----PGGFGAQGPKGGSGSGPTIEVD 258
DB 624 GGGGMPGAAGAAGAGGAGGPTIEVD 651

RESULT 31
S09036
dnak-type molecular chaperone HSPA6 - human
N;Alternate names: heat shock protein 70B
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S09036; I37563
R;Leung, T.K.C.; Rajendran, M.Y.; Monfries, C.; Hall, C.; Lim, L.
Biochem. J. 267, 125-132, 1990
A;Title: The human heat-shock protein family. Expression of a novel heat-inducible HSP70
A;Reference number: S09036; MUID:90226304; PMID:2327978
A;Accession: S09036
A;Molecule type: DNA
A;Residues: 1-643 <LEU>
A;Cross-references: UNIPROT:P17066; EMBL:X51757; NID:g35221; PIDN:CAA36061.1; PID:g35222
R;Schiller, P.; Amin, J.; Ananthan, J.; Brown, M.E.; Scott, W.A.; Voellmy, R.
J. Mol. Biol. 203, 97-105, 1988
A;Title: Cis-acting elements involved in the regulated expression of a human HSP70 gene.
A;Reference number: I37563; MUID:89037198; PMID:3184191
A;Accession: I37563
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-6 <RES>
A;Cross-references: EMBL:X13229; NID:g32484; PIDN:CAA31616.1; PID:g579988
C;Genetics:
A;Gene: GDB:HSPA6
A;Cross-references: GDB:127963; OMIM:140555
A;Map position: 1cen-1qter
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 77.0%; Score 1012; DB 2; Length 643;
Best Local Similarity 74.4%; Pred. No. 4.4e-58;
Matches 192; Conservative 33; Mismatches 33; Indels 0; Gaps 0;

QY 1 KSENVQDLLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQTFTTYSNQPQGVLIQVY 60
DB 386 KCEKVQDLLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQTFTTYSNQPQGVLIQVY 445

QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVATDSTGKANKITI 120
DB 446 EGERAMTKDNNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVATDSTGKANKITI 505

QY 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSANAKLESYAFNMKSAVEDGLGKGIS 180
DB 506 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSANAKLESYAFNMKSAVEDGLGKGIS 565

QY 181 EADKKVKLDKQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGGPGGFG 240
DB 566 EEDRRKMDKCREVLAWLEHNQLAKREYEHQKRELEQICRPISRLYGGPGVPGGSSCG 625

QY 241 AQGPKGGSGSGPTIEVD 258
DB 626 TQARQGDPTGTPIIEVD 643

RESULT 32
JC5642

dnak-type molecular chaperone hac70 - Iberian ribbed newt
N;Alternate names: heat shock cognate 70K protein
C;Species: Pleurodeles waltlii (Iberian ribbed newt)
C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 09-Jul-2004
C;Accession: J05642
R;Delellis-Fantien, C.; Penrad-Mobayed, M.; Angelier, N.
Biochem. Biophys. Res. Commun. 238, 159-164, 1997
A;Title: Molecular cloning of a cDNA encoding the amphibian Pleurodeles waltli 70-kDa heat shock protein
A;Reference number: J05642; MUID:97445144; PMID:9299471
A;Accession: J05642
A;Molecule type: mRNA
A;Residues: 1-645
A;Cross-references: UNIPROT:O13120; GB:Y13663; NID:g2196881; PIDN:CAA74012.1; PID:g219688
A;Experimental source: embryo
A;Note: the sequence of residues 8-17 and 18-27 are interchanged in authors' translation
C;Genetics:
A;Gene: hac70
C;Function:
C;Description: involved in protein folding and assembling/disassembling of protein complex
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
F;122-264/Domain: ATP-binding #status predicted <ATP>
F;246-262/Region: nuclear location signal
F;521-645/Domain: peptide-binding #status predicted <PEB>

Query Match 76.8%; Score 1009; DB 2; Length 645;
Best Local Similarity 78.5%; Pred. No. 6.9e-58;
Matches 208; Conservative 24; Mismatches 23; Indels 10; Gaps 8;
Qy 1 KSENVQDLLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTQITFTYSDNQPGVLIQVY 60
Db KSENVQDLLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTQITFTYSDNQPGVLIQVY 60
Qy 384 KSENVQDLLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTQITFTYSDNQPGVLIQVY 442
Db KSENVQDLLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTQITFTYSDNQPGVLIQVY 442
Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPQIETVDFDANGILNVATATDKSTGKANKIT 119
Db EGERAMTKDNNLLGRFELSGIPAPRGVPQIETVDFDANGILNVATATDKSTGKANKIT 119
Qy 443 EGERAMTKDNNLLGRFELSGIPAPRGVPQIETVDFDANGILNVATATDKSTGKANKIT 501
Db EGERAMTKDNNLLGRFELSGIPAPRGVPQIETVDFDANGILNVATATDKSTGKANKIT 501
Qy 120 ITNDKGRLSKEIEIRMVQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 179
Db ITNDKGRLSKEIEIRMVQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 179
Qy 502 ITNDKGRLSKEIEIRMVQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 560
Db ITNDKGRLSKEIEIRMVQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 560
Qy 180 SEADKKVLDKQCVISWLDANTLAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 236
Db SEADKKVLDKQCVISWLDANTLAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 236
Qy 561 IDEDKQKILEKNCNIIIAWLDKQKAEDEPHQKLEKVCNPIITKLQYAGGMPGGM 620
Db IDEDKQKILEKNCNIIIAWLDKQKAEDEPHQKLEKVCNPIITKLQYAGGMPGGM 620
Qy 237 GGFGAQQ--PKG--GSGSGPTIEEVD 258
Db GGFGAQQ--PKG--GSGSGPTIEEVD 258

RESULT 33
S25585
dnak-type molecular chaperone Hsp70 - pig
N;Alternate names: heat shock protein 70
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S34625
R;Dezeure, F.; Vaiman, M.; Chardon, P.
Biochim. Biophys. Acta 1174, 17-26, 1993
A;Title: Characterization of a polymorphic heat shock protein 70 gene in swine outside the pig
A;Reference number: S34625; MUID:93326632; PMID:7687468
A;Accession: S34625
A;Molecule type: mRNA
A;Residues: 1-643 <DEZ>
A;Cross-references: UNIPROT:Q04967; EMBL:X68213; NID:g1977; PIDN:CAA48295.1; PID:g1978
C;Genetics:
A;Gene: Hsp70
C;Function:
C;Description: involved in protein folding and assembling/disassembling of protein complex
C;Superfamily: heat shock protein 70
C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 76.7%; Score 1008; DB 2; Length 643;

Best Local Similarity 74.4%; Pred. No. 8e-58;
Matches 192; Conservative 32; Mismatches 34; Indels 0; Gaps 0;
Qy 1 KSENVQDLLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTQITFTYSDNQPGVLIQVY 60
Db KSENVQDLLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTQITFTYSDNQPGVLIQVY 60
Qy 386 KCEKQVQDLLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTQITFTYSDNQPGVLIQVY 445
Db KCEKQVQDLLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTQITFTYSDNQPGVLIQVY 445
Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPQIETVDFDANGILNVATATDKSTGKANKIT 120
Db EGERAMTKDNNLLGRFELSGIPAPRGVPQIETVDFDANGILNVATATDKSTGKANKIT 120
Qy 446 EGERAMTKDNNLLGRFELSGIPAPRGVPQIETVDFDANGILNVATATDKSTGKANKIT 505
Db EGERAMTKDNNLLGRFELSGIPAPRGVPQIETVDFDANGILNVATATDKSTGKANKIT 505
Qy 121 TNDKGRLSKEIEIRMVQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 180
Db TNDKGRLSKEIEIRMVQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 180
Qy 506 TNDKGRLSKEIEIRMVQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 565
Db TNDKGRLSKEIEIRMVQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 565
Qy 181 EADKKVLDKQCVISWLDANTLAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 240
Db EADKKVLDKQCVISWLDANTLAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 240
Qy 566 EEDCKVQDQKQCVLTWLEHNLAKKEEYHQRKLEQICRPIFSRLYGAQIPGSGCG 625
Db EEDCKVQDQKQCVLTWLEHNLAKKEEYHQRKLEQICRPIFSRLYGAQIPGSGCG 625
Qy 241 AQSPKGGSGPTIEEVD 258
Db AQSPKGGSGPTIEEVD 258

RESULT 34

S27004
dnak-type molecular chaperone hsp70.1 - Hydra magnipapillata
N;Alternate names: heat shock protein 70.1
C;Species: Hydra magnipapillata
A;Variety: strain 105
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: S27004
R;Gallner, K.; Praetzel, G.; Bosch, T.C.G.
Eur. J. Biochem. 210, 683-691, 1992
A;Title: Cloning and expression of a heat-inducible hsp70 gene in two species of Hydra w
A;Reference number: S27004; MUID:93130891; PMID:1483453
A;Accession: S27004
A;Molecule type: DNA
A;Residues: 1-654 <GSL>
A;Cross-references: UNIPROT:Q05944; EMBL:M84019; NID:g159267; PIDN:AAA29213.1; PID:g1592
C;Genetics:
A;Gene: hsp70.1
A;Introns: 69/1; 93/3
C;Function:
C;Description: involved in protein folding and assembling/disassembling of protein compl
C;Superfamily: heat shock protein 70
C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 76.6%; Score 1007; DB 2; Length 654;
Best Local Similarity 74.0%; Pred. No. 9.5e-58;
Matches 196; Conservative 27; Mismatches 34; Indels 8; Gaps 3;

Qy 1 KSENVQDLLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTQITFTYSDNQPGVLIQVY 60
Db KSENVQDLLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTQITFTYSDNQPGVLIQVY 60
Qy 391 KHEAVQDLLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTQITFTYSDNQPGVLIQVY 450
Db KHEAVQDLLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTQITFTYSDNQPGVLIQVY 450
Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPQIETVDFDANGILNVATATDKSTGKANKIT 120
Db EGERAMTKDNNLLGRFELSGIPAPRGVPQIETVDFDANGILNVATATDKSTGKANKIT 120
Qy 451 EGERAMTKDNNLLGRFELSGIPAPRGVPQIETVDFDANGILNVATATDKSTGKANKIT 510
Db EGERAMTKDNNLLGRFELSGIPAPRGVPQIETVDFDANGILNVATATDKSTGKANKIT 510
Qy 121 TNDKGRLSKEIEIRMVQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 180
Db TNDKGRLSKEIEIRMVQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 180
Qy 511 TNDKGRLSKEIEIRMVQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 570
Db TNDKGRLSKEIEIRMVQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 570
Qy 181 EADKKVLDKQCVISWLDANTLAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 235
Db EADKKVLDKQCVISWLDANTLAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 235
Qy 571 EEDKKTIIKKCNVETVWVDKQKAEDEPHQKLEKVCNPIITKLQYAGGMPGGM 630
Db EEDKKTIIKKCNVETVWVDKQKAEDEPHQKLEKVCNPIITKLQYAGGMPGGM 630
Qy 236 --PGFGAQQ--PKGSGSGPTIEEVD 258
Db --PGFGAQQ--PKGSGSGPTIEEVD 258
Qy 631 GMPGMPGSGSGSKASSG-GPTIEEVD 654
Db GMPGMPGSGSGSKASSG-GPTIEEVD 654

RESULT 35

HKW7A

dnak-type molecular chaperone hsp70A - Caenorhabditis elegans

N/Alternate names: heat shock protein 70 A

C/Species: Caenorhabditis elegans

C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004

C/Accession: J070285

R/Submitted, T.P.; Heschl, M.F.P.; Baillie, D.L.

Gene 64, 241-255, 1988

A/Title: The Caenorhabditis elegans hsp70 gene family: a molecular genetic characterization

A/Reference number: J070285; MUID:88297155; PMID:2841196

A/Accession: J070285

A/Molecule type: DNA; mRNA

A/Residues: 1-640 <SN>

A/Cross-references: UNIPROT:P09446; GB:M18540; NID:g156351; PIDN:AAA28078.1; PID:g156352

A/Note: genomic clones representing six distinct members of the hsp70 gene family were

A/Note: transcripts of hsp70A are abundant in control worms and also increase two- to si

A/Note: one of the three introns in hsp70A is in a position similar to an intron in Dro

C/Genetics:

A/Gene: hsp70A

A/Map position: IV

A/Introns: 69/1; 331/3; 558/3

C/Function:

A/Description: involved in protein folding and assembling/diseassembling of protein comp

C/Superfamily: heat shock protein 70

C/Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 75.6%; Score 994; DB 1; Length 640;

Best Local Similarity 75.2%; Pred. No. 6.4e-57;

Matches 194; Conservative 23; Mismatches 39; Indels 2; Gaps 1;

Qy 1 KSENVQDLLLLDVAPLSGLGTAGVMTALIKRNTSTPTKTQITFTTYSNQPGLVQVY 60

Db 385 KSEAVQDLLLLDVAPLSGLGTAGVMTALIKRNTTPTTKAQITFTTYSNQPGLVQVY 444

Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120

Db 445 EGERAMTKDNNLLGKFLSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKAKQITI 504

Qy 121 TNDKGRLSKEIERMVOEAEKYKAEDVQERVSAKNALSYAFNMKSASVEDGLKGKIS 180

Db 505 TNDKGRFSKDIERNVNEAEKYKADDEAQDKQAKNGLESYAFNLKQTIDEKLGKDKIS 564

Qy 181 EADKKVLDKQEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGPGFG 240

Db 565 PEDKKKIEDKDEILKWLDSNQTAEKEEFESQKDLGLAKFDLSKLYQSAGGAPPG--A 622

Qy 241 AQPGKGGSGGPTIEVD 258

Db 623 APGGAAGGAGGPTIEVD 640

RESULT 36

A48469

dnak-type molecular chaperone hsp70 - fluke (Schistosoma mansoni)

N/Alternate names: heat shock protein hsp70; major surface antigen

C/Species: Schistosoma mansoni

C/Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C/Accession: A48469; J00314

R/Neumann, S.; Ziv, E.; Lantner, F.; Schechter, I.

Mol. Biochem. Parasitol. 56, 357-360, 1992

A/Title: Cloning and sequencing of an hsp70 gene of Schistosoma mansoni.

A/Reference number: A48469; MUID:93133227; PMID:1484560

A/Accession: A48469

A/Status: preliminary

A/Molecule type: nucleic acid

A/Residues: 1-637 <NU>

A/Cross-references: UNIPROT:P08418; GB:L02415; NID:g161025; PIDN:AAA29898.1; PID:g552242

A/Note: sequence extracted from NCBI backbone (NCBIN:122799, NCBI:P122802)

R/Hedstrom, R.; Culpepper, J.; Harrison, R.A.; Agabian, N.; Newport, G.

J. Exp. Med. 165, 1430-1435, 1987

A/Title: A major immunogen in Schistosoma mansoni infections is homologous to the heat-s

A/Reference number: J00314; MUID:87197073; PMID:3106556

A/Accession: J00314

A/Molecule type: mRNA

A/Residues: 19-68, 'T', 70-113, 'P', 115-252, 'FH', 255-288, 'I', 290-299, 'G', 301-326, 'A', 328-38

A/Note: the authors translated the codon GAT for residue 59 as Pro

C/Genetics:

A/Gene: hsp70

C/Function:

A/Description: involved in protein folding and assembling/diseassembling of protein comp

C/Superfamily: heat shock protein 70

C/Keywords: ATP; molecular chaperone; surface antigen

Query Match 75.2%; Score 988; DB 2; Length 637;

Best Local Similarity 76.4%; Pred. No. 1.6e-56;

Matches 197; Conservative 23; Mismatches 36; Indels 2; Gaps 2;

Qy 1 KSENVQDLLLLDVAPLSGLGTAGVMTALIKRNTSTPTKTQITFTTYSNQPGLVQVY 60

Db 382 KCEAVQDLLLLDVAPLSGLGTAGVMTALIKRNTTPTTKQTFTTYSNQPGLVQVY 441

Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120

Db 442 EGERALTNDNNLLGKFLSGIPPPAPRGVPOIEVTFDIDANGILNVSAVDKGTGKQNKITI 501

Qy 121 TNDKGRLSKEIERMVOEAEKYKAEDVQERVSAKNALSYAFNMKSASVEDGLKGKIS 180

Db 502 TNDKGRLSKEIERMVAADAKYKAEDKQDRVSAKNSLESYVYTMKQVVEGE-LKEKIP 560

Qy 181 EADKKVLDKQEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGPGFG 240

Db 561 ESDRQVITISCEPTISWLDVHSAEKHEYESKRELEKVCAPITTKYQAGMPG-QMHE 619

Qy 241 AQPGKGGSGGPTIEVD 258

Db 620 ASGAGSGSGGPTIEVD 637

RESULT 37

T45522

heat shock protein HSC70-1, cytosolic [imported] - spinach

C/Species: Spinacia oleracea (spinach)

C/Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004

C/Accession: T45522

R/Li, Q.B.; Guy, C.L.

A/Description: The organization and evolution of the spinach stress 70 molecular chaperon

A/Reference number: Z22998

A/Accession: T45522

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-647 <LIQ>

A/Cross-references: UNIPROT:Q41374; EMBL:AF034618; PIDN:AAB88134.1

C/Genetics:

A/Gene: HSC70-1

A/Introns: 72/1

C/Superfamily: heat shock protein 70

Query Match 73.4%; Score 964; DB 2; Length 647;

Best Local Similarity 71.6%; Pred. No. 5.7e-55;

Matches 184; Conservative 31; Mismatches 42; Indels 0; Gaps 0;

Qy 2 SENVDQLLLDVAPLSGLGTAGVMTALIKRNTSTPTKTQITFTTYSNQPGLVQVYE 61

Db 391 NEKVQDLLLLDVTFPLSLGTAGVMTVLIPTNTTPTTKKEQVFSTYSNQPGLVQVYE 450

Qy 62 GERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 121

Db 451 GEETRTDNNLLGKFLSGIPPPAPRGVPOINVCFDIDANGILNVSAEDKTTGQNKKITIT 510

Qy 122 NDKGRLSKEIERMVOEAEKYKAEDVQERVSAKNALSYAFNMKSASVEDGLKGKISE 181

Db 511 NDKGRLSKEIERMVOEAEKYKSEDEEHKKVSKALENYA YNMRTVYDEKIGAKLSE 570

Qy 182 ADKKKVLDKQEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGPGFGA 241

Db 571 ADKKKIEAIDASIQWLDGNLADEFDKMKELIESCNPIIAKMYQGAGDGMGGMED 630
Qy 242 QGPKGGSGGPTIEVD 258
Db 631 EGPTSGGAGPKIEVD 647

RESULT 38
JN0668
dnak-type molecular chaperone hsc1 - fruit fly (Drosophila melanogaster)
N;Alternate names: heat-shock cognate protein 1
C;Species: Drosophila melanogaster
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: JN0668
R;Rubin, D.M.; Mehta, A.D.; Zhu, J.; Shoham, S.; Chen, X.; Wells, Q.R.; Palter, K.B.
Gene 128, 155-163, 1993
A;Title: Genomic structure and sequence analysis of Drosophila melanogaster HSC70 genes.
A;Reference number: JN0666; MUID:93292982; PMID:8514184
A;Accession: JN0668
A;Molecule type: DNA
A;Residues: 1-641 <RUB>
A;Cross-references: UNIPROT:P29843; GB:L01500
C;Comment: This protein is a member of the heat-shock cognate proteins that are implicated in endocytotic vesicles.
C;Genetics:
A;Gene: hsc1
A;Cross-references: FlyBase:FBgn0001219
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein complex
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 72.9%; Score 958; DB 2; Length 641;
Best Local Similarity 70.9%; Pred. No. 1.4e-54;
Matches 183; Conservative 32; Mismatches 43; Indels 0; Gaps 0;

Qy 1 KSENVQDILLDVLAPLSIGLETAGVMTALIKRNSTIPTKTQITFTYSDNQPGVLIQVY 60
Db 384 KSEAVQDILLDVLTPSLIGTAGVMTLLKRNITPTKTQITFTYADNQPGVLIQV 443
Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
Db 444 EGERAMTRDNNLSLGRFELSAIPAPRGVPOIEVTFDIDANGILNVATLEKSTGKRNITI 503
Qy 121 TNDGRLSKEIERMVOEAKYKADEVORERSAKNALESYAFNMKSAVEDEGLKGIS 180
Db 504 TNDGRLSKEDIERNVDNAEAYROADEQORIRNAKQLESYCFQLRSTLDDHLSSRFS 563
Qy 181 EADKKKVLDDKQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQGAGPGPGFG 240
Db 564 PADRETIQORSSEITAWLDANQLAERQEFHKKQELERICSPIITRLYQGAGMAPPTAG 623
Qy 241 AQGPKGGSGGPTIEVD 258
Db 624 GSNFGATGGSGPTIEVD 641

RESULT 39
S46302
dnak-type molecular chaperone hsc70.1 - Arabidopsis thaliana
N;Alternate names: heat shock cognate protein 70.1
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S46302; S41402; JAO169; S36623
R;Wu, S.H.; Wang, C.; Chen, J.; Lin, B.L.
Plant Mol. Biol. 25, 577-583, 1994
A;Title: Isolation of a cDNA encoding a 70 kDa heat-shock cognate protein expressed in
A;Reference number: S46302; MUID:94325483; PMID:8049382
A;Accession: S46302
A;Molecule type: mRNA
A;Residues: 1-651 <WUS>
A;Cross-references: UNIPROT:P22953; EMBL:X74604; NID:G397481; PIDN:CAA52684.1; PID:G3974

R;King, K.
submitted to the EMBL Data Library, January 1994
A;Reference number: S41402
A;Accession: S41402
A;Molecule type: DNA
A;Residues: 15-64, 'S', 66-194, 'R', 196-371, 'V', 373-375, 'V', 377-506, 'V', 508-651 <KIN>
A;Cross-references: EMBL:X77199; NID:G450879; PIDN:CAA54419.1; PID:G450880
R;Wu, C.H.; Caspar, T.; Browne, J.; Lindquist, S.; Somerville, C.
Plant Physiol. 88, 731-740, 1988
A;Title: Characterization of an HSP70 cognate gene family in Arabidopsis.
A;Reference number: JAO169
A;Accession: JAO169
A;Molecule type: DNA
A;Residues: 1-120 <WUC>
A;Cross-references: GB:M23105
A;Experimental source: Leaf
C;Genetics:
A;Gene: HSC70-1
A;Introns: 71/3
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein complex
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 72.7%; Score 955; DB 2; Length 651;
Best Local Similarity 70.1%; Pred. No. 2.2e-54;
Matches 183; Conservative 31; Mismatches 43; Indels 4; Gaps 1;

Qy 2 SENVDILLDVLAPLSIGLETAGVMTALIKRNSTIPTKTQITFTYSDNQPGVLIQVYE 61
Db 391 NEKVQDILLDVLTPSLIGTAGVMTLLIPRNTIPTKEQVFSTYSDNQPGVLIQVYE 450
Qy 62 GERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 121
Db 451 GERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 510
Qy 122 NDKGRLSKEIERMVOEAKYKADEVORERSAKNALESYAFNMKSAVEDEGLKGIKISE 181
Db 511 NDKGRLSKDBIEKMVQEAKEYKSEDEHKKVKAENALYVNNRNTIQDEKIGELPA 570
Qy 182 ADKKKVLDDKQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQV-----AGGPGPG 237
Db 571 ADKKKIEDSIEQALQWLEGNQLAEDEFDKMKELESICNPITIAKMYQGAGGAGGPGAS 630
Qy 238 GFGAQGPKGSGGSGPTIEVD 258
Db 631 GMDDDAPPASGAGPKIEVD 651

RESULT 40
T48271
dnak-type molecular chaperone hsc70.1 - Arabidopsis thaliana
N;Alternate names: protein T22P11.90
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48271
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24490
A;Accession: T48271
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-651 <BEV>
A;Cross-references: UNIPROT:P22953; EMBL:AJ162971
A;Experimental source: cultivar Columbia; BAC clone T22P11
C;Genetics:
A;Map position: 5
A;Introns: 72/1
A;Note: T22P11.90
C;Superfamily: heat shock protein 70

Query Match 72.7%; Score 955; DB 2; Length 651;
Best Local Similarity 70.1%; Pred. No. 2.2e-54;

Db 391 NEKVDLLLDVTPLSLGLETAGGVTTLIPRNTTPTKKEQVSTYSDNQPGVLIQVYE 450
Qy 62 GERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 121
Db 451 GERATRDNNLLGKFLTGIPPA PRGVPQITVCDFIDANGILNVSADKTTTGQKNKITIT 510
Qy 122 NDKGRLSKEETRMVQAEKKADEQVRERVSNAKNALESYAFNMKSAVEDGLKGIKISE 181
Db 511 NDKGRLSKDETEKMWQAEKKADEEHKKKVEAKNALENAYNNRNTIKDDKTIASKLSP 570
Qy 182 ADKKKVLDDKQEVTSWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGGPG-PCGFG 240
Db 571 DEKKKIEIDASQIOWLDGNQLAEDEFDDKMKLESICNPIIAKMTQGRAGPDMAGGMD 630
Qy 241 AQGPKGG---SGSGPTIEVD 258
Db 631 EDGFSAGASSAGAPKIEVD 651

RESULT 44
A42582
dnak-type molecular chaperone SCE70 - spinach
N:Alternate names: heat shock protein SCE70
C:Species: Spinacia oleracea (spinach)
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A42582; S21943
R:Ko, K.; Bornemisza, O.; Kourtz, L.; Ko, Z.W.; Plaxton, W.C.; Cashmore, A.R.
J. Biol. Chem. 267, 2986-2993, 1992
A:Title: Isolation and characterization of a cDNA clone encoding a cognate 70-kDa heat s
A:Reference number: A42582; MUID:92147640; PMID:1371110
A:Accession: A42582
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-653 <KOK>
A:Cross-references: UNIPROT:P29357; EMBL:X61491; NID:G21337; PIDN:CAA43711.1; PID:G21338
A:Note: sequence extracted from NCBI Backbone (NCBIN:80804, NCBIIP:80805)
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein comp
C:Superfamily: heat shock protein 70
C:Keywords: ATP; chloroplast; molecular chaperone

Query Match 71.8%; Score 943; DB 2; Length 653;
Best Local Similarity 70.6%; Pred. No. 1.3e-53;
Matches 180; Conservative 31; Mismatches 44; Indels 0; Gaps 0;

Qy 2 SENVDLLLDVAPLSLGLETAGGVTALIKRNTIPTKQITFTTYSNDQPGVLIQVYE 61
Db 391 NEKVDLLLDVTPLSLGLETAGGVTTLIPRNTTPTKKEQVSTYSDNQPGVLIQVYE 450
Qy 62 GERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 121
Db 451 GERATRDNNLLGKFLTGIPPPAPRGVPQINVCDFIDANGILNVSADKTTTGQKNKITIT 510
Qy 122 NDKGRLSKEETRMVQAEKKADEQVRERVSNAKNALESYAFNMKSAVEDGLKGIKISE 181
Db 511 NDKGRLSKDETEKMWQAEKKADEEHKKKVEAKNALENAYNNRNTIKDDKTIASKLSE 570
Qy 182 ADKKKVLDDKQEVTSWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGGPGGFGA 241
Db 571 ADKKKIEIDASQIOWLDGNQLAEDEFDDKMKLESICNPIIAKMTQGRAGPDMAGGMD 630
Qy 242 QGPKGGSGPTIEVD 258
Db 631 EGPTSGGAGPKIEE 645

RESULT 45
S53126
dnak-type molecular chaperone hap70 - rice (fragment)
N:Alternate names: heat shock cognate protein 70
C:Species: Oryza sativa (rice)
C>Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S53126

R:Qun, W.; Rong-Xiang, F.
submitted to the EMBL Data Library, July 1994
A:Description: Structure and expression of a rice hsp 70 cognate gene.
A:Reference number: S53126
A:Accession: S53126
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-649 <QUN>
A:Cross-references: UNIPROT:Q40693; EMBL:X67711; NID:G736271; PIDN:CAA47948.1; PID:G7631
C:Genetics:
A:Gene: hsp70
A:Introns: 72/1
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein comp
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match 71.5%; Score 939; DB 2; Length 649;
Best Local Similarity 69.9%; Pred. No. 2.4e-53;
Matches 181; Conservative 31; Mismatches 45; Indels 2; Gaps 1;

Qy 2 SENVDLLLDVAPLSLGLETAGGVTALIKRNTIPTKQITFTTYSNDQPGVLIQVYE 61
Db 391 NEKVDLLLDVTPLSLGLETAGGVTTLIPRNTTPTKKEQVSTYSDNQPGVLIQVYE 450
Qy 62 GERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 121
Db 451 GERATRDNNLLGKFLTGIPPPAPRGVPQITVCDFIDANGILNVSADKTTTGQKNKITIT 510
Qy 122 NDKGRLSKEETRMVQAEKKADEQVRERVSNAKNALESYAFNMKSAVEDGLKGIKISE 181
Db 511 NDKGRLSKDETEKMWQAEKKADEEHKKKVEAKNALENAYNNRNTIKDDKTIASKLDP 570
Qy 182 ADKKKVLDDKQEVTSWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGGPGGFGA 241
Db 571 ADKKKIEIDASQIOWLDGNQLAEDEFDDKMKLEGCNPIIAKMTQGRAGDMAGGMD 630
Qy 242 QG--PKGGSGPTIEVD 258
Db 631 DDAPPAGGSGAGPKIEVD 649

RESULT 46
T45517
heat shock protein 70, cytosolic [imported] - spinach
C:Species: Spinacia oleracea (spinach)
C>Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
C:Accession: T45517
R:Li, Q.B.; Haskell, D.W.; Guy, C.L.
Plant Mol. Biol. 39, 21-34, 1999
A:Title: Coordinate and non-coordinate expression of the stress 70 family and other mole
A:Reference number: Z16516; MUID:99178791; PMID:10080706
A:Accession: T45517
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-651 <LIQ>
A:Cross-references: UNIPROT:O22664; EMBL:AF033852; NID:G2642647; PIDN:AAB97316.1; PID:G2
A:Experimental source: strain Bloomsdale
C:Genetics:
A:Gene: HSC70
C:Superfamily: heat shock protein 70

Query Match 71.4%; Score 938; DB 2; Length 651;
Best Local Similarity 70.6%; Pred. No. 2.8e-53;
Matches 185; Conservative 31; Mismatches 40; Indels 6; Gaps 3;

Qy 2 SENVDLLLDVAPLSLGLETAGGVTALIKRNTIPTKQITFTTYSNDQPGVLIQVYE 61
Db 391 NEKVDLLLDVTPLSLGLETAGGVTTLIPRNTTPTKKEQVSTYSDNQPGVLIQVYE 450
Qy 62 GERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 121
Db 451 GERATRDNNLLGKFLTGIPPPAPRGVPQITVCDFIDANGILNVSADKTTTGQKNKITIT 510

Qy 122 NDKGRLSKEEIERVMQAEAKYKADEVQREVRSKNALESYAFNMKSAVEDGLKGIKISE 181
 Db 511 NDKGRLSKEEIERVMQAEAKYKADEVQREVRSKNALESYAFNMKSAVEDGLKGIKISE 570

Qy 182 ADKKKVLDDKQEVISWLDANTLAEDKPEHKKRKELEQVNCPIISGLYQAGGPGPGGF-- 239
 Db 571 ADKKKIEESIDNAINWLESNOLAEADPEDKMKLESICNPPIAKMYQAGGGEA-GGVPM 629

Qy 240 -GAQGPKG--SGSGPTIEEVD 258
 Db 630 DDDEVPSAGASSGPGKIEEVD 651

RESULT 47
 S37165
 dnak-type molecular chaperone - Eimeria acervulina
 N;Alternate names: heat shock protein
 C;Species: Eimeria acervulina
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C;Accession: S37165
 R;Laurent, F.; Bourdieu, C.; Yvor, P.; Pry, P.
 submitted to the EMBL Data Library, September 1993
 A;Description: Cloning of a 70 kDa protein of E.acervulina sporozoite which is related
 A;Reference number: S37165
 A;Accession: S37165
 A;Molecule type: mRNA
 A;Residues: 1-646 <LAI>
 A;Cross-references: UNIPROT:Q24768; EMBL:Z26134; NID:G401828; PIDN:CAA81135.1; PID:G4018
 C;Function:
 A;Description: involved in protein folding and assembling/disassembling of protein comp
 C;Superfamily: heat shock protein 70
 C;Keywords: ATP; molecular chaperone

Query Match 70.7%; Score 928.5; DB 2; Length 646;
 Best Local Similarity 68.8%; Pred. No. 1.1e-52;
 Matches 179; Conservative 34; Mismatches 44; Indels 3; Gaps 1;

Qy 2 SENVQDILLDVAPLSLGLETAGGVTALIKRNSTIPTKQIETFTYSDNPGVLIQVYE 61
 Db 387 SSQVQDILLDVAPLSLGLETAGGVTALIKRNSTIPTKQIETFTYSDNPGVLIQVYE 446

Qy 62 GERAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 121
 Db 447 GERAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 506

Qy 122 NDKGRLSKEEIERVMQAEAKYKADEVQREVRSKNALESYAFNMKSAVEDGLKGIKISE 181
 Db 507 NDKGRLSQGEIDRMVAEAKYKADEVQREVRSKNALESYAFNMKSAVEDGLKGIKISE 566

Qy 182 ADKKKVLDDKQEVISWLDANTLAEDKPEHKKRKELEQVNCPIISGLYQ--GAGGPGGG 238
 Db 567 EDREAATSAIQALDLDKQAEKPEAKQKEVEAVCTPIVTMTQSAAGAAGGMPGG 626

Qy 239 FGAQGPKGSGSGPTIEEVD 258
 Db 627 MPDMSAAAGAGGPTIEEVD 646

RESULT 48
 S03250
 dnak-type molecular chaperone hsp70 (clone pMON9743) - garden petunia
 N;Alternate names: heat shock protein 70
 C;Species: Petunia x hybrida (garden petunia)
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C;Accession: S03250
 R;Winter, J.; Wright, R.; Duck, N.; Gasser, C.; Fraley, R.; Shah, D.
 Mol. Gen. Genet. 211, 315-319, 1988
 A;Title: The inhibition of petunia hsp70 mRNA processing during CdCl(2) stress.
 A;Reference number: S03250
 A;Accession: S03250
 A;Molecule type: DNA
 A;Residues: 1-651 <DNA>

A;Cross-references: UNIPROT:P09189; EMBL:X06932; NID:G20556; PIDN:CAA30018.1; PID:G20556
 A;Experimental source: var. Mitchell diploid
 C;Genetics:
 A;Gene: hsp70
 A;Introns: 72/1
 C;Function:
 A;Description: involved in protein folding and assembling/disassembling of protein comp
 C;Superfamily: heat shock protein 70
 C;Keywords: ATP; molecular chaperone

Query Match 70.6%; Score 928; DB 2; Length 651;
 Best Local Similarity 70.0%; Pred. No. 1.2e-52;
 Matches 184; Conservative 32; Mismatches 39; Indels 8; Gaps 3;

Qy 2 SENVQDILLDVAPLSLGLETAGGVTALIKRNSTIPTKQIETFTYSDNPGVLIQVYE 61
 Db 391 NEKVQDILLDVAPLSLGLETAGGVTALIPRNTIPTKKEQVFSTYSDNPGVLIQVYE 450

Qy 62 GERAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 121
 Db 451 GERAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 510

Qy 122 NDKGRLSKEEIERVMQAEAKYKADEVQREVRSKNALESYAFNMKSAVEDGLKGIKISE 181
 Db 511 NDKGRLSKEEIERVMQAEAKYKADEVQREVRSKNALESYAFNMKSAVEDGLKGIKISE 570

Qy 182 ADKKKVLDDKQEVISWLDANTLAEDKPEHKKRKELEQVNCPIISGLYQ-GAGG----PG 235
 Db 571 ADKKRIEIDAIDEAKLWLDNQLAEADFEKMKLESICNPPIAKMYQGGAGGATMDEG 630

Qy 236 PGGFGAQPKGSGSGPTIEEVD 258
 Db 631 PSVGSAGSQ--TGAGPKIEEVD 651

RESULT 49
 S14950
 dnak-type molecular chaperone hsc-2 - tomato
 N;Alternate names: heat shock cognate protein 70
 C;Species: Lycopersicon esculentum (tomato)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C;Accession: S14950
 R;Lin, T.Y.; Duck, N.B.; Winter, J.; Folk, W.R.
 Plant Mol. Biol. 16, 475-478, 1991
 A;Title: Sequences of two hsc 70 cDNAs from Lycopersicon esculentum.
 A;Reference number: S14949; MUID:91370894; PMID:1893113
 A;Accession: S14950
 A;Molecule type: mRNA
 A;Residues: 1-644 <LIN>
 A;Cross-references: UNIPROT:P27322; EMBL:X54030; NID:G19257; PIDN:CAA37971.1; PID:G19258
 C;Genetics:
 A;Gene: hsc-2
 C;Function:
 A;Description: involved in protein folding and assembling/disassembling of protein comp
 C;Superfamily: heat shock protein 70
 C;Keywords: ATP; molecular chaperone

Query Match 70.1%; Score 921.5; DB 2; Length 644;
 Best Local Similarity 69.0%; Pred. No. 3.2e-52;
 Matches 180; Conservative 32; Mismatches 38; Indels 11; Gaps 3;

Qy 2 SENVQDILLDVAPLSLGLETAGGVTALIKRNSTIPTKQIETFTYSDNPGVLIQVYE 61
 Db 391 NEKVQDILLDVAPLSLGLETAGGVTALIPRNTIPTKKEQVFSTYSDNPGVLIQVYE 450

Qy 62 GERAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 121
 Db 451 GERTRDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 510

Qy 122 NDKGRLSKEEIERVMQAEAKYKADEVQREVRSKNALESYAFNMKSAVEDGLKGIKISE 181
 Db 511 NDKGRLSKEEIERVMQAEAKYKADEVQREVRSKNALESYAFNMKSAVEDGLKGIKISE 570

Qy 182 ADKKVLDKQEVISWLDANTLAERKDEFEHKKRKELEQVNCNPIISGLYQAGG-----PGPG 237
Db 571 DRTKIDAEATQIQWIDGNQLAEAEFEFKMKELESCLNPIIAKMYQAGGDMDDRGP- 629
Qy 238 GFAGQGPKGSGSGPTIEEVD 258
Db 630 -----APSGG-GAGPKIEEVD 644

RESULT 50
A25089
N;Alternate names: molecular chaperone - maize
C;Species: Zea mays (maize)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C;Accession: A25089
R;Rocheater, D.E.; Winer, J.A.; Shah, D.M.
EMBO J. 5, 451-458, 1986
A;Title: The structure and expression of maize genes encoding the major heat shock prote
A;Reference number: A25089
A;Accession: A25089
A;Molecule type: DNA
A;Residues: 1-645 <ROC>
A;Cross-references: UNIPROT:P11143
A;Note: the authors translated the codon CTG for residue 22 as Val and GAG for residues
C;Genetics:
A;Introns: 48/1
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Qy 7 DILLVDVAPLSGLGTAGGVTALIKRNSTIPTKQTOIFTTYSNDQPGVLIQVYGERAM 66
Db 392 DILLVDVAPLSGLGTAGGVTALIKRNSTIPTKQTOIFTTYSNDQPGVLIQVYGERAR 451
Qy 67 TKNNLLGRFELSGIPAPRGVPOIETFTDIDANGILNVATDKSTGKANKITITNDKGR 126
Db 452 TKNNLLGRFELSGIPAPRGVPOIETFTDIDVNNILNVSAEDKTTGCKNKITITNDKGR 511
Qy 127 LSKEEIERMVOEAEKYKAEDVQERVSNAKNALESYAFNMKSAAVEDGLKGISEAADKK 186
Db 512 LSKEEIERMVOEAEKYKAEDVQERVSNAKNALESYAFNMKSAAVEDGLKGISEAADKK 571
Qy 187 VLDKQCVISWLDANTLAERKDEFEHKKRKELEQVNCNPIISGLY--QGAGGPGGFGAQQP 244
Db 572 IEDAVDGAISWLDNSQLAEVEEPEDKMKLEGINCPPIIAKMYXGEGAGMGAAAGMDREDAP 631
Qy 245 KGGSGSGPTIEEVD 258
Db 632 SGGSGAGPKIEEVD 645

RESULT 51
S51682
N;Alternate names: molecular chaperone hsp70 - Eimeria maxima (fragment)
C;Species: Eimeria maxima
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S51682
R;Dunn, P.P.J.; Billington, K.J.; Bumstead, J.M.; Tomley, F.M.
submitted to the EMBL Data Library, December 1994
A;Description: Isolation and sequences of cDNA clones for cytosolic and organellar hsp70
A;Reference number: S51682
A;Accession: S51682
A;Molecule type: DNA
A;Residues: 1-521 <DUN>
A;Cross-references: UNIPROT:Q24896; EMBL:Z46964; NID:G603811; PIDN:CAA87085.1; PID:G6038
C;Genetics:

A;Gene: hsp70
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 69.5%; Score 913.5; DB 2; Length 521;
Best Local Similarity 66.8%; Pred. No. 8.1e-52;
Matches 179; Conservative 35; Mismatches 43; Indels 11; Gaps 3;

Qy 2 SENVDLLLDVAPLSGLGTAGGVTALIKRNSTIPTKQTOIFTTYSNDQPGVLIQVY 61
Db 254 STQVQDLLLLDVAPLSGLGTAGGVTALIKRNSTIPTKQTOIFTTYSNDQPGVLIQVY 313
Qy 62 GERATKDNLLGRFELSGIPAPRGVPOIETFTDIDANGILNVATDKSTGKANKITIT 121
Db 314 GERATKDNLLGRFELSGIPAPRGVPOIETFTDIDANGILNVATDKSTGKANKITIT 373
Qy 122 NDKGRLSKEEIERMVOEAEKYKAEDVQERVSNAKNALESYAFNMKSAAVEDGLKGI 181
Db 374 NDKGRLSQGEIDRMVAEAEKYKAEDVQERVSNAKNALESYAFNMKSAAVEDGLKGI 433
Qy 182 ADKKVLDKQEVISWLDANTLAERKDEFEHKKRKELEQVNCNPIISGLYQAGG-----PG- 235
Db 434 EDKDTAAAIQKTDLDWLNQLAKEEYESKLKEIEGVCPTIVTKMTQAAAGAGMPGA 493
Qy 236 ----PGGF-GAOGPKGSGSGPTIEEVD 258
Db 494 AAGMPGMPDMSGAAAPGAGPTVEEVD 521

RESULT 52
JQ1515
N;Alternate names: molecular chaperone HSP70 - Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 09-Jul-2004
C;Accession: JQ1515
R;Mueller, F.W.; Igloi, G.L.; Beck, C.F.
Gene 111, 165-173, 1992
A;Title: Structure of a gene encoding heat-shock protein HSP70 from the unicellular alga
A;Reference number: JQ1515; MUID:92175520; PMID:1541398
A;Accession: JQ1515
A;Molecule type: DNA
A;Residues: 1-649 <MUE>
A;Cross-references: UNIPROT:P25840; GB:M76725; NID:g167420; PIDN:AAB00730.1; PID:g167421
A;Note: the authors translated the codon GAC for residue 371 as Asn
C;Comment: This protein is inducible by light as well as by elevated temperature.
C;Genetics:
A;Introns: 17/2; 59/3; 106/1; 159/3; 193/2; 550/1
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; calmodulin binding; molecular chaperone
F;205-213/Region: ATP binding #status predicted
F;222-228/Region: ATP binding #status predicted
F;263-281/Region: calmodulin binding #status predicted

Query Match 69.4%; Score 911.5; DB 2; Length 649;
Best Local Similarity 68.8%; Pred. No. 1.4e-51;
Matches 179; Conservative 33; Mismatches 43; Indels 5; Gaps 3;

Qy 3 ENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTIPTKQTOIFTTYSNDQPGVLIQVY 62
Db 391 EKVDQDLLLLDVAPLSGLGTAGGVTALIKRNSTIPTKQTOIFTTYSNDQPGVLIQVY 450
Qy 63 ERATKDNLLGRFELSGIPAPRGVPOIETFTDIDANGILNVATDKSTGKANKITITN 122
Db 451 ERATKDNLLGRFELSGIPAPRGVPOIETFTDIDANGILNVSAEDKTTGCKNKITITN 510
Qy 123 DKGRLSKEEIERMVOEAEKYKAEDVQERVSNAKNALESYAFNMKSAAVEDGLKGISEA 182
Db 511 DKGRLSKEEIERMVOEAEKYKAEDVQERVSNAKNALESYAFNMKSAAVEDGLKGISEA 569

Query Match 69.3%; Score 910; DB 2; Length 652;
Best Local Similarity 66.2%; Pred. No. 1.8e-51;
Matches 176; Conservative 39; Mismatches 41; Indels

A;Gene: cahsp70

Query Match	69.3%	Score 911	DB 2	Length 656
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N;Alternate names: heat shock protein 70

A;Residues: I-644 <C02>
A:Cross-references: EMRI:Z69729: PIDN:CAA93590.1: GSPDB:GN00066: SPDB:SPAC13G7.02C

A;Description: involved in protein folding and assembling/disassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

	Query Match	69.2%;	Score	909.5;	DB 2;	Length	644;	
	Best Local Similarity	67.6%;	Pred.	No. 1.9e-51;				
	Matches	177;	Conservative	37;	Mismatches	43;	Indels	5; Gaps 3;

Qy 2 SENVQDLLLLDVAPLSLGLETAGGVNMTALKRNSTIPTKTQTQTFTTYSNQPGVLQIYVE 61
 | | | | | |
Db 383 SEKTDQLLLLDVAPISLGIETAGGVTPLTKRNTTIPTKKSEVFSTADNPQGVLQIVPE 442

Qy 62 GERAMTYKNNNLRGFELSGIPPAARGVPQIEVTFDDANGILNVATDTSKGANKITIT 121
 ||||| | | | | |
Db 443 GERARWDCNLGLKFELSGIPPAARGVPQIEVTFDDANGILNVSALEKGTGKTQKITIT 502
 ||||| | | | | |

Qy 122 NDGRLSKKEIERVMQAEKKAEDVQRRVSAKNALESYAFNMKSAVEDGLKGIKE 181
Db 503 NDGRLSKKEIDRMVSEAEKKAEDAEATSRIQAKNHLESVAYSLSRLSDDPNLKDKVDA 562
Qy 182 ADKKKVLKDCQEVISWLDANTLAEDFEHKKKELEQVNCPIISGLYQAGGPG--PGGP 239
Db 563 SKKAIDKAVKETIEMLDHNTAAKDEYEDKQLEGVANPIMAKIYQAGGAPGGM 622
Qy 240 --GAQ-GPKGGSGSGPTIEVD 258
Db 623 PGAPGAGGADNGPVEEVD 644

RESULT 56
S14949
dnak-type molecular chaperone hsc-1 - tomato
N:Alternate names: heat shock cognate protein 70
C:Species: Lycopersicon esculentum (tomato)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S14949
R:Lin, T.Y.; Duck, N.B.; Winter, J.; Folk, W.R.
Plant Mol. Biol. 16, 475-478, 1991
A:Title: Sequences of two hsc 70 cDNAs from Lycopersicon esculentum.
A:Reference number: S14949; MUID:91370894; PMID:1893113
A:Accession: S14949
A:Molecule type: mRNA
A:Residues: 1-650 <LIN>
A:Cross-references: UNIPROT:P24629; EMBL:X54029; NID:g19255; PIDN:CAA37970.1; PID:g19256
C:Genetics:
A:Gene: hsc-1
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein comp
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match 69.2%; Score 909; DB 2; Length 650;
Best Local Similarity 70.4%; Pred. No. 2.1e-51;
Matches 183; Conservative 31; Mismatches 42; Indels 4; Gaps 3;

Qy 2 SENVDLLLDVAPLSGLTAGGVTALIKRNSIPTKQTQIFFTYSNQPGLVLIQVFE 61
Db 392 NEKVDLLLDVTPUSLGLTAGGVTMLIPRNTIPTPKKEQVSTYSNQPGLVLIQVFE 451

Qy 62 GE-RAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 452 GERRARTDNLLGKFLSVIPAPRVQPIVCFDIDANGILNVSAEDKTTGQNKITI 511

Qy 121 TNDKRLSKKEIERVMQAEKKAEDVQRRVSAKNALESYAFNMKSAVEDGLKGIKE 180
Db 512 TNDKRLSKKEIERVMQAEKKAEDVQRRVSAKNALESYAFNMKSAVEDGLKGIKE 571

Qy 181 EADKKVLKDCQEVISWLDANTLAEDFEHKKKELEQVNCPIISGLYQAGGPG--PGG 238
Db 572 SDDKKKIEDAVDQALSWLESQLAEDFEHKKKELEQVNCPIISGLYQAGGPG--PGG 631

Qy 239 FGAQGPKGSGSGPTIEVD 258
Db 632 DDAP-PSGGSSAGPKIEVD 650

RESULT 57
S53498
dnak-type molecular chaperone HSP71.2 - garden pea
N:Alternate names: heat shock protein HSP71.2
C:Species: Pisum sativum (garden pea)
C>Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S53498
R:DeRocher, A.; Vierling, E.
Plant Mol. Biol. 27, 441-456, 1995
A:Title: Cytoplasmic HSP70 homologues of pea: differential expression in vegetative and
A:Reference number: S53498; MUID:95201239; PMID:7894010
A:Accession: S53498

A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-648 <DER>
A:Cross-references: UNIPROT:Q40980; GB:U08848; NID:g562005; PIDN:AAA82975.1; PID:g562006
C:Genetics:
A:Gene: HSP71.2
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein comp
C:Superfamily: heat shock protein 70
C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 68.9%; Score 906; DB 2; Length 648;
Best Local Similarity 69.0%; Pred. No. 3.2e-51;
Matches 178; Conservative 33; Mismatches 45; Indels 2; Gaps 2;

Qy 3 ENVQDLLLDVAPLSGLTAGGVTALIKRNSIPTKQTQIFFTYSNQPGLVLIQVYEG 62
Db 391 EKVDLLLDVTPUSLGLTAGGVTMLIPRNTIPTPKKEQIFSTYSNQPGLVLIQVYEG 450

Qy 63 ERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITITN 122
Db 451 ERAMTKDNLLGKFLSGIPAPRGVQVNVCFDIDANGILNVSAEDKTAGVKNKITITN 510

Qy 123 DKGRLSKEIERVMQAEKKAEDVQRRVSAKNALESYAFNMKSAVEDGLKGIKESEA 182
Db 511 DKGRLSKEIERVMQAEKKAEDVQRRVSAKNALESYAFNMKSAVEDGLKGIKESEA 570

Qy 183 DKKVLKDCQEVISWLDANTLAEDFEHKKKELEQVNCPIISGLYQ--GAGGPGGPGGA 241
Db 571 DREKIEKAVEAIOQLGNEQLGEVEFEDKQLEGVNCPIIAKMYQGGAGGDPVMDGDM 630

Qy 242 Q-GPKGGSGSGPTIEVD 258
Db 631 PGGSNGSGPGPKIEVD 648

RESULT 58
S14992
dnak-type molecular chaperone hsp70 - soybean
N:Alternate names: heat shock protein, 70K
C:Species: Glycine max (soybean)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S14992
R:Roberts, J.K.; Key, J.L.
Plant Mol. Biol. 16, 671-683, 1991
A:Title: Isolation and characterization of a soybean hsp70 gene.
A:Reference number: S14992; MUID:91329700; PMID:1714321
A:Accession: S14992
A:Molecule type: DNA
A:Residues: 1-645 <PLA>
A:Cross-references: UNIPROT:P26413; EMBL:X62799; NID:g18662; PIDN:CAA44620.1; PID:g18663
C:Genetics:
A:Gene: hsp70
A:Introns: #status absent
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein comp
C:Superfamily: heat shock protein 70
C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 68.8%; Score 904.5; DB 2; Length 645;
Best Local Similarity 68.1%; Pred. No. 4e-51;
Matches 175; Conservative 38; Mismatches 41; Indels 3; Gaps 2;

Qy 3 ENVQDLLLDVAPLSGLTAGGVTALIKRNSIPTKQTQIFFTYSNQPGLVLIQVYEG 62
Db 391 EKVDLLLDVTPUSLGLTAGGVTMLIPRNTIPTPKKEQIFSTYSNQPGLVLIQVYEG 450

Qy 63 ERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITITN 122
Db 451 ERAMTKDNLLGKFLSGIPAPRGVQVNVCFDIDANGILNVSAEDKTAGVKNKITITN 510

Qy 123 DKGRLSKEIERVMQAEKKAEDVQRRVSAKNALESYAFNMKSAVEDGLKGIKESEA 182
Db 511 DKGRLSKEIERVMQAEKKAEDVQRRVSAKNALESYAFNMKSAVEDGLKGIKESEA 182

Db 511 DKGRSLKEETKVMYKAEDEEVKKVKAQNSLENVAYNMRNTIKDEKIGKLSPD 570
Qy 183 DKKKVLDKQEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGG-GFGA 241
Db 571 EKQIERAVEDAIQWLEGNOVAEYDEFEKQKELEGICNPITIAKMYQGAAGPGDPMGA 630
Qy 242 QGPKGGSGGPTIEVD 258
Db 631 DMP--AAGAGPKIEVD 645
RESULT 59
JC7132
heat shock protein 70 - Rhizopus nigricans
C:Species: Rhizopus nigricans
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: JC7132
R:Cernila, B.; Cresnar, B.; Brekvar, K.
Biochem. Biophys. Res. Commun. 265, 494-498, 1999
A:Title: Induction of Hsp70 in the fungus Rhizopus nigricans.
A:Reference number: JC7132; MUID:20025372; PMID:10558896
A:Accession: JC7132
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-651 <CER>
A:Cross-references: UNIPROT:Q9UVM1; GB:AF188288
C:Superfamily: heat shock protein 70
Query Match 68.8%; Score 904; DB 2; Length 651;
Best Local Similarity 66.3%; Pred. No. 4.4e-51;
Matches 177; Conservative 36; Mismatches 44; Indels 10; Gaps 3;
Qy 2 SENVDLLLDVAPLSGLTAGGVTALIKRNSIPTKQTOIFTTYSNDQPGVLIQVYE 61
Db 385 SEKTQDLLLDVAPLSGLTAGGVTALIKRNTVPTKSEVSTYADNQPGLIQVFE 444
Qy 62 GERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVTATDKSTGKANKITIT 121
Db 445 GERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVSALDKTKGSKNITIT 504
Qy 122 NDGRSLKEETRMVQEAQKAEDEVQVRVSAKNALESYAFNMKSAVEDGLKGKISE 181
Db 505 NDGRSLKEETRMVQEAQKAEDEAAASIAQKNGLESYAYNLNTLQDERSVGALPE 564
Qy 182 ADKKVLDKQEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGG----PG- 235
Db 565 EDTKLNAVDSEIKWLDESKAESEYKQKELEETANFIMKFTQQAGGAPGAPGA 624
Qy 236 -PGGFGAGQPKGGS---GGSGPTIEVD 258
Db 625 AFGGPPGAGAPGSDTDTGFSIEVD 651
RESULT 60
T43730
dnaK-type molecular chaperone 70A2 [imported] - Anopheles albimanus
N:Alternate names: heat shock protein hsp70A2
C:Species: Anopheles albimanus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43730; T43729
R:Benedict, M.Q.; Cockburn, A.F.; Seawright, J.A.
Insect Mol. Biol. 2, 93-102, 1993
A:Title: The Hsp70 heat-shock gene family of the mosquito Anopheles albimanus.
A:Reference number: Z22652; MUID:97242549; PMID:9087548
A:Accession: T43730
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-640 <BEN>
A:Cross-references: UNIPROT:P41827; EMBL:M96661; NID:g159591; PIDN:AAC41543.1; PID:g159591
A:Accession: T43729
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-502 <BE2>

A:Cross-references: EMBL:M96661; NID:g159591; PIDN:AAC41542.1; PID:g159592
C:Genetics:
A:Gene: hsp70
C:Superfamily: heat shock protein 70
Query Match 68.7%; Score 903; DB 2; Length 640;
Best Local Similarity 65.6%; Pred. No. 5e-51;
Matches 170; Conservative 43; Mismatches 44; Indels 2; Gaps 2;
Qy 1 KSENVQDLLLDVAPLSGLTAGGVTALIKRNSIPTKQTOIFTTYSNDQPGVLIQVY 60
Db 383 KDDKIQDVLVLDVAPLSGLTAGGVTALIKRNSIPCKQTOIFSTYADNQPGLIQVFE 442
Qy 61 EGERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVTATDKSTGKANKITIT 120
Db 443 EGERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVAEKSTGKKNITIT 502
Qy 121 TNDKGRSLKEETRMVQEAQKAEDEVQVRVSAKNALESYAFNMKSAVEDGLKGKISE 180
Db 503 KNDKGRLSQADIDRMVSEAEKFEDEKQREKISARNQLEAYCNLQSLDGGG-ASKLS 561
Qy 181 EADKKVLDKQEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLY-QGAGGPGPGG 239
Db 562 DADRKTVDRCETLRWDGNTWADKEEFHKKMQELTKACSPIMTKLHQQAAGGPGSPSSC 621
Qy 240 GAQPKGSGSGGPTIEVD 258
Db 622 AQAAGGFGGTGPTVEVD 640
RESULT 61
T41121
heat shock protein 70 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T41121; T43342
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z21969
A:Accession: T41121
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-647 <LYN>
A:Cross-references: UNIPROT:O59855; EMBL:AL031540; PIDN:CAA20787.1; GSPDB:GN00068; SPDB:8
A:Experimental source: strain 972h-; cosmid c1739
R:Kawamukai, M.
submitted to the EMBL Data Library, March 1998
A:Description: S.pombe heat shock protein of HSP70 family.
A:Reference number: Z22442
A:Accession: T43342
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-647 <KAW>
A:Cross-references: EMBL:AB012387; PIDN:BAA25322.1
C:Genetics:
A:Gene: SPCC1739.13
A:Map position: 3
C:Superfamily: heat shock protein 70
Query Match 68.6%; Score 902; DB 2; Length 647;
Best Local Similarity 66.8%; Pred. No. 5.9e-51;
Matches 177; Conservative 34; Mismatches 46; Indels 8; Gaps 2;
Qy 2 SENVDLLLDVAPLSGLTAGGVTALIKRNSIPTKQTOIFTTYSNDQPGVLIQVYE 61
Db 383 SEKTQDLLLDVAPLSGLTAGGVTALIKRNTVPTKSEIYSTYADNQPGLIQVFE 442
Qy 62 GERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVTATDKSTGKANKITIT 121
Db 443 GERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVSALDKTKGKTKITIT 502
Qy 122 NDKGRSLKEETRMVQEAQKAEDEVQVRVSAKNALESYAFNMKSAVEDGLKGKISE 181
A:Residues: 1-502 <BE2>

[illegible]

R;MacFarlane, J.; Blaxter, M.L.; Bishop, R.P.; Miles, M.A.; Kelly, J.M.
Eur. J. Biochem. 190, 377-384, 1990
A>Title: Identification and characterisation of a Leishmania donovani antigen belonging
A:Reference number: S11448; MUID:90306037; PMID:2163842
A:Accession: S11448
A:Molecule type: DNA
A:Residues: 1-653 <MAC1>
A:CROSS-references: UNIPROT:P17804; EMBL:X52314
R;MacFarlane, J.
submitted to the EMBL Data Library, April 1990
A:Reference number: S11572
A:Accession: S11572
A:Molecule type: DNA
A:Residues: 1-208,'S',210-653 <MAC2>
A:CROSS-references: EMBL:X52314; NID:g9495; PIDN:CAA36551.1; PID:g9496
C:Genetics:
A:Gene: hsc70
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein comp
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match 67.7%; Score 890; DB 2; Length 653;
Best Local Similarity 63.8%; Pred.No.3.6e-50;
Matches 171; Conservative 42; Mismatches 45; Indels 10; Gaps 2;

Qy 1 KSENVQDLLLDVAPLSLGLETAGGVMTALIKRNSTIPTKTQTIFTTSDNQPGVLIOY 60
Db ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
386 KSKQTGELLDDVTPLTIGIETAGGVMTALIKRNTIPTPKSQIFSTYADNQPGVLIQVF 445
Qy 61 EGERAMTKONNLGRFELSGIPPAPRGVPQIEVTFDIDANGILNVATDTKSTGKANKITI 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
446 EGERAMTKOCHLLGTFLDSGIPPAPRGVPQIEVTFDIDANGILNVSAEKGTCGRNQITI 505
Qy 121 TNDGRLSKEIERMVQAEBKYKAEDVQRENVSAKNALSYAFNMKSAVEDGLKKGIS 180
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
506 TNDGRLSKDRIERMVDNKYEADDRAQRDEAKNGLENAYSMMKNTLGDNSNVSGKID 565
Qy 181 EADKKVKLVDCQEVISWILDANTLAEKDRFEHKKRKELEQCNPITISGLYQ---GAGGPGPG 237
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
566 DSDKATLNKEIDVLEWLSNQEQATKEEYEHKKELSVCNPTIMTKMYQSMGGAGGMGP 625
Qy 238 GF-----GAQPKGKGSQGTIBEVD 258
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
626 GMPDMSGMGGAGPAGGASSGPKVEVD 653

RESULT 69
I46588
dnak-type molecular chaperone hsp70 - pig (fragment)
N:Alternate names: heat shock protein 70
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: I46588
R;Buchman, T.G.; Cabin, D.E.; Vickers, S.; Deutschman, C.S.; Delgado, E.; Sussman, M.M.;
Surgery 108, 559-566, 1990
A>Title: Molecular biology of circulatory shock. Part II. Expression of four groups of h
A:Reference number: I46588; MUID:90371455; PMID:1697703
A:Accession: I46588
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-379 <BUC>
A:CROSS-references: UNIPROT:P34934; GB:M29506; NID:gi64494; PIDN:AAA02938.1; PID:g164495
A:Description: involved in protein folding and assembling/disassembling of protein comp
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match 67.2%; Score 883; DB 2; Length 379;
Best Local Similarity 69.1%; Pred.No.5.2e-50;
Matches 181; Conservative 33; Mismatches 38; Indels 10; Gaps 5;

Qy 1 KSENVQDLLLDVAPLSLGLETAGGVMTALIKRNSTIPTKTQTIF-TTYS DNQPGVLIQV 59

Db 124 KCEVQDLLLLDVAPLSLGLETAGVMTTLTQRTNATPTKQTQNFHYLLQNNQPGVLIQV 183
 Qy 60 YEGERAMTKONNLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKIT 119
 Db 184 YEGERAMTRONNLGRFELSGIPPTPGVPOIEVTFDIDANGILNVTATDRTGRANKMT 243
 Qy 120 ITNDKGRLSKEEIERMVOEAKYKAEDVQRRYSAKNALESYAFNMKSAAVEDGLKGI 179
 Db 244 LTKDGRLSKEEIERMVOEAKYKAEDVQRRYSAKNALESYAFNMKSAAVEDGLKGI 303
 Qy 180 SEADKKVLDKQEVTSWLDANTLAEDKDEFEHKKRKELEQVCPNPIISGLYQAGGPGPG 238
 Db 304 PEEDRCVKQDCQVPLWLEHNLAEKEEYHQRELEQIAS--ISQLL----GPGTGW 357
 Qy 239 --FGAQQPKGGSGGPTIEVD 258
 Db 358 SSCGAQPKGPGSTGPTIEVD 379
 RESULT 70
 PC7036
 heat shock protein 70 - Rhizopus nigricans (fragment)
 C;Species: Rhizopus nigricans
 C;Date: 03-Nov-2000 #sequence_revision 03-Nov-2000 #text_change 09-Jul-2004
 C;Accession: PC7036
 R;Cernila, B.; Cresnar, B.; Breakvar, K.
 Biochem. Biophys. Res. Commun. 265, 494-498, 1999
 A;Title: Induction of Hsp70 in the fungus Rhizopus nigricans.
 A;Reference number: JC7132; MUID:20025372; PMID:10558896
 A;Accession: PC7036
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-641 <CER>
 A;Cross-references: UNIPROT:Q9UVM0; GB:AF188289
 C;Superfamily: heat shock protein 70
 Query Match 67.2%; Score 883; DB 2; Length 641;
 Best Local Similarity 64.6%; Pred. No. 9.9e-50;
 Matches 170; Conservative 42; Mismatches 45; Indels 6; Gaps 3;
 Qy 2 SENVDLLLLDVAPLSLGLETAGVMTALIKRNTIPTKQTQIFTTYSNQPGLVLIQVE 61
 Db 379 SEKTDLSRLLDVAPLSLGLETAGVMTPLIKRNTIPTKQSEVFTYADNQPGLVLIQVE 438
 Qy 62 GERAMTKONNLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITIT 121
 Db 439 GELARTKONNLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITIT 498
 Qy 122 NDKGRLSKEEIERMVOEAKYKAEDVQRRYSAKNALESYAFNMKSAAVEDGLKGIKISE 181
 Db 499 NDKGRLSKEEIERMVOEAKYKAEDVQRRYSAKNALESYAFNMKSAAVEDGLKGIKISE 558
 Qy 182 ADKKVLDKQEVTSWLDANTLAEDKDEFEHKKRKELEQVCPNPIISGLYQAGGPGPG 239
 Db 559 GDKEKLERAVKQADMDNSQASKEEYHQRELEQIAS--ISQLL----GPGTGW 618
 Qy 240 --GAQQ--PKGGSGGPTIEVD 258
 Db 619 GGGAPGGFPGDGTGGEPTIEVD 641

RESULT 71
 S52727
 dnaK-type molecular chaperone hsp70 - Leishmania donovani infantum (fragment)
 N;Alternate names: heat shock protein hsp70; immunodominant antigen
 C;Species: Leishmania donovani infantum
 C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
 C;Accession: S52727
 R;Quijada, L.; Requena, J.M.; Soto, M.; Alonso, C.
 submitted to the EMBL Data Library, March 1995
 A;Description: In canine viscero-cutaneous leishmaniasis the anti-hsp70 antibodies are s
 A;Reference number: S52727

A;Accession: S52727
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-653 <QUI>
 A;Cross-references: UNIPROT:Q25292; EMBL:X85798; NID:g758135; PIDN:CAAS9793.1; PID:g758135
 C;Genetics:
 A;Gene: hsp70
 C;Function:
 A;Description: involved in protein folding and assembling/disassembling of protein complex
 C;Superfamily: heat shock protein 70
 C;Keywords: ATP; molecular chaperone
 Query Match 67.2%; Score 883; DB 2; Length 653;
 Best Local Similarity 63.1%; Pred. No. 1e-49;
 Matches 169; Conservative 44; Mismatches 45; Indels 10; Gaps 2;
 Qy 1 KSENVQDLLLLDVAPLSLGLETAGVMTALIKRNTIPTKQTQIFTTYSNQPGLVLIQV 60
 Db 386 KSKQTEGLLLLDVTPLTGLTETAGVMTALIKRNTIPTKKSQIFSTYADNQPGLVLIQV 445
 Qy 61 EGERAMTKONNLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITIT 120
 Db 446 EGERAMTKONNLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITIT 505
 Qy 121 TNDKGRLSKEEIERMVOEAKYKAEDVQRRYSAKNALESYAFNMKSAAVEDGLKGIKISE 180
 Db 506 TNDKGRLSKEEIERMVOEAKYKAEDVQRRYSAKNALESYAFNMKSAAVEDGLKGIKISE 565
 Qy 181 EADKKVLDKQEVTSWLDANTLAEDKDEFEHKKRKELEQVCPNPIISGLYQ--GAGGPGPG 237
 Db 566 DSDKATLNKEIDVVLWLSNQAEEYHKKRKELEQVCPNPIISGLYQ--GAGGPGPG 625
 Qy 238 GF-----GAQPKGGSGGPTIEVD 258
 Db 626 GMPGMSGMSGAGPAGGASGPKVEVD 653
 RESULT 72
 HHFF72
 dnaK-type molecular chaperone Hsp70Bc - fruit fly (Drosophila melanogaster)
 N;Alternate names: major heat shock protein 70 2
 C;Species: Drosophila melanogaster
 C;Date: 31-Dec-1980 #sequence_revision 31-Dec-1980 #text_change 09-Jul-2004
 C;Accession: A03307
 R;Ingolia, T.D.; Craig, E.A.; McCarthy, B.J.
 Cell 21, 669-679, 1980
 A;Title: Sequence of three copies of the gene for the major Drosophila heat shock induc
 A;Reference number: A03307; MUID:81064669; PMID:6777045
 A;Accession: A03307
 A;Molecule type: DNA
 A;Residues: 1-641 <ING>
 A;Cross-references: UNIPROT:Q9BIR7; GB:J01104; GB:J01105; NID:g157720; PIDN:AAD15226.1; f
 C;Comment: Heat shock induces the synthesis of seven proteins at five otherwise inactive
 pectively, code for the 70K protein. The function of heat shock proteins is unknown.
 C;Genetics:
 A;Gene: FlyBase:Hsp70Bc
 A;Cross-references: FlyBase:FBgn0013279
 C;Function:
 A;Description: involved in protein folding and assembling/disassembling of protein complex
 C;Superfamily: heat shock protein 70
 C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein
 Query Match 67.0%; Score 881; DB 1; Length 641;
 Best Local Similarity 65.3%; Pred. No. 1.3e-49;
 Matches 175; Conservative 34; Mismatches 41; Indels 18; Gaps 4;
 Qy 1 KSENVQDLLLLDVAPLSLGLETAGVMTALIKRNTIPTKQTQIFTTYSNQPGLVLIQV 60
 Db 382 QSKQIQDVLVLDVAPLSLGLETAGVMTALIKRNTIPTKQIFSTYADNQPGLVLIQV 441
 Qy 61 EGERAMTKONNLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITIT 120
 Db 442 EGERAMTKONNLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITIT 501

[illegible]

A;Map position: 2L

C;Function:

A;Description: involved in protein folding and assembling/diseassembling of protein comp

C;Superfamily: heat shock protein 70

C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 66.5%; Score 874; DB 2; Length 649;
Best Local Similarity 63.3%; Pred. No. 3.8e-49;
Matches 171; Conservative 37; Mismatches 48; Indels 14; Gaps 3;

Qy 1 KSENVQDILLDLVAPLSIGLGTAGGVNTALIKRNSTIPTKQTQIFTTYSNDQPGVLIOVY 60
Db 382 QSTKTQDILLDLVAPLSIGLGTAGGINTKILPRNSTIPTKKSETFTSYADNPQVLIQVF 441
Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 442 EGEKTRTKDNNLLGRFELSGIPPPAPRGVPOIDVTFDIDANGILNVSLEKGTGKSNKITI 501
Qy 121 TNDKGRLSKEBIEIRMVQEAKEYKAEDVEQRRVSAKNALYESYAFNMKSAYEDELGKGKIS 180
Db 502 TNDKGRLSKDDIDRMVSEAEKYRADDERAEERVOAKNQLESYAFTLKANTINEASFKEKVG 561
Qy 181 EADKKKVLDKQEVISWLDANTLAEKDEFEHKKRKELEQVCNPIISGLYQAGAGGPGP---- 236
Db 562 EDDAKRLKETASQETIDWLDSQAASSTDEYKDRQKEGIANPIMTKFYGAGAGPGPAGE 621
Qy 237 -GGP-----GAQPKGGSGSGPTIEEVD 258
Db 622 SGGFPGSGMPNSGATG--GGEDTGTVEVD 649

RESULT 78

A34041

dnak-type molecular chaperone - mouse

N;Alternate names: heat shock protein 70-related protein

C;Species: Mus musculus (house mouse)

C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004

C;Accession: A34041

R;Matsumoto, M.; Fujimoto, H.
Biochem. Biophys. Res. Commun. 166, 43-49, 1990

A;Title: Cloning of a hsp70-related gene expressed in mouse spermatids.

A;Reference number: A34041; MUID:90147735; PMID:2302214

A;Accession: A34041

A;Molecule type: DNA; mRNA

A;Residues: 1-630 <MAT>

A;Cross-references: UNIPROT:p16627; GB:M32218

C;Function:

A;Description: involved in protein folding and assembling/diseassembling of protein comp

C;Superfamily: heat shock protein 70

C;Keywords: ATP; molecular chaperone

Query Match	66.4%;	Score 873;	DB 2;	Length 630;
Best Local Similarity	72.2%;	Pred. No. 4.3e-49;		
Matches 187;	Conservative 17;	Mismatches 45;	Indels 10;	Gaps 5;
Qy	1	KSENVQDLLLLDVAPLSLGLETAGGVMVTLKRNSTPTKQTQFTTYSNDQNPQVLQVY	60	
Db	381	KSEKVDLLLLDVAPLSLGLETAGGVMVTLKRNSTPTKQTQFTTYSNDQNPQVLQTC-	439	
Qy	61	EGERAMTKDNNLLGRFELSGIPPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI	120	
Db	440	--TRQTPIDNNLVGPFDLTGIPAP-SVPQIEVTFDIARNGILNVATMDKSTGKANKITI	496	
Qy	121	TNDGRLSKEEIERMVQAEKVKAEDEVQREVSRVSKNALESYAFNMKSAVEDEGLGKGIS	180	
Db	497	TNDGRLSKEEID-SIESRTAYKREDEGQREKIAAKNALESYAFNMKSAACDDEGLKDKIT	555	
Qy	181	EADKKKVLDKQEVYSIWDANTLAEKDFEHRKRELEQVNCNPIISGLYQ-GAGGPGPGGF	239	
Db	556	ESDKKKILDKNEVPFLLSQTLAEKVEFDHKKRELENNCNPIITKLQSGCTGPTV---	612	
Qy	240	GAQPGKGSGSGPTIEVD	258	

Db	613	-RGILRQSGTGPTIEVD	630
RESULT 79			
A48872			
dnak-type molecular chaperone hspB -			
N:Alternate names: 70k heat shock cogn			
C:Species: Dictyostelium discoideum			
C:Date: 19-May-1995 #sequence_revisio			
C:Accession: A48872			
R:Eddy, R.J.; Sauter, R.A.; Condeelis			
J. Biol. Chem. 268, 23267-23274, 1993			
A:Title: Aginactin, an agonist-regula			
A:Reference number: A48872; MUID:94040			
A:Accession: A48872			
A>Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-636 <EDD>			
A:Cross-references: UNIPROT:P36415; G			
A:Note: authors translated the codon			
C:Function:			
A:Description: involved in protein fo			
C:Superfamily: heat shock protein 70			
C:Keywords: ATP; molecular chaperone			
Query Match 66.1%; Score			
Best Local Similarity 65.9%; Pre			
Matches 170; Conservative 35;			
Qy	5	VQDLILLVAPILSLGLETAGGVMMV	65
Db	382	VADLLLLDVAPISLMSGLTAGGVMMV	65
Qy	65	AMTKNNLLGRFELSGIPAPRGR	65
Db	442	AMTKNNLLGKELSGIPAPRGR	65
Qy	125	GRLSKEEIERMVOEAKYKADE	65
Db	502	GRLSKEEIERMVADEAKFKQD	65
Qy	185	KKVLDKQCVISWLDANTLAED	65
Db	562	STIESETEVLKWLNSNTQAKD	65
Qy	241	AQQPKGGSGSGPTIEVD	258
Db	622	NDSFK--SSNNKVDEL	636
RESULT 80			
S37394			
dnak-type molecular chaperone hsc70 -			
N:Alternate names: heat shock cognate			
C:Species: Dictyostelium discoideum			
C:Date: 31-Dec-1993 #sequence_revisio			
C:Accession: S37394			
R:Haus, U.; Trommler, P.; Fisher, P.R.			
EMBO J. 12, 3763-3771, 1993			
A:Title: The heat shock cognate prote			
A:Reference number: S37394; MUID:94000			
A:Accession: S37394			
A:Molecule type: mRNA			
A:Residues: 1-640 <HAU>			
A:Cross-references: UNIPROT:P36415; E			
C:Genetics:			
A:Gene: hsc70			
C:Function:			
A:Description: involved in protein fo			
C:Superfamily: heat shock protein 70			
C:Keywords: ATP; molecular chaperone			
Query Match 66.1%; Score			

Query Match 66.1%; Score 868.5; DB 2; Length 640;

```

Best Local Similarity   65.9%, Pred. No. 8.6e-49;
Matches 170; Conservative 35; Mismatches 46; Indels 7; Gaps 2;

Qy      5 VQDLLLLDVAPLSGLGTAGGVTMLTKRNSTIPTKQTIFTVYSDNQPGVLIOVYGER    64
Db      386 VADLLLLDVAPLSMGLGTAGGVTMLTPRNTTIFCKTIQTFSTVDNQPGVLIOVYGER    445

Qy     65 AMTKDNLLGRFELSGIPPRGPVPQIEVTFIDANGILNVATDKSTGKANKITITNDK    124
Db     446 AMTKDNLLGKFELSGIPPRGPVPQIEVTFVDANGILNVAEDKSTGNKQKITITNDK    505

Qy     125 GRLSKEBIERNVQAABKYKAEDVFQRERVSANNALESYAFNMKSADVDEGLKGKISADK    184
Db     506 GRLSKEBIEKNVADAABKFQKDQQOKDRVESKNLENYAFTVKNSIKDEKVAAKISDSK    565

Qy     185 KKVLDDKCQEVTSWLDANTLAEKDFEHRKRKELEOVCPNIISGLYQGAGGGP-----PCGFG    240
Db     566 STIESFETSVLKULESNQTAEKEDIEDNKKALEAVNPIMSKLYQEGLMPGGGMPGGMGS    625

Qy     241 AQPKGGSGSGPTTIEEVD    258
Db     626 NDSFK---SSNNKKVDELQ    640

```

RESULT 81
JU0164
dnak-type molecular chaperone - malaria parasite (Plasmodium falciparum)
N:Alternate names: heat shock protein 70-related protein
C:Species: Plasmodium falciparum
C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C/Accession: JU0164
R:/Yang, Y.P.; Tan-ariya, P.; Sharma, Y.D.; Kilejian, A.
Mol. Biochem. Parasitol. 26, 61-68, 1987
A:/Title: The primary structure of a Plasmodium falciparum polypeptide related to heat shock protein 70
A:/Reference number: JU0164; MUID:88122267; PMID:2448622
A:/Accession: JU0164
A:/Molecule type: mRNA
A:/Residues: 1-681 <VAN>
A:/Cross-references: UNIPROT:P11144; GB:M19753; NID:G309689; PIDN:AAA29626.1; PID:G309650
C:/Function:
A:/Description: involved in protein folding and assembling/disassembling of protein complex
C:/Superfamily: heat shock protein 70
C:/Keywords: ATP; molecular chaperone; tandem repeat
F:/632-661/Region: 4-residue repeats

[illegible]

RESULT 82
A49242
dnaK-type molecular chaperone hsp70 - Plasmodium cynomolgi

N:Alternate names: heat shock protein hsp70
C:Species: Plasmodium cynomolgi
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A49242
R:Eckert, V.; Sanchez, L.; Cochrane, A.; Enea, V.
Exp. Parasitol. 75, 323-328, 1992
A:Title: Plasmodium cynomolgi: the hsp 70 gene.
A:Reference number: A49242; MUID:93050041; PMID:1426134
A:Accession: A49242
A:Status: Preliminary
A:Molecule type: nucleic acid
A:Residues: 1-686 <ECK>
A:Cross-references: UNIPROT.Q05746; GB:M90978; NID:G160349; PIDN:AAA29625.1; PID:G160350
A:Note: sequence extracted from NCBI Backbone (NCBIN:118975, NCBIP:118976)
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein complex
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

[illegible]

RESULT 83
JC4610
dnaK-type molecular chaperone hsp70 - Oxytricha nova
N/Alternate names: heat-shock protein 70; Hsp 70
C/Species: Oxytricha nova
C/Date: 10-Apr-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C/Accession: JC4610
R/Anderson, R.C.; Lindauer, K.R.; Prescott, D.M.
Gene 168, 103-107, 1996
A/Title: A gene-sized DNA molecule encoding heat-shock protein 70 in Oxytricha nova.
A/Reference number: JC4610; MUID:96186964; PMID:8626054
A/Accession: JC4610
A/Molecule type: DNA
A/Residues: 1-651 <AND>
A/Cross-references: UNIPROT:Q27150; GB:U37280; NID:gl051275; PIDN:AA804940.1; PID:gl051275
C/Comment: The expression of hsp70 gene is regulated at the transcriptional level.
C/Genetics:
A/Gene: hsp70
A/Genetic code: SGC5
C/Function:
A/Description: involved in protein folding and assembling/diseassembling of protein complex
C/Superfamily: heat shock protein 70
C/Keywords: ATP; heat shock; molecular chaperone; stress-induced protein
F/1-355/Domain: ATPase active #status predicted <ATA>
F/356-519/Domain: polypeptide binding #status predicted <POB>

Query Match	65.6%	Score	862.5	DB	2	Length	651
Best Local Similarity	66.0%	Pred. No.	2.1e-48				
Matches 169	Conservative	33	Mismatches	47	Indels	7	Gaps

QY 4 NVQDLLLLDVAPLSLGLSTAGGWTALIKRNSITPTKQTQIFTTYSDNQPGVLIOVVE 63
 DB 387 NVQDLLLLDVAPLSLGLSTAGGWTALIGRNTTPTKKSQIFTTYADNQPGVLIOVVE 446
 QY 64 RAMTKDNMLGRPELSGIPAPRGVPQIETVFDIDANGILNVTATDKSTGKANKITITND 123
 DB 447 RSMTKDNMLGKNLEGIIPAPRGVPQIETVFDIDANGILNVSADVKGTKINKITITND 506
 QY 124 KGRLSKEEIERMVOEAEKYKAEDVQRRVRSYAKNALESYAFNMKSAVEDEGLKGKISEAD 183
 DB 507 KGRLSKEEIEKWVNDAEKPKGEDEKMKRIEAKNSPENYCFQMKNTLNDEKLEKFTEDD 566
 QY 184 KKKVLDKQEVISWLDANTLAEKDFEHRKKELEBOVCNPIISGLYQAGG-----PG--P 236
 DB 567 KKVIEDASKEGLOWLEGNPMAEPETEIAKQKEVEAKYNPIIMRVYQAAGMPGGMFGMP 626
 QY 237 GGFQGAQPGKGGSGGP 252
 DB 627 GGMPPGGPFGAGGAAP 642

RESULT 84
 T46650
 heat shock protein 70 [imported] - Neurospora crassa
 C:Species: Neurospora crassa
 C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004
 C:Accession: T46650
 R:Kapoor, M.; Cutler, C.A.; Runham, C.
 J. Bacteriol. 177, 212-221, 1995
 A:Title: The hsp70 gene family of Neurospora crassa: cloning, sequence analysis, expression
 A:Reference number: T23115; MUID:95095970; PMID:7798134
 A:Accession: T46650
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-646 <KAP>
 A:Cross-references: UNIPROT:Q01233; EMBL:U10443; MID:g607817; PIDN:AAA82183.1; PID:g607817
 C:Genetics:
 A:Gene: hsp70
 A:Map position: LGII
 A:Introns: 23/3; 247/1; 353/1; 360/3
 C:Superfamily: heat shock protein 70

Query Match 65.5%; Score 861; DB 2; Length 646;
 Best Local Similarity 60.5%; Pred. No. 2.6e-48;
 Matches 159; Conservative 48; Mismatches 50; Indels 6; Gaps 1;

QY 2 SENVQDLLLLDVAPLSLGLSTAGGWTALIKRNSITPTKQTQIFTTYSDNQPGVLIOVVE 61
 DB 384 SKSTSEILLDDVAPLSLGIETAGGWTCLKIPRNTTPTKKSVEFSTFSDNQPGVLIOVVE 443
 QY 62 GERAMTKDNMLGRPELSGIPAPRGVPQIETVFDIDANGILNVTATDKSTGKANKITIT 121
 DB 444 GERQRTKDNMLGKPELTGTPAPRGVPQIETVFDVDANGIMNVSALEKGTGKTNQITIT 503
 QY 122 NDKGRLSKEEIERMVOEAEKYKAEDVQRRVRSYAKNALESYAFNMKSAVEDEGLKGKISE 181
 DB 504 NDKGRLSKEEIERMLAEAEKFEDEAEAKVAAKNGLESYAYSLRNTLSDSKVDEKIDA 563
 QY 182 ADKKVLDKQEVISWLDANTLAEKDFEHRKKELEBOVCNPIISGLYQAGGPG----- 235
 DB 564 ADKEKLKSEIDKIVAWLDENQQAQTRBEYERQKELEAIANPIIMKVFYAGGAGPGMGAA 623
 QY 236 PGGFQGAQPGKGGSGGPTIEVD 258
 DB 624 PGGFPGGAPGSDNEGPTVEVD 646

RESULT 85
 A26485
 dnak-type molecular chaperone - malaria parasite (Plasmodium falciparum) (fragments)
 N:Alternate names: cytoplasmic antigen
 C:Species: Plasmodium falciparum

C>Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 09-Jul-2004

R/Accession: A26485
R/Bianco, A.E.; Favalaro, J.M.; Burkot, T.R.; Culvenor, J.G.; Crewther, P.E.; Brown, G.V.
Proc. Natl. Acad. Sci. U.S.A. 83, 8713-8717, 1986
A>Title: A repetitive antigen of Plasmodium falciparum that is homologous to heat shock
A/Reference number: A26485; MUID:87041522; PMID:3095842
A/Accession: A26485
A/Molecule type: mRNA
A/Residues: 1-313 <BIA>
A/Cross-references: UNIPROT:Q25791; GB:M14655; NID:g160111; PIDN:AAC12678.1; PID:g160112
C/Function:
A/Description: involved in protein folding and assembling/diseassembling of protein comp
C/Superfamily: heat shock protein 70
C/Keywords: ATP; molecular chaperone

Query Match 65.5%; Score 860.5; DB 2; Length 313;
Best Local Similarity 61.4%; Pred. No. 1.2e-48;
Matches 172; Conservative 37; Mismatches 48; Indels 23; Gaps 3;

Qy 1 KSENVQDLLLLDVAPLSLGLETAGGVTALIKRNSTIPTKQTQIFFTYSDNQPGVLIQVY 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
31 QSNVQDLLLLDVCSLSGLSETAGGVTAKLIERNTTTPAKSKQIFTTYADNQPGVLIQVY 90
Qy 61 EGERAMTKDNLLGRFELSGLPPAPRGVPQLEVTFDIDANGILNVTTATDKSTGKANKITI 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
91 EGERALTKDNLLGKFHLDGIPPAPRKVPQLEVTFDIDANGILNVTTAVKSTGKQNHTI 150
Qy 121 TNDGRSLKEBIERMVOAEKYKAEDVQRVSNAKNALESYAFNMKSVADEGLKGKIS 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
151 TNDGRISOEIDRWVDNAEKYKAEDENRRKRIEARNLSLENICYGVKSLSLEDQKIIEKLQ 210
Qy 181 EADKKVKLVDCQEIVSMILDANTLAEBKBFHKRKELEVCPNPPIISGLYQGAGG----- 233
Db : : : : : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
211 PAETETCMKTITITLEWLEKQLAGSVEAYEQEAESVCAPIMSKIYQDAAGAAGMPG 270
Qy 234 -----PG-----PGCGAQGPKG--SGSGPTIEEV 257
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
271 GMPGPMGGPMGGMNFPGMGAGMGNAPAGSGPTVEEV 310

RESULT 86
B31238
dnak-type molecular chaperone - malarial parasite (Plasmodium falciparum) (fragments)
N/Alternate names: heat shock protein 70-related protein
C/Species: Plasmodium falciparum
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jun-2000
C/Accession: B31238
R/Kumar, N.; Synn, C.; Carter, R.; Quakyi, I.; Miller, L.H.
Proc. Natl. Acad. Sci. U.S.A. 85, 6277-6281, 1988
A>Title: Plasmodium falciparum gene encoding a protein similar to the 78-kDa rat glucose
A/Reference number: A94204; MUID:88320425; PMID:3045815
A/Accession: B31238
A/Molecule type: DNA
A/Residues: 1-313 <KUM>
A/Note: the sequence shown in Fig.2 is lacking residue 181-Aen
C/Function:
A/Description: involved in protein folding and assembling/diseassembling of protein comp
C/Superfamily: heat shock protein 70
C/Keywords: ATP; molecular chaperone

Query Match 65.3%; Score 857.5; DB 2; Length 313;
Best Local Similarity 61.6%; Pred. No. 1.8e-48;
Matches 173; Conservative 37; Mismatches 48; Indels 23; Gaps 4;

Qy 1 KSENVQDLLLLDVAPLSLGLETAGGVTALIKRNSTIPTKQTQIFFTYSDNQPGVLIQVY 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
33 QSNVQDLLLLDVCSLSGLSETAGGVTAKLIERNTTTPAKSKQIFTTYADNQPGVLIQVY 92
Qy 61 EGERAMTKDNLLGRFELSGLPPAPRGVPQLEVTFDIDANGILNVTTATDKSTGKANKITI 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
93 EGERALTKDNLLGKFHLDGIPPAPRKVPQLEVTFDIDANGILNVTTAVKSTGKQNHTI 152
Qy 121 TNDGRSLKEBIERMVOAEKYKAEDVQRVSNAKNALESYAFNMKSVADEGLKGKIS 180

A;Description: Sequence and IgB-binding sites of an allergen, Cla h IV, of Cladosporium
A;Reference number: S49303
A;Accession: S49303
A:Molecule type: mRNA
A;Residues: 1-643 <SHA>
A;Cross-references: UNIPROT:P40918; EMBL:X81860; NID:g551227; PIDN:CMA57452.1; PID:g5512
A;Experimental source: tissue type mycelia
C;Genetics:
A;Gene: hsp70
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein compo
C;Superfamily: heat shock protein 70
C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 64.1%; Score 842.5; DB 2; Length 643;
Best Local Similarity 61.7%; Pred. No. 4.1e-47;
Matches 161; Conservative 45; Mismatches 50; Indels 5; Gaps 2;

Qy 2 SENVODLLLDVAPLSGLGTAGGVTALIKRNSTIPTKTQTFTTYSNDQNPGVLIOVYE 61
Db : :: : ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
 384 SKSKTEILLDVAPLSLGIETAGGVMTALIKRNTTIPTKSETFSTFSNDNQPVGLIQVF 443

Qy 62 GERAMTKDNMLGRFELSGIIPPARGVPQLVEVTFDDANGILNVATDKSTGKANITIT 121
Db : ||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 444 GERARTKDINLMGFELSGIRPARGPVQLVEVTFDDLNGIMNVSALEKGTGTKNKIVIT 503

Qy 122 NDGRLSKEIERMVQAEKYKAEDYQRRERSAKNALESYAFNMKSASAVEDEGLKGKISE 181
Db : ||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 504 NDGRLSKEIERMLDAEKYKEEDEAEAGR IQAKNGLESYAVSLKNVTSDPKVEEKL SA 563

Qy 182 ADKKVVLDCKOEVI SWILDANTLAQRFEHKKRKELEVCHNPISIGLYQGAGGPPGGFGA 241
Db : :: : : | | : | | : | | : | | : | | : | | : | | : | | : | | | | |
 564 EDKETLTGAIDKTVAMDENQTA TKEEYAEQK QLESVANPVMVKIY - GAEGGAPGGMPG 622

Qy 242 QG-----PKGGSGSGPTIEEVD 258
Db 623 QGAGAPPGAGDDGPTVEEVD 643

RESULT 90
A44985
dnaak-type molecular chaperone 70.1 - Theileria annulata
N;Alternate names: heat shock protein 70.1
C;Species: Theileria annulata
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change_07-May-1999
C;Accession: A44985
R;Mason, P.J.; Shields, B.R.; Tait, A.; Beck, P.; Hall, R.
Mol. Biochem. Parasitol. 37, 27-36, 1989
A;Title: Sequence and expression of a gene from Theileria annulata coding for a 70-kilod
A;Reference number: A44985; MUID:90136713; PMID:2515435
A;Accession: A44985
A;Status: preliminary
A:Molecule type: DNA
A;Residues: 1-646 <MAS>
A;Cross-references: GB:J04653
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein compo
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 64.1%; Score 842; DB 2; Length 646;
Best Local Similarity 62.6%; Pred. No. 4.5e-47;
Matches 164; Conservative 38; Mismatches 56; Indels 4; Gaps 1;

Qy 1 KSENVODLLLDVAPLSGLGTAGGVTALIKRNSTIPTKTQTFTTYSNDQNPGVLIOVY 60
Db : ||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 385 QSERKIQLLEDVAPLSGLGTAGGVTMLIKRNTTIPTKKNQIFTTNEDEQEVGLIQVF 444

Qy 61 EGERAMTKDNMLGRFELSGIIPPARGVPQLVEVTFDDANGILNVATDKSTGKANITI 120
Db : ||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 445 EGERAMTKDNMLLGKFLHTGAPRGVPQLVEVTFDDLNGILNVATANDKSTGKSEHTI 504

Qy 121 TNDRGLRSKEIERMVQAEKYKAEDYQRRERSAKNALESYAFNMKSASAVEDEGLKGKIS 180


```

Qy 15 PLSLGLETAGGVMTALIKRNSTIPTKQTQIETFTYSDNQPVLVIQVVEGERAMTKNNLLG 74.
Db 1 PLTGIEIAGGVMVSLIKRNTTIPTKSQIFSTYDPDQPGVHIQVFEGERAMTKDCHLLG 60
Qy 75 RFELSGIPPAIPRGVPQIEVTFDIDANGILNVATATDKSTGKANKITITNDKGRLSKEIER 134
Db 61 TFDLSGIPPAIPRGVPQIEVTFDLDANGILNVSAEEKGTGRNQIVITNDKGRLSKADIER 120
Qy 135 MVQBAEKYKAEDVQORVRSNAKNALESVAFNMKSAVEDEGLKKGKISEADKKVKLDKQREV 194
Db 121 MVSEAAKYEADQKQDRIDAKGLNGLYAFNMKNTVNEPNVAGKTEADKNTITTSABVEEA 180
Qy 195 ISWLDANTLAEKDFEHRKKELEOVCPNIISGLYO--GAGGPGPGCGFCAQGPKG----- 246
Db 181 LQWLNNOQASKEEVEHROKELENLCTPIMTKYQGMGAGGGMFGMFGMFGMFGMFGMGP 240
Qy 247 -----GSGSGPTTIEVD 258
Db 241 GMPGGANPSSSSGPKVEVD 261

RESULT 96
T45468
dnak-type molecular chaperone Hsp70 [imported] - bloodfluke planorb
N;Alternate names: heat shock protein 70
C;Species: Biomphalaria glabrata (bloodfluke planorb)
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
C;Accession: T45468
R;Yoshino, T.P.; Wu, X.J.; Liu, H.D.
submitted to the EMBL Data Library, November 1997
A;Description: Transfection and heat-inducible expression of a molluscan promot
A;Reference number: 222978
A;Accession: T45468
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-636 <YOS>
A;Cross-references: UNIPROT:O4343; EMBL:AF025477; PIDN:AMB99911.1
A;Experimental source: strain PR albino
C;Genetics:
C;Superfamily: heat shock protein 70

```

C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A48439
C;R;Ortner, S.; Plaimauer, B.; Binder, M.; Wiedermann, G.; Scheiner, O.; Duchens, M.
Mol. Biochem. Parasitol. 54, 175-183, 1992
A;Title: Humoral immune response against a 70-kilodalton heat shock protein of *Entamoeba*
A;Reference number: A48439; MUID:93063033; PMID:1435858
A;Accession: A48439
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-656 <ORT>
A;Cross-references: UNIPROT:Q24842; GB:M84652; NID:gi58955; PIDN:AAA29102.1; PID:gi58956
A;Experimental source: SPL-3 trophozoites
A;Note: sequence extracted from NCB1 backbone (NCBIN:117218, NCBIP:117219)
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein compl
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Result No.	Score	Query Match	DB ID	Length	Description	
1	1314	100.0	641	2	AAW54349	Human hea
2	1314	100.0	641	3	AAE23652	Human hea
3	1314	100.0	641	4	AAE82534	Human hea
4	1314	100.0	641	4	AAE12986	Human Hsp
5	1314	100.0	641	6	ABU89711	Protein d
6	1314	100.0	641	7	ADD74759	Human Pro
7	1314	100.0	641	7	ADJ27279	Human HSP
8	1314	100.0	641	8	ADJ76981	Human pro
9	1314	100.0	641	8	ADL82939	Human PRO
10	1314	100.0	641	8	ABM80760	Tumour-as
11	1312	99.8	641	7	ADL20102	Hsp70. 4/
12	1309	99.6	476	7	ADM04781	Human pro
13	1309	99.6	641	6	ABR40400	Human HSP
14	1309	99.6	641	7	ADF76349	Novel hum
15	1309	99.6	641	8	ABM80759	Tumour-as
16	1298.5	98.8	554	3	AAV88410	Human hea
17	1298.5	98.8	554	3	AAV88409	Human hea
18	1298.5	98.8	640	3	AAE23653	Human hea
19	1298.5	98.8	640	7	ADD14137	Human src
20	1298.5	98.8	640	7	ADJ68449	Human hea
21	1295	98.6	641	6	ABR40399	Bovine HS
22	1290.5	98.2	640	3	AAW10065	Human hea
23	1290.5	98.2	640	3	AAV88408	Human hea
24	1282	97.6	640	2	AAR03929	Homo sapi
25	1278.5	97.3	640	3	AAV88411	Human hea

99 1012 77.0 643 8 ADP12947 Protein e
100 1012 77.0 643 8 ADRI4395 Human NF-

ALIGNMENTS

RESULT 1
AAW54349
ID AAW54349 standard; protein; 641 AA.

XX AC AAW54349;
XX 14-AUG-1998 (first entry)
XX Human heat shock 70 kD protein 1.
XX Endometrium; hyperplasia; adenocarcinoma; proliferative phase;
XX 2D gel electrophoresis; detection.

XX Homo sapiens.
XX OS
XX WO9810291-A1.
XX 12-MAR-1998.

XX 05-SEP-1997; 97WO-GB002394.
XX 06-SEP-1996; 96GB-00018600.
XX 08-APR-1997; 97GB-00007132.

XX (CLIN-) CENT CLINICAL & BASIC RES.
XX Byrjalsen I, Larsen P, Fey SJ;
XX WPI; 1998-207057/18.

XX Biochemical markers of human endometrium - useful for, e.g. diagnosis of
XX hyperplasia and adenocarcinoma.
XX Disclosure; Page 19; 77pp; English.

XX Proteins AAW54349-W54364 are examples of proteins produced in the
XX endometrium during the hyperplasia, adenocarcinoma or proliferative phase
XX of the endometrium. The presence and quantities of these proteins can be
XX detected using 2D gel electrophoresis comparison of cell lysates. The
XX proteins can be used as biochemical markers to detect the phase of the
XX endometrium and can be measured in body fluids, obviating the need for
XX endometrial biopsies

XX Sequence 641 AA;
Query Match 100.0%; Score 1314; DB 2; Length 641;
Best Local Similarity 100.0%; Pred. No. 8.8e-101;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSENVQDILLDDVAPLSLGLTAGGVTALIKRNSITPTKQTOIFTTYSNQPGVLIQVY 60
DB 384 KSENVQDILLDDVAPLSLGLTAGGVTALIKRNSITPTKQTOIFTTYSNQPGVLIQVY 443

QY 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVQIETVFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKDNNLLGRFELSGIPPPAPRGVQIETVFDIDANGILNVTATDKSTGKANKITI 503

QY 121 TNDKGRLSKEIERMVOEAKYKAEDVQERVSAKNALESYAFNMKSAVEDGLKCKIS 180
DB 504 TNDKGRLSKEIERMVOEAKYKAEDVQERVSAKNALESYAFNMKSAVEDGLKCKIS 563

QY 181 EADKKKVLDDKQEVISWLDANTLAEKDFEHRKELEQVCNPIISGLYQAGGPGPGFG 240
DB 564 EADKKKVLDDKQEVISWLDANTLAEKDFEHRKELEQVCNPIISGLYQAGGPGPGFG 623

QY 241 AOGPKGGSGSGPTIEVD 258

DB 624 AOGPKGGSGSGPTIEVD 641

RESULT 2
AAB23652
ID AAB23652 standard; protein; 641 AA.

XX AC AAB23652;
XX 05-JAN-2001 (first entry)
XX Human heat shock protein Hsp70.1 protein sequence SEQ ID NO:4.
XX ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;
XX immune response; infectious disease; malaria; cytotoxic T cell;
XX cytototoxic; immunostimulant; cellular immune response inducer;
XX protozoicide; leukaemia; cancer.

XX Homo sapiens.
XX OS
XX WO200049041-A1.
XX 24-AUG-2000.

XX 18-FEB-2000; 2000WO-JP000941.
XX 19-FEB-1999; 99JP-00041535.

XX (SUME) SUMITOMO ELECTRIC IND CO.
XX Shinbara N, Udono H, Yui K;
XX WPI; 2000-543748/49.

XX Fused protein capable of inducing cellular immune response, useful as
XX active ingredient for drug compositions in preventing and/or treating
XX infectious diseases such as malaria or cancer.
XX Claim 3; Page 46-48; 72pp; Japanese.

XX The present invention describes a fused protein (I) prepared from a
XX peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by
XX cytotoxic T cells and a protein containing the ATPase domain of a heat
XX shock protein. Also described are: (1) a drug composition containing (I)
XX as active ingredient; (2) a DNA encoding (I); (3) an expression vector
XX containing the DNA of (2); and (4) a transformant which can retain the
XX expression vector of (3). (I) has cytostatic, immunostimulant and
XX protozoicide activities, and can be used as a cellular immune response
XX inducer. The protein is useful as an active ingredient for drug
XX compositions in preventing and/or treating infectious diseases such as
XX malaria or cancer e.g. to provide systemic immunity against leukaemia.
XX The present sequence represents a specifically claimed heat shock protein
XX for use in a fused protein of the present invention

XX Sequence 641 AA;

Query Match 100.0%; Score 1314; DB 3; Length 641;
Best Local Similarity 100.0%; Pred. No. 8.8e-101;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSENVQDILLDDVAPLSLGLTAGGVTALIKRNSITPTKQTOIFTTYSNQPGVLIQVY 60
DB 384 KSENVQDILLDDVAPLSLGLTAGGVTALIKRNSITPTKQTOIFTTYSNQPGVLIQVY 443

QY 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVQIETVFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKDNNLLGRFELSGIPPPAPRGVQIETVFDIDANGILNVTATDKSTGKANKITI 503

QY 121 TNDKGRLSKEIERMVOEAKYKAEDVQERVSAKNALESYAFNMKSAVEDGLKCKIS 180
DB 504 TNDKGRLSKEIERMVOEAKYKAEDVQERVSAKNALESYAFNMKSAVEDGLKCKIS 563

QY 181 EADKKVLDKQCVISWLDANTLAEDFEHKKKELEQVCNPIISGLYQAGGPGGPG 240
 DB 564 EADKKVLDKQCVISWLDANTLAEDFEHKKKELEQVCNPIISGLYQAGGPGGPG 623

QY 241 AQPCKGSGSGPTIEVD 258
 DB 624 AQPCKGSGSGPTIEVD 641

RESULT 3
 AAB82534
 ID AAB82534 standard; protein; 641 AA.
 XX
 AC AAB82534;
 XX
 DT 17-SEP-2001 (first entry)
 XX
 DE Human heat shock protein Hsp71.
 XX
 KW Hsp71; human; heat shock protein; immunotherapy; therapy; cancer;
 KW infection; vaccine.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Binding-site 391..615
 FT /note= "peptide-binding domain"
 FT Region 395..502
 FT /note= "beta-helix motif"
 FT Binding-site 400..440
 FT /note= "peptide-binding core"
 FT
 XX WO200152791-A2.
 PN
 XX
 PD 26-JUL-2001.
 XX
 PF 18-JAN-2001; 2001WO-US001781.
 XX
 PR 20-JAN-2000; 2000US-00488393.
 XX
 PA (UYCO-) UNIV CONNECTICUT HEALTH CENT.
 XX
 PI Srivastava PK;
 XX
 XX WPI; 2001-457506/49.
 XX
 PT Pharmaceutical composition, used to treat or prevent infection or cancer,
 PT comprises a complex comprising a heat shock protein-binding fragment
 PT associated with a molecule displaying antigenicity of an infectious agent
 PT or cancer cell.
 XX
 PS Claim 46; Fig 1C; 106pp; English.
 XX
 CC The present sequence is that of human heat shock protein (HSP) Hsp71, an
 CC inducible form of a Hsp70 family protein. The invention relates to
 CC complexes of peptide-binding fragments of HSPs with antigenic molecules
 CC and their use in immunotherapy for the treatment of infectious diseases
 CC and cancer. Claimed methods of treating or preventing cancer/infectious
 CC disease involve culturing a cancer cell/infected cell transformed with a
 CC nucleic acid encoding a HSP peptide-binding domain, recovering complexes
 CC of the HSP fragments noncovalently associated with peptides from the
 CC cancer cell/infected cell, and administering the recovered complexes.
 CC These methods can use Hsp71 peptide-binding fragments comprising amino
 CC acids 391-615 and 400-440 of the present sequence, i.e. the peptide-
 CC binding domain and peptide-binding core
 XX
 SQ Sequence 641 AA;
 Query Match 100.0%; Score 1314; DB 4; Length 641;
 Best Local Similarity 100.0%; Pred. No. 8.8e-101;
 Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSENVQDLLLDVAPLSLGTAGVMTALIKRNSTIPTKTQTIFFTSYDQGVLIQVY 60

DB 384 KSENVQDLLLDVAPLSLGTAGVMTALIKRNSTIPTKTQTIFFTSYDQGVLIQVY 443
 QY 61 EGERAMTKDNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 444 EGERAMTKDNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEEIERMVQEAKEYKAEDVQERVSAAKNALESYAFNMKSAVEDSLGKGKIS 180
 DB 504 TNDKGRLSKEEIERMVQEAKEYKAEDVQERVSAAKNALESYAFNMKSAVEDSLGKGKIS 563
 QY 181 EADKKVLDKQCVISWLDANTLAEDFEHKKKELEQVCNPIISGLYQAGGPGGPG 240
 DB 564 EADKKVLDKQCVISWLDANTLAEDFEHKKKELEQVCNPIISGLYQAGGPGGPG 623

QY 241 AQPCKGSGSGPTIEVD 258
 DB 624 AQPCKGSGSGPTIEVD 641

RESULT 4
 AAE12986
 ID AAE12986 standard; protein; 641 AA.
 XX
 AC AAE12986;
 XX
 DT 28-JAN-2002 (first entry)
 XX
 DE Human Hsp70 family homologue, Hsp71.
 XX
 KW Heat shock protein; HSP; HSP peptide-binding fragment; HSPB; vaccine;
 KW cytotoxic T cell response; hepatitis virus; herpes simplex virus;
 KW human immunodeficiency virus; bacteria; Mycobacteria; Rickettsia;
 KW protozoa; Leishmani; Trypanosoma; intracellular parasite; Chlamydia;
 KW sarcoma; carcinoma; cancer; human; Hsp70 homologue; Hsp71.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Binding-site 391..615
 FT /note= "peptide binding domain"
 FT Binding-site 396..502
 FT /note= "p-helix motif"
 FT Domain 402..442
 FT /note= "Central core of peptide binding domain"
 FT
 XX US2001034042-A1.
 PN
 XX 25-OCT-2001.
 PD
 XX 12-JAN-2001; 2001US-00759010.
 PF
 XX 20-JAN-2000; 2000US-00488393.
 PR
 XX (SRIV/) SRIVASTAVA P K.
 XX
 PI Srivastava PK;
 XX
 XX WPI; 2001-656559/75.
 XX
 PT Vaccine compositions for vaccinating against cancers and infections,
 PT comprises peptide-binding fragments (PBPs) of heat shock proteins (HSPs)
 PT and non-covalent complexes of PBPs of HSPs and antigenic molecules.
 XX
 PS Disclosure; Fig 1C; 39pp; English.
 XX
 CC The invention relates to pharmaceutical compositions comprising peptide
 CC binding fragments of heat shock proteins (HSPs) and non-covalent
 CC complexes of HSP peptide-binding fragments (HSPB) in non-covalent
 CC association with antigenic molecules. Vaccines comprising peptide
 CC fragments of the invention may be used to stimulate an immune response,
 CC in particular cytotoxic T cell responses against cells infected with
 CC viruses (including hepatitis type A, B and C, influenza, varicella,

CC adenovirus, herpes simplex (HSV) type I and type II, rinderpest
CC rhinovirus, echovirus, rotavirus, respiratory syncytial virus, mumps
CC virus, papova virus, papilloma virus, arbovirus, cytomegalovirus,
CC echinovirus, hantavirus, coxsackie virus, measles virus, rubella virus,
CC polio virus, HIV-I, and HIV-II; bacteria including (including
CC Mycobacteria, Rickettsia, Mycoplasma, Neisseria and Legionella); protozoa
CC (including Leishmania, Kokzidioa and Trypanosoma) and intracellular
CC parasites (including Chlamydia and Rickettsia). The vaccines may be used
CC to treat cancers such as human sarcomas and carcinomas, pancreatic
CC cancer, breast cancer, ovarian cancer, prostate cancer, squamous cell
CC carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma,
CC sebaceous gland carcinoma, papillary carcinoma, papillary
CC adenocarcinomas, medullary carcinoma, cystadenocarcinoma, bronchogenic
CC carcinoma, renal cell carcinoma, hepatoma, bile duct carcinoma,
CC choriocarcinoma, seminoma and embryonal carcinoma. The present sequence
CC is human Hsp70 family homologue, Hsp71
XX
SQ Sequence 641 AA;

Query Match 100.0%; Score 1314; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 8.8e-101;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KSENVODLLLDVAPLSGLGLETAGGVMTALIKRNSTIPTKTQIFFTYSDNQPGVLIQVY 60
DB 384 KSENVODLLLDVAPLSGLGLETAGGVMTALIKRNSTIPTKTQIFFTYSDNQPGVLIQVY 443
QY 61 EGERAMTKONNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVTTATDKSTGKANKITI 120
DB 444 EGERAMTKONNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVTTATDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMWQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDGLGKGIS 180
DB 504 TNDKGRLSKEEIERMWQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDGLGKGIS 563
QY 181 EADKKVLDKQCEVISWLDANTLAEKDFEHRKKELEQVCNPIISGLYQAGGPGGFG 240
DB 564 EADKKVLDKQCEVISWLDANTLAEKDFEHRKKELEQVCNPIISGLYQAGGPGGFG 623
QY 241 AQGPKGGSGSGPTIEVD 258
DB 624 AQGPKGGSGSGPTIEVD 641

RESULT 5
ABU89711
ID ABU89711 standard; protein; 641 AA.
XX
AC ABU89711;
XX
DT 10-JUL-2003 (first entry)
XX
DE Protein differentially expressed in cardiovascular disease #5.
XX
KW Cardiovascular disease; arteriosclerosis; ischaemia; angina pectoris;
KW myocardial infarction; cardiast; antiarteriosclerotic; antianginal;
KW gene therapy; differential gene expression.
XX
OS Homo sapiens.
XX
PN WO2003031650-A2.
XX
PD 17-APR-2003.
XX
PF 02-OCT-2002; 2002WO-EP011034.
XX
PR 08-OCT-2001; 2001GB-00024145.
XX
PA (FARB) BAYER AG.
XX
PI Munnes M, Gehrman M, Wick M, Schmitz G;
XX WPI; 2003-403108/38.
DR

DR N-PSDB; ACA89884.
XX
PT Predicting, diagnosing or prognosing a cardiovascular disease, e.g.
PT angina, ischemia, myocardial infarction or arteriosclerosis by detection
PT of a polynucleotide in a biological sample comprises detecting a
PT hybridization complex.
XX
PS Claim 3; Page 260-263; 454pp; English.
XX
CC The invention describes a method of predicting, diagnosing or prognosing
CC a cardiovascular disease by detection of a polynucleotide in a biological
CC sample comprises hybridising at least one of the polynucleotide to a
CC nucleic acid material of a biological sample, thus forming a
CC hybridisation complex, and detecting the hybridisation complex. The
CC polynucleotides, polypeptides, antisense molecule, antibody and reagent
CC are useful for preparing compositions for preventing, predicting or
CC diagnosing, or a medicament for treating a cardiovascular disease, e.g.
CC arteriosclerosis, ischaemia, angina pectoris, or myocardial infarction.
CC This sequence represents a protein identified in the invention a being
CC differentially expressed in individuals with cardiovascular disease
XX
SQ Sequence 641 AA;

Query Match 100.0%; Score 1314; DB 6; Length 641;
Best Local Similarity 100.0%; Pred. No. 8.8e-101;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KSENVODLLLDVAPLSGLGLETAGGVMTALIKRNSTIPTKTQIFFTYSDNQPGVLIQVY 60
DB 384 KSENVODLLLDVAPLSGLGLETAGGVMTALIKRNSTIPTKTQIFFTYSDNQPGVLIQVY 443
QY 61 EGERAMTKONNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVTTATDKSTGKANKITI 120
DB 444 EGERAMTKONNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVTTATDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMWQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDGLGKGIS 180
DB 504 TNDKGRLSKEEIERMWQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDGLGKGIS 563
QY 181 EADKKVLDKQCEVISWLDANTLAEKDFEHRKKELEQVCNPIISGLYQAGGPGGFG 240
DB 564 EADKKVLDKQCEVISWLDANTLAEKDFEHRKKELEQVCNPIISGLYQAGGPGGFG 623
QY 241 AQGPKGGSGSGPTIEVD 258
DB 624 AQGPKGGSGSGPTIEVD 641

RESULT 6
ADD47459
ID ADD47459 standard; protein; 641 AA.
XX
AC ADD47459;
XX
DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
DE Human Protein AAA52697, SEQ ID NO 13154.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
OS Unidentified.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346392P.
 XX 26-NOV-2001; 2001US-0333347P.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; AAA52697.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Example 1; Page: 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (described in Table 3
 CC of the specification) which is differentially expressed during pain.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 641 AA;
 Query Match 100.0%; Score 1314; DB 7; Length 641;
 Best Local Similarity 100.0%; Pred. No. 8.8e-101;
 Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KSNVODLLLLDVAPLSLGLTAGGVTALIKNSTIPTKQTQIFFTYSDNQPGVLIQVY 60
 DB 384 KSNVODLLLLDVAPLSLGLTAGGVTALIKNSTIPTKQTQIFFTYSDNQPGVLIQVY 443
 QY 61 EGERAMTKONNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 444 EGERAMTKONNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEEIERMWQEAKEYAEDVQERVSNAKNALESYAFNMKSAVEDEGLGKIS 180
 DB 504 TNDKGRLSKEEIERMWQEAKEYAEDVQERVSNAKNALESYAFNMKSAVEDEGLGKIS 563
 QY 181 EADKKVKLVKQCEVISWLDANTLAEDFEHKKKELEQVNCNPIISGLYQAGGPGGPGG 240
 DB 564 EADKKVKLVKQCEVISWLDANTLAEDFEHKKKELEQVNCNPIISGLYQAGGPGGPGG 623
 QY 241 AOGPKGGSGSGPTIEVD 258
 DB 624 AOGPKGGSGSGPTIEVD 641
 RESULT 7
 ADJ27279

ID ADJ27279 standard; protein; 641 AA.
 XX
 AC ADJ27279;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human HSP70.1.
 XX
 KW heat shock protein-70; HSP70; HSP70.1; HSP70.3; inducible; induction;
 KW heat; tumour necrosis factor; TNF; interferon-gamma; tumour.
 XX
 OS Homo sapiens.
 XX
 PN WO2003061684-A2.
 XX
 PD 31-JUL-2003.
 XX
 PF 24-JAN-2003; 2003WO-EP000786.
 XX
 PR 24-JAN-2002; 2002EP-00075297.
 XX
 PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
 XX
 PI Libert C, Wielockx B, Van Molle W, Mahieu T;
 XX WPI; 2003-608168/57.
 DR N-PSDB; ADJ27278.
 XX
 PT New pharmaceutical composition comprising HSP70 that is endogenously
 PT induced by heat and TNF, useful for the manufacture of a medicament for
 PT treating systemic tumor.
 XX
 PS Disclosure; SEQ ID NO 6; 53pp; English.
 XX
 CC This sequence represents human heat shock protein-70.1 (HSP70.1). HSP70.1
 CC and HSP70.3 are inducible members of the HSP70 family of proteins. The
 CC heat shock proteins of the invention are endogenously induced by heat and
 CC tumour necrosis factor (TNF). This heat shock protein may be used in a
 CC composition which further comprises interferon-gamma, and/or a
 CC chemotherapeutic compound. The pharmaceutical composition is useful for
 CC the manufacture of a medicament for treating systemic tumour.
 XX
 SQ Sequence 641 AA;
 Query Match 100.0%; Score 1314; DB 7; Length 641;
 Best Local Similarity 100.0%; Pred. No. 8.8e-101;
 Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KSNVODLLLLDVAPLSLGLTAGGVTALIKNSTIPTKQTQIFFTYSDNQPGVLIQVY 60
 DB 384 KSNVODLLLLDVAPLSLGLTAGGVTALIKNSTIPTKQTQIFFTYSDNQPGVLIQVY 443
 QY 61 EGERAMTKONNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 444 EGERAMTKONNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEEIERMWQEAKEYAEDVQERVSNAKNALESYAFNMKSAVEDEGLGKIS 180
 DB 504 TNDKGRLSKEEIERMWQEAKEYAEDVQERVSNAKNALESYAFNMKSAVEDEGLGKIS 563
 QY 181 EADKKVKLVKQCEVISWLDANTLAEDFEHKKKELEQVNCNPIISGLYQAGGPGGPGG 240
 DB 564 EADKKVKLVKQCEVISWLDANTLAEDFEHKKKELEQVNCNPIISGLYQAGGPGGPGG 623
 QY 241 AOGPKGGSGSGPTIEVD 258
 DB 624 AOGPKGGSGSGPTIEVD 641
 RESULT 8
 ADE76981
 ID ADE76981 standard; protein; 641 AA.
 XX

AC ADE76981;
XX 29-JAN-2004 (first entry)
XX Human protein expressed in a liver disorder #42.
XX human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;
XX tumour; liver; inflammatory disorder; immune response disorder;
XX high-throughput screening; differential gene expression; gene therapy.
XX Homo sapiens.
XX US2003108871-A1.
XX 12-JUN-2003.
XX 30-JUL-2001; 2001US-00919039.
XX 28-JUL-2000; 2000US-0222113P.
XX (KASE/) KASER M R.
XX Kaser MR;
XX WPI; 2004-031227/03.
XX N-PSDB; ADE76980.
XX Composition comprising several cDNAs that are differentially expressed in
XX treated human C3A liver cell cultures, useful for treating liver
XX disorders.
XX Claim 1; SEQ ID NO 146; 41pp; English.
XX The invention relates to a composition comprising several cDNAs that are
XX differentially expressed in a liver disorder. The composition is useful
XX for treating liver disorder such as hyperlipidaemia, hypertension, type
XX II diabetes, tumours of the liver and disorders of the inflammatory and
XX immune response. The composition is useful for a high-throughput method
XX of screening several molecules or compounds to identify a ligand which
XX specifically binds a cDNA. A protein encoded by the cDNA is useful for a
XX high-throughput method for using a protein to screen several molecules or
XX compounds to identify at least one ligand which specifically binds the
XX protein which involves combining the protein encoded by the cDNA with
XX several of molecules or compounds under conditions to allow specific
XX binding, and detecting specific binding between the protein and a
XX molecule or compound, therefore identifying a ligand which specifically
XX binds the protein. The composition is useful for detecting and
XX quantifying differential gene expression, can be used in gene therapy, to
XX formulate prognosis and to design a treatment regimen and to monitor the
XX efficacy of treatment. The present sequence represents the amino acid
XX sequence of a protein encoded by a cDNA differentially expressed in a
XX liver disorder.
XX Sequence 641 AA;
SQ Query Match 100.0%; Score 1314; DB 8; Length 641;
Best Local Similarity 100.0%; Pred. No. 8.8e-101;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KSENVQDLLLLDVAPLSLGLETAGGVTALIKRNSITPTKQTQITFTTSDNQPGVLIQVY 60
DB 384 KSENVQDLLLLDVAPLSLGLETAGGVTALIKRNSITPTKQTQITFTTSDNQPGVLIQVY 443
QY 61 EGERAMTKDNNLGRFELSGIPAPRGVQFTEVTIDANGILNVATDKSTGKANKITI 120
DB 444 EGERAMTKDNNLGRFELSGIPAPRGVQFTEVTIDANGILNVATDKSTGKANKITI 503
QY 121 TNDKRLSKSEIERMVQAEKYKAEDVQERVSNAKNALESYAFNMKSAVDEGLGKGIS 180
DB 504 TNDKRLSKSEIERMVQAEKYKAEDVQERVSNAKNALESYAFNMKSAVDEGLGKGIS 563
QY 181 BADKKKVLDKCOEIVISWLDANTLAEKDFEHRKELEQVCNPIISGLYQGAGGPGPGFG 240

DB 564 EADKKKVLDKCOEIVISWLDANTLAEKDFEHRKELEQVCNPIISGLYQGAGGPGPGFG 623
QY 241 AQCPKGGSGSGPTIEEVD 258
DB 624 AQCPKGGSGSGPTIEEVD 641
RESULT 9
ADL82939
ID ADL82939 standard; protein; 641 AA.
XX AC ADL82939;
XX 17-JUN-2004 (first entry)
XX Human PRO71095, SEQ ID 141.
XX Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
XX Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;
XX Gene Therapy; PRO; B cell related disorder; cancer;
XX immune-mediated inflammatory disease; human.
XX Homo sapiens.
XX WO2004024097-A2.
XX 25-MAR-2004.
XX 15-SEP-2003; 2003WO-US029097.
XX 16-SEP-2002; 2002US-0411392P.
XX (GETH) GENENTECH INC.
XX Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;
XX Wu TD;
XX WPI; 2004-329389/30.
XX N-PSDB; ADL82938.
XX New PRO polypeptide, useful for diagnosing and treating a B cell related
XX disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
XX mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
XX Claim 10; Fig 141; 695pp; English.
XX The present invention relates to PRO proteins and their coding sequences.
XX The PRO proteins are useful for diagnosing and treating a B cell related
XX disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide
XX antigen unresponsiveness, selective IgA deficiency, selective IgM
XX deficiency, selective deficiency of IgG subclasses, immunodeficiency with
XX hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's
XX lymphoma, intermediate lymphoma, follicular lymphoma, type II
XX hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic
XX anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
XX ankylosing spondylitis. The PRO proteins are also useful for preparing a
XX medicament for treating a condition that is responsive to the PRO
XX protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
XX coding sequences are useful as hybridization probes in chromosome and
XX gene mapping, in preparing PRO proteins, or in generating transgenic
XX animals or knockout animals, which in turn are useful in the development
XX and screening of therapeutically useful reagents.
XX Sequence 641 AA;
SQ Query Match 100.0%; Score 1314; DB 8; Length 641;
Best Local Similarity 100.0%; Pred. No. 8.8e-101;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KSENVQDLLLLDVAPLSLGLETAGGVTALIKRNSITPTKQTQITFTTSDNQPGVLIQVY 60
DB 384 KSENVQDLLLLDVAPLSLGLETAGGVTALIKRNSITPTKQTQITFTTSDNQPGVLIQVY 443

QY 61 EGERAMTKONLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 444 EGERAMTKONLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEEIERMVOEAEKYAEDEVQERVSANNALESYAFNMKSAVEDSLGKGKIS 180
 DB 504 TNDKGRLSKEEIERMVOEAEKYAEDEVQERVSANNALESYAFNMKSAVEDSLGKGKIS 563
 QY 181 EADKKVLDKQEVISWLDANTLAEKDEFEHKKKELEQVNCNPIISGLYQAGGPGGPGF 240
 DB 564 EADKKVLDKQEVISWLDANTLAEKDEFEHKKKELEQVNCNPIISGLYQAGGPGGPGF 623
 QY 241 AOGPKGSGSGPTIEVD 258
 DB 624 AOGPKGSGSGPTIEVD 641

RESULT 10
 ABM80760
 ID ABM80760 standard; protein; 641 AA.
 XX
 AC ABM80760;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Tumour-associated antigenic target (TAT) polypeptide PRO71095, SEQ:1964.
 XX
 KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KW tumour; diagnosis; cell proliferative disorder; breast cancer;
 KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KW central nervous system cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; melanoma; leukaemia; hybridisation probe;
 KW chromosome identification; chromosome mapping; gene mapping;
 KW gene therapy; cytostatic.
 XX
 OS Homo sapiens..
 XX
 PN WO2004030615-A2.
 XX
 PD 15-APR-2004.
 XX
 PF 29-SEP-2003; 2003WO-US028547.
 XX
 PR 02-OCT-2002; 2002US-0414971P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Wu TD, Zhang Z, Zhou Y;
 XX
 DR WPI; 2004-347921/32.
 DR N-PSDB; ACN38447.
 XX
 PT New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.
 XX
 PS Claim 12; SEQ ID NO 1964; 7273pp; English.
 XX
 CC The invention relates to human tumour-associated antigenic target (TAT)
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAT nucleic acids and
 CC polypeptides; expression vectors and host cells comprising a TAT nucleic
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
 CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
 CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,

CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
 CC used as hybridisation probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAT polypeptide of the invention
 XX
 SQ Sequence 641 AA;
 Query Match 100.0%; Score 1314; DB 8; Length 641;
 Best Local Similarity 100.0%; Pred. No. 8.8e-101;
 Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KSENVQDLLLLDVAPLSLGLTAGGVMTALIKENSTIPTKQTQIFTTYSNQPGVLIQVY 60
 DB 384 KSENVQDLLLLDVAPLSLGLTAGGVMTALIKENSTIPTKQTQIFTTYSNQPGVLIQVY 443
 QY 61 EGERAMTKONLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 444 EGERAMTKONLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEEIERMVOEAEKYAEDEVQERVSANNALESYAFNMKSAVEDSLGKGKIS 180
 DB 504 TNDKGRLSKEEIERMVOEAEKYAEDEVQERVSANNALESYAFNMKSAVEDSLGKGKIS 563
 QY 181 EADKKVLDKQEVISWLDANTLAEKDEFEHKKKELEQVNCNPIISGLYQAGGPGGPGF 240
 DB 564 EADKKVLDKQEVISWLDANTLAEKDEFEHKKKELEQVNCNPIISGLYQAGGPGGPGF 623
 QY 241 AOGPKGSGSGPTIEVD 258
 DB 624 AOGPKGSGSGPTIEVD 641

RESULT 11
 ADI20102
 ID ADI20102 standard; protein; 641 AA.
 XX
 AC ADI20102;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Hep70.
 XX
 KW Inducible heat shock protein; Hsp70; constitutive heat shock protein;
 KW Hsc70; human leukocyte antigen; HLA.
 XX
 OS Unidentified.
 XX
 PN WO2003029288-A2.
 XX
 PD 10-APR-2003.
 XX
 PF 26-SEP-2002; 2002WO-EP010821.
 XX
 PR 27-SEP-2001; 2001EP-00402496.
 XX
 PA (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.
 PA (INSR) INST ROUSSY GUSTAVE.
 PA (INRM) INSERM.
 XX
 PI Faure O, Kosmatopoulos K;
 XX WPI; 2003-449139/42.
 XX
 PT Novel peptide derived from inducible heat shock protein Hsp70, useful for
 PT inducing cytotoxic T lymphocyte response that targets cells expressing
 PT inducible Hsp70, and for preparing drugs for treating cancer.
 XX
 PS Disclosure; SEQ ID NO 1; 49pp; English.
 XX
 CC The present invention relates to a peptide comprising a sequence of at
 CC least 8 contiguous amino acids, having at least 65 % identity to a

CC portion inducible heat shock protein (Hsp)-70 sequence, differing from a
CC sequence of constitutive heat shock protein Hsc70 by at least one amino
CC acid, and capable of inducing cytotoxic T lymphocytes that specifically
CC recognize cells naturally producing inducible Hsp70, in vitro or in vivo.
CC The peptides are stable, and has high affinity for human leukocyte
CC antigen (HLA) class I molecules. The present sequence represents Hsp 70.
XX
SQ Sequence 641 AA;

Query Match 99.8%; Score 1312; DB 7; Length 641;
Best Local Similarity 99.6%; Pred. No. 1.3e-100;
Matches 257; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KSENVQDLLLLDVAPLSGLGTAGGVTALIKENSTIPTKQTOIFTTYSNQPGLIOVY 60
DB 384 KSENVQDLLLLDVAPLSGLGTAGGVTALIKENSTIPTKQTOIFTTYSNQPGLIOVY 443
QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDGLGKGIS 180
DB 504 TNDKGRLSKEEIERMVQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDGLGKGIS 563
QY 181 EADKKKVLDKCOVSWLDANTLAEDKDEFEHKKRKELEQVNCNPIISGLYQAGGPGGFG 240
DB 564 EADKKKVLDKCOVSWLDANTLAEDKDEFEHKKRKELEQVNCNPIISGLYQAGGPGGFG 623
QY 241 AQPKGGSGSGPTIEVD 258
DB 624 AQPKGGSGSGPTIEVD 641

RESULT 12
ADM04781
ID ADM04781 standard; protein; 476 AA.
AC ADM04781;
XX
XX 20-MAY-2004 (first entry)
XX Human protein of the invention SEQ ID NO:3466.
XX human; gene therapy; diagnostic marker; pharmaceutical.
XX
XX Homo sapiens.
XX OS
XX EPI347046-A1.
XX
XX 24-SEP-2003.
XX
XX 12-APR-2002; 2002EP-00008400.
XX
XX 22-MAR-2002; 2002JP-00137785.
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
XX Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
XX Seki N, Yoshikawa T, Otsuka M, Nagahara K, Masuho Y;
XX
XX WPI; 2003-723558/69.
XX N-PSDB; ADM02338.
XX
XX New polynucleotides and polypeptides are useful in gene therapy, for
XX developing a diagnostic marker or medicines for regulating their
XX expression and activity, or as a target of gene therapy.
XX
XX Claim 1; SEQ ID NO 3466; 305pp; English.
XX
XX The invention relates to a novel human polynucleotide and the encoded
XX polypeptide. A polynucleotide of the invention may have a use in gene
CC

CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC protein sequence of the invention.
XX
SQ Sequence 476 AA;

Query Match 99.6%; Score 1309; DB 7; Length 476;
Best Local Similarity 99.6%; Pred. No. 1.6e-100;
Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KSENVQDLLLLDVAPLSGLGTAGGVTALIKENSTIPTKQTOIFTTYSNQPGLIOVY 60
DB 219 KSENVQDLLLLDVAPLSGLGTAGGVTALIKENSTIPTKQTOIFTTYSNQPGLIOVY 278
QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 279 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSAGKANKITI 338
QY 121 TNDKGRLSKEEIERMVQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDGLGKGIS 180
DB 339 TNDKGRLSKEEIERMVQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDGLGKGIS 398
QY 181 EADKKKVLDKCOVSWLDANTLAEDKDEFEHKKRKELEQVNCNPIISGLYQAGGPGGFG 240
DB 399 EADKKKVLDKCOVSWLDANTLAEDKDEFEHKKRKELEQVNCNPIISGLYQAGGPGGFG 458
QY 241 AQPKGGSGSGPTIEVD 258
DB 459 AQPKGGSGSGPTIEVD 476

RESULT 13
ABR40400
ID ABR40400 standard; protein; 641 AA.
XX
XX ABR40400;
AC
XX 08-AUG-2003 (first entry)
XX Human Hsp70 protein.
XX
XX heat shock protein; HSP; cytokine; CC chemokine; nitric oxide; cancer;
XX antimicrobial; virucide; cytostatic; microbial infection; anti-HIV;
XX viral infection; immune system disorder; vaccine; HSP70; human.
XX
XX Homo sapiens.
XX
XX WO2003029289-A2.
XX
XX 10-APR-2003.
XX
XX 03-OCT-2002; 2002WO-GB004475.
XX
XX 03-OCT-2001; 2001GB-00023756.
XX (UNLO) KINGS COLLEGE LONDON.
XX
XX Lehner T, Kelly CG, Singh M, Wang Y;
XX WPI; 2003-430189/40.
XX
XX Novel heat shock protein fragment useful for treating microbial
XX infection, viral infection of cancer, that can increase the level of
XX cytokines and/or CC chemokines and/or nitric oxide produced by a cell.
XX
XX Example 3; Page 17-20; 30pp; English.
XX
XX The invention relates to a novel heat shock protein fragment (HSP) that
CC

CC can increase the level of one or more cytokines and/or one or more CC
CC chemokines and/or nitric oxide produced by a cell, above that caused by
CC the corresponding full length heat shock protein. The protein fragment of
CC the invention has antimicrobial, virucide, and cytostatic activity. The
CC protein fragment is useful in therapy, in treatment or prophylaxis of a
CC disease and in the manufacture of a medicament for treatment or
CC prophylaxis of a disease such as microbial infection, viral infection,
CC disease of the immune system or cancer. The fragment is also useful as an
CC adjuvant in vaccines, preferably, anti-HIV vaccines. The present sequence
CC represents the human HSP70 protein
XX
SQ Sequence 641 AA;

Query Match 99.6%; Score 1309; DB 6; Length 641;
Best Local Similarity 99.6%; Pred. No. 2.3e-100;
Matches 257; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KSENVQDLLLDVAPLSGLGTAGGVTALIKRNSTIPTKQTQIFTTYSNQPGVLIQVY 60
Db 384 KSENVQDLLLDVAPLSGLGTAGGVTALIKRNSTIPTKQTQIFTTYSNQPGVLIQVY 443
Qy 61 EGERAMTKONNLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTKONNLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 503
Qy 121 TNDKGRLSKEEIERMVQEAKEYAEDVQERVSQAKNALESYAFNMKSAVEDGLGKGIS 180
Db 504 TNDKGRLSKEEIERMVQEAKEYAEDVQERVSQAKNALESYAFNMKSAVEDGLGKGIS 563
Qy 181 EADKKVLDKCOEIVSWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGGPGF 240
Db 564 EADKKVLDKCOEIVSWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGGPGF 623
Qy 241 AQGPKGGSGSGPTIEVD 258
Db 624 AQGPKGGSGSGPTIEVD 641

RESULT 14
ID ADF76349
XX ADF76349 standard; protein; 641 AA.
AC ADF76349;
XX
DT 26-FEB-2004 (first entry)
XX
DE Novel human secreted and transmembrane protein SeqID 22.
XX
KW human; PRO; membrane bound protein; membrane bound receptor;
KW cell proliferation; cell migration; cell differentiation;
KW mitogenic factor; survival factor; cytotoxic factor;
KW differentiation factor; neuropeptide; hormone; cell receptor;
KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.
XX
OS Homo sapiens.
XX
XX WO2003072035-A2.
XX
XX 04-SEP-2003.
XX
XX 21-FEB-2003; 2003WO-US005241.
XX
XX 22-FEB-2002; 2002US-0359461P.
XX
XX (GETH) GENENTECH INC.
XX
XX Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;
XX Williams PM, Wood WI, Wu TD;
XX WPI; 2003-721702/68.
XX
XX N-PSDB; ADF76348.
XX
XX New PRO polypeptides, useful for diagnosing and treating an immune

PT related disorder, e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or
XX diabetes mellitus.
PS Claim 10; SEQ ID NO 22; 918pp; English.
XX
CC This invention relates to novel nucleic acids encoding human PRO secreted
CC and transmembrane proteins. Extracellular proteins play important roles
CC in the formation, differentiation and maintenance of multicellular
CC organisms. The fate of many individual cells (for example proliferation,
CC migration or differentiation) is typically governed by information
CC received from other cells and the immediate environment. The information
CC is often transmitted by secreted polypeptides (for example mitogenic
CC factors, survival factors, cytotoxic factors, differentiation factors,
CC neuropeptides and hormones) which are received and interpreted by diverse
CC cell receptors or membrane bound proteins. These membrane bound proteins
CC and receptors may be of use as pharmaceutical and diagnostic agents, such
CC as in the blocking of receptor-ligand interactions. The current invention
CC provides the amino acid sequences of novel human membrane bound receptors
CC and proteins, along with the cDNA sequences encoding them. The novel
CC proteins of the invention may have cytostatic activities through the
CC stimulation of chondrocytes. The nucleic acids of the invention may be
CC useful for the manufacture of a medicament for diagnosing or treating a
CC tumour in a mammal. In addition, they may be useful for measuring or
CC detecting the expression of a tumour associated gene. The present
CC sequence is the amino acid sequence of a human PRO protein of the
CC invention.
XX
SQ Sequence 641 AA;

Query Match 99.6%; Score 1309; DB 7; Length 641;
Best Local Similarity 99.6%; Pred. No. 2.3e-100;
Matches 257; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KSENVQDLLLDVAPLSGLGTAGGVTALIKRNSTIPTKQTQIFTTYSNQPGVLIQVY 60
Db 384 KSENVQDLLLDVAPLSGLGTAGGVTALIKRNSTIPTKQTQIFTTYSNQPGVLIQVY 443
Qy 61 EGERAMTKONNLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTKONNLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 503
Qy 121 TNDKGRLSKEEIERMVQEAKEYAEDVQERVSQAKNALESYAFNMKSAVEDGLGKGIS 180
Db 504 TNDKGRLSKEEIERMVQEAKEYAEDVQERVSQAKNALESYAFNMKSAVEDGLGKGIS 563
Qy 181 EADKKVLDKCOEIVSWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGGPGF 240
Db 564 EADKKVLDKCOEIVSWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGGPGF 623
Qy 241 AQGPKGGSGSGPTIEVD 258
Db 624 AQGPKGGSGSGPTIEVD 641

RESULT 15
ID ADF76349
XX ADF76349 standard; protein; 641 AA.
AC ADF76349;
XX
DT 18-NOV-2004 (first entry)
XX
DE Tumour-associated antigenic target (TAT) polypeptide PRO38070, SEQ:1962.
XX
KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.
XX

OS Homo sapiens.
XX W02004030615-A2.
XX 15-APR-2004.
XX 29-SEP-2003; 2003WO-US028547.
XX 02-OCT-2002; 2002US-0414971P.
XX (GETH) GENENTECH INC.
XX Wu TD, Zhang Z, Zhou Y;
XX WPI; 2004-347921/32.
XX N-PSDB; ACN38446.
XX New tumor-associated antigenic target polypeptides and nucleic acids,
XX useful in preparing a medicament for treating or detecting a
XX proliferative disorder, e.g. breast, lung, colorectal, ovarian or
XX prostate cancer or tumor.
XX Claim 12; SEQ ID NO 1962; 7273pp; English.
XX The invention relates to human tumour-associated antigenic target (TAT)
XX polypeptides, and their related nucleic acids. The TAT polypeptides are
XX overexpressed in cancer tissues compared to normal tissues, and may thus
XX serve as effective targets for the diagnosis and treatment of cancer in
XX mammals. The invention also relates to nucleic acid and polypeptide
XX sequences at least 80% identical to the TAT nucleic acids and
XX polypeptides; expression vectors and host cells comprising a TAT nucleic
XX acid; an antibody specific for a TAT polypeptide; a peptide or organic
XX molecule which binds to a TAT polypeptide; fusion proteins comprising a
XX TAT polypeptide; and methods and compositions for the treatment or
XX diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
XX antibodies, antagonists, binding molecules and compositions are useful
XX for diagnosing or treating a cell proliferative disorder associated with
XX increased TAT expression, particularly cancers such as breast cancer,
XX colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
XX cancer, pancreatic cancer, cervical cancer, cancers of the central
XX nervous system, melanoma and leukaemia. TAT nucleic acids may further be
XX used as hybridisation probes, in chromosome and gene mapping, in
XX chromosome identification and in gene therapy. The present sequence
XX represents a TAT polypeptide of the invention
XX
XX Sequence 641 AA;
XX
XX Query Match 99.6%; Score 1309; DB 8; Length 641;
XX Best Local Similarity 99.6%; Pred. No. 2.3e-100;
XX Matches 257; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVY 60
XX 384 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVY 443
XX
XX 61 EGERAMTKONLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
XX 444 EGERAMTKONLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503
XX
XX 121 TNDKGRLSKEEIERMVQAEKKAEDVQERVSNAKNALESYAFNMKSAVEDGLGKGIS 180
XX 504 TNDKGRLSKEEIERMVQAEKKAEDVQERVSNAKNALESYAFNMKSAVEDGLGKGIS 563
XX
XX 181 EADKKVLDKQCQEVISWLDANTLAEKDFEHRKKELEQVCNPIISGLYQAGGPGPGFG 240
XX 564 EADKKVLDKQCQEVISWLDANTLAEKDFEHRKKELEQVCNPIISGLYQAGGPGPGFG 623
XX
XX 241 AQGPKGGSGSGPTIEVD 258
XX 624 AQGPKGGSGSGPTIEVD 641
XX
XX RESULT 16

RAY88410
ID AAY88410 standard; protein; 554 AA.
XX
XX AAY88410;
XX
XX 31-JUL-2000 (first entry)
XX
XX Human heat shock protein SHSP70 amino acid sequence.
XX
XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
XX chromosome 14q22-24; transcription; rheumatism; schizophrenia;
XX depression; nephrotic syndrome; SHSP70.
XX
XX Homo sapiens.
XX
XX JP2000069999-A.
XX
XX 07-MAR-2000.
XX
XX 01-JUN-1995; 99JP-00257146.
XX
XX 01-JUN-1995; 95JP-00158581.
XX
XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
XX
XX WPI; 2000-264458/23.
XX
XX N-PSDB; AAA15622.
XX
XX Abnormal transcription of intracellular HSP70mRNA under acute and chronic
XX continuous load of stress in a human being and its application.
XX
XX Disclosure; Fig 3; 11pp; Japanese.
XX
XX This sequence represents the human heat shock protein SHSP70 amino acid
XX sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
XX and 14q22-24. The invention relates to the abnormal transcription of
XX intracellular HSP70mRNA under acute and chronic stress load in a human.
XX The abnormal transcription of HSP70 can be used in the improvement of
XX stress and response and diagnosis of stress diseases including
XX rheumatism, schizophrenia, depression and nephrotic syndrome
XX
XX Sequence 554 AA;
XX
XX Query Match 98.8%; Score 1298.5; DB 3; Length 554;
XX Best Local Similarity 99.6%; Pred. No. 1.4e-99;
XX Matches 257; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
XX 1 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVY 60
XX 298 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVY 357
XX
XX 61 EGERAMTKONLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
XX 358 EGERAMTKONLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 416
XX
XX 121 TNDKGRLSKEEIERMVQAEKKAEDVQERVSNAKNALESYAFNMKSAVEDGLGKGIS 180
XX 417 TNDKGRLSKEEIERMVQAEKKAEDVQERVSNAKNALESYAFNMKSAVEDGLGKGIS 476
XX
XX 181 EADKKVLDKQCQEVISWLDANTLAEKDFEHRKKELEQVCNPIISGLYQAGGPGPGFG 240
XX 477 EADKKVLDKQCQEVISWLDANTLAEKDFEHRKKELEQVCNPIISGLYQAGGPGPGFG 536
XX
XX 241 AQGPKGGSGSGPTIEVD 258
XX 537 AQGPKGGSGSGPTIEVD 554
XX
XX RESULT 17
XX AAY88409
XX ID AAY88409 standard; protein; 554 AA.
XX
XX AAY88409;

XX DT 31-JUL-2000 (first entry)
XX DE Human heat shock protein SHSP70 amino acid sequence.
XX DE Human heat shock protein SHSP70; chromosome 6p21.3-22; stress;
XX KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;
XX KW depression; nephrotic syndrome; SHSP70.
XX OS Homo sapiens.
XX PN JP2000069999-A.
XX PD 07-MAR-2000.
XX PF 01-JUN-1995; 99JP-002571146.
XX PR 01-JUN-1995; 95JP-00158581.
XX PA (HOKU-) HOKEN KAGAKU KENKYUSHO KK.
XX DR WPI; 2000-264458/23.
XX DR N-PSDB; AAA15621.
XX PT Abnormal transcription of intracellular HSP70mRNA under acute and chronic
XX PT continuous load of stress in a human being and its application.
XX PS Example; Fig 2; 11pp; Japanese.
XX CC This sequence represents the human heat shock protein SHSP70 amino acid
XX CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
XX CC and 14q22-24. The invention relates to the abnormal transcription of
XX CC intracellular HSP70mRNA under acute and chronic stress load in a human.
XX CC The abnormal transcription of HSP70 can be used in the improvement of
XX CC stress and response and diagnosis of stress diseases including
XX CC rheumatism, schizophrenia, depression and nephrotic syndrome
XX SQ Sequence 554 AA;
Query Match 98.8%; Score 1298.5; DB 3; Length 554;
Best Local Similarity 99.6%; Pred. No. 1.4e-99;
Matches 257; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 KSENVQDLLLLDVAPLSLGLGTAGGVTALIKRNSTIPTKTQIIFTTYSNDQPGVLIQVY 60
DB 298 KSENVQDLLLLDVAPLSLGLGTAGGVTALIKRNSTIPTKTQIIFTTYSNDQPGVLIQVY 357
QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 358 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 416
QY 121 TNDKGRLSKEEIERMWQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDSGLGKGIS 180
DB 417 TNDKGRLSKEEIERMWQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDSGLGKGIS 476
QY 181 EADKKVLDKQCQEVISWLDANTLAEKDEFEHKKRKELEQVCNPIISGLYQAGGPGGPGF 240
DB 477 EADKKVLDKQCQEVISWLDANTLAEKDEFEHKKRKELEQVCNPIISGLYQAGGPGGPGF 536
QY 241 AQGPKGGSGSGPTIEVD 258
DB 537 AQGPKGGSGSGPTIEVD 554
RESULT 18
AAB23653
ID AAB23653 standard; protein; 640 AA.
XX AC AAB23653;
XX AC AAB23653;
XX DT 05-JAN-2001 (first entry)
XX DE Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.

XX ATCase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;
XX KW immune response; infectious disease; malaria; cytotoxic T cell;
XX KW cytotaxtic; immunostimulant; cellular immune response inducer;
XX KW protozoacide; leukaemia; cancer.
XX OS Homo sapiens.
XX PN WO200049041-A1.
XX PD 24-AUG-2000.
XX PF 18-FEB-2000; 2000WO-JP000941.
XX PR 19-FEB-1999; 99JP-00041535.
XX PA (SUME) SUMITOMO ELECTRIC IND CO.
XX PI Shinbara N, Udono H, Yui K;
XX WIPI; 2000-543748/49.
XX DR Fused protein capable of inducing cellular immune response, useful as
XX PT active ingredient for drug compositions in preventing and/or treating
XX PT infectious diseases such as malaria or cancer.
XX PS Claim 3; Page 49-52; 72pp; Japanese.
XX CC The present invention describes a fused protein (I) prepared from a
XX CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by
XX CC cytotoxic T cells and a protein containing the Arpase domain of a heat
XX CC shock protein. Also described are: (1) a drug composition containing (I)
XX CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector
XX CC containing the DNA of (2); and (4) a transformant which can retain the
XX CC expression vector of (3). (1) has cytotoxic, immunostimulant and
XX CC protozoacide activities, and can be used as a cellular immune response
XX CC inducer. The protein is useful as an active ingredient for drug
XX CC compositions in preventing and/or treating infectious diseases such as
XX CC malaria or cancer e.g. to provide systemic immunity against leukaemia.
XX CC The present sequence represents a specifically claimed heat shock protein
XX CC for use in a fused protein of the present invention
XX SQ Sequence 640 AA;
Query Match 98.8%; Score 1298.5; DB 3; Length 640;
Best Local Similarity 99.6%; Pred. No. 1.7e-99;
Matches 257; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 KSENVQDLLLLDVAPLSLGLGTAGGVTALIKRNSTIPTKTQIIFTTYSNDQPGVLIQVY 60
DB 384 KSENVQDLLLLDVAPLSLGLGTAGGVTALIKRNSTIPTKTQIIFTTYSNDQPGVLIQVY 443
QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 502
QY 121 TNDKGRLSKEEIERMWQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDSGLGKGIS 180
DB 503 TNDKGRLSKEEIERMWQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDSGLGKGIS 562
QY 181 EADKKVLDKQCQEVISWLDANTLAEKDEFEHKKRKELEQVCNPIISGLYQAGGPGGPGF 240
DB 563 EADKKVLDKQCQEVISWLDANTLAEKDEFEHKKRKELEQVCNPIISGLYQAGGPGGPGF 622
QY 241 AQGPKGGSGSGPTIEVD 258
DB 623 AQGPKGGSGSGPTIEVD 640
RESULT 19
ADD14137
ID ADD14137 standard; protein; 640 AA.
XX

ADD14137;
01-JAN-2004 (first entry)
Human src biomarker polypeptide SEQ ID NO:326.
predictor set; protein tyrosine kinase activity modulator;
protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;
gene therapy; drug sensitivity; genetic profile; cancer; human.
Homo sapiens.
W02003062395-A2.
31-JUL-2003.
17-JAN-2003; 2003WO-US001981.
18-JAN-2002; 2002US-0350061P.
(BRIM) BRISTOL-MYERS SQUIBB CO.
Huang F, Fairchild CR, Lee FY, Shaw P;
WPI; 2003-636735/60.
N-PSDB; ADD14739.
New polynucleotides and polypeptides for predicting the activity of
compounds that interact with protein tyrosine kinases and/or protein
tyrosine kinase pathways.
Claim 10; SEQ ID NO 326; 139pp; English.
The present invention describes a predictor set comprising a plurality of
polynucleotides or polypeptides whose expression pattern is predictive of
the response of cells to treatment with a compound that modulates protein
tyrosine kinase activity or members of the protein tyrosine kinase
pathway. Also described: (1) predicting whether a compound is capable of
modulating the activity of cells, comprising obtaining a sample of cells,
determining whether the cells express a plurality of markers, and
correlating the expression of the markers to the compound's ability to
modulate the activity of the cells; (2) a plurality of cell lines for
identifying polynucleotides and polypeptides whose expression levels
correlate with compound sensitivity or resistance of cells associated
with a disease state; and (3) identifying polynucleotides and
polypeptides that predict compound sensitivity or resistance of cells
associated with a disease state, comprising subjecting the plurality of
cell lines to one or more compounds, analysing the expression pattern of
a microarray of polynucleotides or polypeptides, and selecting
polynucleotides or polypeptides that predict the sensitivity or
resistance of cells associated with a disease state by using the
expression pattern of the microarray. The polynucleotides and
polypeptides have cytostatic activities, and can be used in gene therapy.
The polynucleotides and polypeptides are useful in predicting the
activity of compounds that interact with protein tyrosine kinases and/or
protein tyrosine kinase pathways. These may be used in determining drug
sensitivity in patients to allow the development of individualized
genetic profiles which aid in treating diseases and disorders (e.g.
cancer) based on patient response at a molecular level. The present
sequence is used in the exemplification of the present invention.
Sequence 640 AA;
Query Match 98.8%; Score 1298.5; DB 7; Length 640;
Best Local Similarity 99.6%; Pred No. 1.7e-99;
Matches 257; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 KSENVQDLLLLLVAPLSLGLTAGVMTALIKRNSTIPTKTQTFTTYSNDQPGVLQVY 60
DB 384 KSENVQDLLLLLVAPLSLGLTAGVMTALIKRNSTIPTKTQTFTTYSNDQPGVLQVY 443.
QY 61 EGERAMTKDNNLLGRFELSGIPAP- GVPQIEVTFDIDANGILNVATDKSTGKANKITI 120

444 EGERAMTKDNNLLGRFELSGIPAP- GVPQIEVTFDIDANGILNVATDKSTGKANKITI 502
121 TNDKGRLSKEELRMVQAEKYKAEDEVQRRVRSNAKNALESYAFNWKSAVEDGLKKGKIS 180
503 TNDKGRLSKEELRMVQAEKYKAEDEVQRRVRSNAKNALESYAFNWKSAVEDGLKKGKIS 562
181 EADKKKVLDDKQEVISWLDANTLAEKDFEHRKKELEQVCNPIISGLYQAGGPGPGGFG 240
563 EADKKKVLDDKQEVISWLDANTLAEKDFEHRKKELEQVCNPIISGLYQAGGPGPGGFG 622
241 AQPCKGGSGSGPTIEVD 258
623 AQPCKGGSGSGPTIEVD 640
RESULT 20
ADJ68449
ID ADJ68449 standard; protein; 640 AA.
XX
AC ADJ68449;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heat mitochondrial protein as a therapeutic target SeqID255.
XX
KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
PN W02003087768-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010870.
XX
PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX
DR WPI; 2003-845369/78.
XX
PT Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
PS Claim 1; SEQ ID NO 255; 180pp; English.
XX
CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and

CC cytosolic activities. This polypeptide sequence is a human heat
 XX mitochondrial protein of the invention.
 SQ Sequence 640 AA;

Query Match 98.8%; Score 1298.5; DB 7; Length 640;
 Best Local Similarity 99.6%; Pred. No. 1.7e-99;
 Matches 257; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 KSENVQDLLLDVAPLSGLGLETAGGVTALIKRSTIPTKTQTFITYSDNQGVLIQVY 60
 Db 384 KSENVQDLLLDVAPLSGLGLETAGGVTALIKRSTIPTKTQTFITYSDNQGVLIQVY 443
 Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVQIETVTFDANGILNVATDKSTGKANKITI 120
 Db 444 EGERAMTKNNLLGRFELSGIPAPRGVQIETVTFDANGILNVATDKSTGKANKITI 502
 Qy 121 TNDKGRLSKEEIERMVOEAEKYAEDEVQERVSANNALESYAFNMKSAVEDSGLGKIS 180
 Db 503 TNDKGRLSKEEIERMVOEAEKYAEDEVQERVSANNALESYAFNMKSAVEDSGLGKIS 562
 Qy 181 EADKKVLDKQCEVISWLDANTLAEKDFEHEKKELEQVNCNPIISGLYQAGGPGGFG 240
 Db 563 EADKKVLDKQCEVISWLDANTLAEKDFEHEKKELEQVNCNPIISGLYQAGGPGGFG 622
 Qy 241 AOGPKGGSGGPTIEVD 258
 Db 623 AOGPKGGSGGPTIEVD 640

RESULT 21
 ABR40399
 ID ABR40399 standard; protein; 641 AA.
 XX
 AC ABR40399;
 DT 08-AUG-2003 (first entry)
 XX
 XX Bovine Hsp70 protein.
 XX
 DE heat shock protein; HSP; cytokine; CC chemokine; nitric oxide; cancer;
 KW antimicrobial; virucide; cytostatic; microbial infection; anti-HIV;
 KW viral infection; immune system disorder; vaccine; HSP70; bovine.
 XX
 OS Bos taurus.
 XX
 PN WO2003029289-A2.
 XX
 PD 10-APR-2003.
 XX
 XX 03-OCT-2002; 2002WO-GB004475.
 XX
 XX 03-OCT-2001; 2001GB-00023756.
 XX
 XX (UNLO) KINGS COLLEGE LONDON.
 XX
 XX Lehner T, Kelly CG, Singh M, Wang Y;
 XX WPI; 2003-430189/40.
 XX
 XX Novel heat shock protein fragment useful for treating microbial
 PT infection, viral infection or cancer, that can increase the level of
 PT cytokines and/or CC chemokines and/or nitric oxide produced by a cell.
 XX
 XX Example 3; Page 17-20; 30pp; English.
 XX
 XX The invention relates to a novel heat shock protein fragment (HSP) that
 CC can increase the level of one or more cytokines and/or one or more CC
 CC chemokines and/or nitric oxide produced by a cell, above that caused by
 CC the corresponding full length heat shock protein. The protein fragment of
 CC the invention has antimicrobial, virucide, and cytostatic activity. The
 CC protein fragment is useful in therapy, in treatment or prophylaxis of a
 CC disease and in the manufacture of a medicament for treatment or

CC prophylaxis of a disease such as microbial infection, viral infection,
 CC disease of the immune system or cancer. The fragment is also useful as an
 CC adjuvant in vaccines, preferably, anti-HIV vaccines. The present sequence
 CC represents the bovine HSP70 protein
 XX
 SQ Sequence 641 AA;

Query Match 98.8%; Score 1295; DB 6; Length 641;
 Best Local Similarity 98.8%; Pred. No. 3.4e-99;
 Matches 255; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLDVAPLSGLGLETAGGVTALIKRSTIPTKTQTFITYSDNQGVLIQVY 60
 Db 384 KSENVQDLLLDVAPLSGLGLETAGGVTALIKRSTIPTKTQTFITYSDNQGVLIQVY 443
 Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVQIETVTFDANGILNVATDKSTGKANKITI 120
 Db 444 EGERAMTKNNLLGRFELSGIPAPRGVQIETVTFDANGILNVATDKSTGKANKITI 503
 Qy 121 TNDKGRLSKEEIERMVOEAEKYAEDEVQERVSANNALESYAFNMKSAVEDSGLGKIS 180
 Db 504 TNDKGRLSKEEIERMVOEAEKYAEDEVQERVSANNALESYAFNMKSAVEDSGLGKIS 563
 Qy 181 EADKKVLDKQCEVISWLDANTLAEKDFEHEKKELEQVNCNPIISGLYQAGGPGGFG 240
 Db 564 EADKKVLDKQCEVISWLDANTLAEKDFEHEKKELEQVNCNPIISGLYQAGGPGGFG 623
 Qy 241 AOGPKGGSGGPTIEVD 258
 Db 624 AOGPKGGSGGPTIEVD 641

RESULT 22
 AAW10065
 ID AAW10065 standard; protein; 640 AA.
 XX
 AC AAW10065;
 DT 24-OCT-1997 (first entry)
 XX
 XX Human heat shock protein 70.
 DE
 XX Human; heat shock protein 70; HSP70; primer; probe; detection;
 KW intracellular; abnormal transcription; acute; chronic; sustained; stress.
 XX
 OS Homo sapiens.
 XX
 PN JP08322577-A.
 XX
 PD 10-DEC-1996.
 XX
 XX 01-JUN-1995; 95JP-00158581.
 XX
 XX 01-JUN-1995; 95JP-00158581.
 PR
 XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
 PA
 XX WPI; 1997-081088/08.
 DR
 XX N-PSDB; AAT58086.
 XX
 XX Detection of abnormal transcription of HSP70 mRNA - using HSP70 specific
 PT primer or probe, used in detection of human acute and chronic sustained
 PT stress load.
 XX
 XX Claim 1; Fig 1; 13pp; Japanese.
 PS
 XX The cDNA encoding the present sequence, human heat shock protein 70
 CC (HSP70), is located on human chromosome 6p 21.3-22 and 14q 22-24 and 21.
 CC Primers and probes based on the HSP70 cDNA coding sequence can be used to
 CC detect the abnormal transcription of intracellular HSP70 mRNA in human
 CC acute and chronic sustained stress load
 CC
 XX Sequence 640 AA;

Query Match 98.2%; Score 1290.5; DB 2; Length 640;
 Best Local Similarity 99.2%; Pred. No. 8e-99; Indels 1; Gaps 1;
 Matches 256; Conservative 0; Mismatches 1;

QY 1 KSENVQDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQTQIFFTYSNQPGVLIQVY 60
 DB 384 KSENVQDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQTQIFFTYSNQPGVLIQVY 443

QY 61 EGERAMTKONLLGRFELSGIPAPRGVPOIETVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 444 EGERAMTKONLLGRFELSGIPAPRGVPOIETVTFDIDANGILNVTATDKSTGKANKITI 502

QY 121 TNDKGRLSKEEIERMWQEAKEYKAEDVQREVRSNAKNALESYAFNMKSAVEDGLGKIS 180
 DB 503 TNDKGRLSKEEIERMWQEAKEYKAEDVQREVRSNAKNALESYAFNMKSAVEDGLGKIS 562

QY 181 EADKKKVLDRKQEVISWLDANTLAEKDFEHRKKELEQVCNPIISGLYQAGGPGPGFG 240
 DB 563 EADKKKVLDRKQEVISWLDANTLAEKDFEHRKKELEQVCNPIISGLYQAGGPGPGFG 622

QY 241 AQPCKGGSGSGPTIEVD 258
 DB 623 AQPCKGGSGSGPTIEVD 640

RESULT 23

AA088408
 ID AAY88408 standard; protein; 640 AA.

AC AAY88408;

DT 31-JUL-2000 (first entry)

DE Human heat shock protein HSP70 amino acid sequence.

KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
 KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;
 KW depression; nephrotic syndrome.

OS Homo sapiens.

PN JP2000069999-A.

PD 07-MAR-2000.

PF 01-JUN-1995; 99JP-00257146.

PR 01-JUN-1995; 95JP-00158581.

PA (HOKI-) HOKEN KAGAKU KENKYUSHO KK.

XX WPI; 2000-264458/23.

DR N-PSDB; AAA15620.

XX Abnormal transcription of intracellular HSP70mRNA under acute and chronic
 PT continuous load of stress in a human being and its application.

PS Claim 2; Fig 1; 11pp; Japanese.

XX This sequence represents the human heat shock protein HSP70 amino acid
 CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
 CC and 14q22-24. The invention relates to the abnormal transcription of
 CC intracellular HSP70mRNA under acute and chronic stress load in a human.
 CC The abnormal transcription of HSP70 can be used in the improvement of
 CC stress and response and diagnosis of stress diseases including
 CC rheumatism, schizophrenia, depression and nephrotic syndrome

XX Sequence 640 AA;

Query Match 98.2%; Score 1290.5; DB 3; Length 640;
 Best Local Similarity 99.2%; Pred. No. 8e-99; Indels 1; Gaps 1;
 Matches 256; Conservative 0; Mismatches 1;

QY 1 KSENVQDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQTQIFFTYSNQPGVLIQVY 60
 DB 384 KSENVQDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQTQIFFTYSNQPGVLIQVY 443

QY 61 EGERAMTKONLLGRFELSGIPAPRGVPOIETVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 444 EGERAMTKONLLGRFELSGIPAPRGVPOIETVTFDIDANGILNVTATDKSTGKANKITI 502

QY 121 TNDKGRLSKEEIERMWQEAKEYKAEDVQREVRSNAKNALESYAFNMKSAVEDGLGKIS 180
 DB 503 TNDKGRLSKEEIERMWQEAKEYKAEDVQREVRSNAKNALESYAFNMKSAVEDGLGKIS 562

QY 181 EADKKKVLDRKQEVISWLDANTLAEKDFEHRKKELEQVCNPIISGLYQAGGPGPGFG 240
 DB 563 EADKKKVLDRKQEVISWLDANTLAEKDFEHRKKELEQVCNPIISGLYQAGGPGPGFG 622

QY 241 AQPCKGGSGSGPTIEVD 258
 DB 623 AQPCKGGSGSGPTIEVD 640

RESULT 24

AA03929
 ID AAR03929 standard; protein; 640 AA.

AC AAR03929;

DT 30-AUG-1990 (first entry)

DE Homo sapiens HSP (humhsp70).

KW Hep70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 640
 FT /note= "residue given as "O" in specification"

XX WO9002564-A.

XX 22-MAR-1990.

XX 12-SEP-1988; 88US-00243474.

XX 12-SEP-1988; 88US-00243474.

XX (CODO-) CODON.

XX Dragon E, Pauls D, Sias S;

XX WPI; 1990-115820/15.

XX Proteins homologous to heat shock proteins of Trypanosoma cruzi - used in
 PT vaccines and diagnosis for species of e.g. muco-plasma or mycobacteria.

XX Disclosure; Fig 2.1-2.14; 86pp; English.

XX According to the legend of Fig 2, the H. sapiens HSP sequence has 641
 CC amino acid residues, the sequence itself has only 640, including "O" (?)
 CC at position 640. Fig. 2 provides an alignment of heat shock proteins from
 CC a variety of organisms: 1. M. hyopneumoniae (Mhysp70 - AAR03922); 2.
 CC Bacillus megaterium (Bmeasp70 - AAR03923); 3. E. coli (dnak - AAR03924);
 CC 4. T. cruzi (tc70kd - AAR03925); 5. T. cruzi (AAR03926); 6. Rat rattus
 CC (rathsp70 - AAR03927); 7. Xenopus laevis (xl170 - AAR03928); 8. Homo
 CC sapiens (humhsp70 - AAR03929); 9. Gallus gallus (chkhsp70 - AAR03930);
 CC 10. Zea mays (mzeasp70 - AAR03931); 11. Serratia marcescens (smahsp70 -
 CC AAR03932). The proteins having homology to hsp's of T. cruzi can be used
 CC in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
 CC Mycobacteria species

XX Sequence 640 AA;

Query Match 97.6%; Score 1282; DB 2; Length 640;
Best Local Similarity 99.2%; Pred. No. 4.1e-98;
Matches 256; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 KSENVODLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQIFFTYSNQPGLIQVY 60
DB 384 KSENVODLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQIFFTYSNQPGLIQVY 443
QY 61 EGERAMTKDNLLGRFELSIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKDNLLGRFELSIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 502
QY 121 TNDKGRLSKEEIERMVEAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLGKIS 180
DB 503 TNDKGRLSKEEIERMVEAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLGKIS 562
QY 181 EADKKKVLKQCVISWLDANTLAEKDFEHRKELEQVCNPIISGLYQAGGPGGPG 240
DB 563 EADKKKVLKQCVISWLDANTLAEKDFEHRKELEQVCNPIISGLYQAGGPGGPG 622
QY 241 AQPCKGGSGSGPTIEVD 258
DB 622 AQPCKGGSGSGPTIEVD 639

RESULT 25
AAY88411
ID AAY88411 standard; protein; 640 AA.
XX AAY88411;
XX
DT 31-JUL-2000 (first entry)
XX Human heat shock protein LHSF70 amino acid sequence.
XX
XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;
KW depression; nephrotic syndrome; LHSF70.
XX
XX Homo sapiens.
XX
XX JP2000069999-A.
XX
XX 07-MAR-2000.
XX
XX 01-JUN-1995; 99JP-00257146.
XX
XX 01-JUN-1995; 95JP-00158581.
XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
XX
XX WPI; 2000-264458/23.
XX
XX Abnormal transcription of intracellular HSP70mRNA under acute and chronic
PT continuous load of stress in a human being and its application.
XX
XX Disclosure; Fig 4; 11pp; Japanese.
XX
XX This sequence represents the human heat shock protein LHSF70 amino acid
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
CC and 14q22-24. The invention relates to the abnormal transcription of
CC intracellular HSP70mRNA under acute and chronic stress load in a human.
CC The abnormal transcription of HSP70 can be used in the improvement of
CC stress and response and diagnosis of stress diseases including
CC rheumatism, schizophrenia, depression and nephrotic syndrome
XX
XX Sequence 640 AA;

Query Match 97.3%; Score 1278.5; DB 3; Length 640;
Best Local Similarity 98.1%; Pred. No. 8e-98;
Matches 253; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 KSENVODLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQIFFTYSNQPGLIQVY 60
DB 384 KSENVODLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQIFFTYSNQPGLIQVY 443
QY 61 EGERAMTKDNLLGRFELSIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKDNLLGRFELSIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 502
QY 121 TNDKGRLSKEEIERMVEAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLGKIS 180
DB 503 TNDKGRLSKEEIERMVEAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLGKIS 562
QY 181 EADKKKVLKQCVISWLDANTLAEKDFEHRKELEQVCNPIISGLYQAGGPGGPG 240
DB 563 EADKKKVLKQCVISWLDANTLAEKDFEHRKELEQVCNPIISGLYQAGGPGGPG 622
QY 241 AQPCKGGSGSGPTIEVD 258
DB 622 AQPCKGGSGSGPTIEVD 640

RESULT 26
ABR40398
ID ABR40398 standard; protein; 641 AA.
XX
AC ABR40398;
XX
DT 08-AUG-2003 (first entry)
XX
DE Rat HSP70 protein.
XX
KW heat shock protein; HSP; cytokine; CC chemokine; nitric oxide; cancer;
KW antimicrobial; virucide; cytostatic; microbial infection; anti-HIV;
KW viral infection; immune system disorder; vaccine; HSP70; rat.
XX
OS Rattus sp.
XX
XX WO2003029289-A2.
XX
XX 10-APR-2003.
XX
XX 03-OCT-2002; 2002WO-GB004475.
XX
XX 03-OCT-2001; 2001GB-00023756.
XX (UNLO) KINGS COLLEGE LONDON.
XX
XX Lehner T, Kelly CG, Singh M, Wang Y;
XX WPI; 2003-430189/40.
XX
XX Novel heat shock protein fragment useful for treating microbial
PT infection, viral infection or cancer, that can increase the level of
PT cytokines and/or CC chemokines and/or nitric oxide produced by a cell.
XX
XX Example 3; Page 17-20; 30pp; English.
XX
XX The invention relates to a novel heat shock protein fragment (HSP) that
CC can increase the level of one or more cytokines and/or one or more CC
CC chemokines and/or nitric oxide produced by a cell, above that caused by
CC the corresponding full length heat shock protein. The protein fragment of
CC the invention has antimicrobial, virucide, and cytostatic activity. The
CC protein fragment is useful in therapy, in treatment or prophylaxis of a
CC disease and in the manufacture of a medicament for treatment or
CC prophylaxis of a disease such as microbial infection, viral infection,
CC disease of the immune system or cancer. The fragment is also useful as an
CC adjuvant in vaccines, preferably, anti-HIV vaccines. The present sequence
CC represents the rat HSP70 protein
XX
XX Sequence 641 AA;

Query Match 95.7%; Score 1258; DB 6; Length 641;
Best Local Similarity 95.3%; Pred. No. 4.1e-96;

Matches 246; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 KSENVODLLLDVAPLSLGLTAGGVTALIKENSTIPTKOTIFTTYSNQPGLIOVY 60
DB 384 KSENVODLLLDVAPLSLGLTAGGVTALIKENSTIPTKOTIFTTYSNQPGLIOVY 443
QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATATDKSTGKANKITI 120
DB 444 EGERAMTRDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATATDKSTGKANKITI 503
QY 121 TNDKGRSLKKEEIERMVOEAEKYAEDVQERVAQNALESYAFNMKSAVEDGLGKIS 180
DB 504 TNDKGRSLKKEEIERMVOEAEKYAEDVQERVAQNALESYAFNMKSAVEDGLGKIS 563
QY 181 EADKKVLDKCOEIVSWLDANTLAEDFEHKEKELEOVNCNPIISGLYQAGGPGGFG 240
DB 564 EADKKVLDKCOEIVSWLDANTLAEDFEHKEKELEOVNCNPIISGLYQAGGPGGFG 623
QY 241 AQPKGGSGSGPTIEVD 258
DB 624 AQPKGGSGSGPTIEVD 641

RESULT 27
ADD46498
ID ADD46498 standard; protein; 641 AA.
AC ADD46498;
XX
XX
XX 29-JAN-2004 (first entry)
XX
XX Rat Protein Q07439, SEQ ID NO 12179.
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
XX Rattus norvegicus.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO) GEN HOSPITAL CORP.
XX PA (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
XX DR GENBANK; Q07439.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a

CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 641 AA;
XX
XX Query Match 95.7%; Score 1258; DB 7; Length 641;
XX Best Local Similarity 95.3%; Pred. No. 4.1e-96;
XX Matches 246; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 KSENVODLLLDVAPLSLGLTAGGVTALIKENSTIPTKOTIFTTYSNQPGLIOVY 60
DB 384 KSENVODLLLDVAPLSLGLTAGGVTALIKENSTIPTKOTIFTTYSNQPGLIOVY 443
QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATATDKSTGKANKITI 120
DB 444 EGERAMTRDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATATDKSTGKANKITI 503
QY 121 TNDKGRSLKKEEIERMVOEAEKYAEDVQERVAQNALESYAFNMKSAVEDGLGKIS 180
DB 504 TNDKGRSLKKEEIERMVOEAEKYAEDVQERVAQNALESYAFNMKSAVEDGLGKIS 563
QY 181 EADKKVLDKCOEIVSWLDANTLAEDFEHKEKELEOVNCNPIISGLYQAGGPGGFG 240
DB 564 EADKKVLDKCOEIVSWLDANTLAEDFEHKEKELEOVNCNPIISGLYQAGGPGGFG 623
QY 241 AQPKGGSGSGPTIEVD 258
DB 624 AQPKGGSGSGPTIEVD 641

RESULT 28
ADE57092
ID ADE57092 standard; protein; 641 AA.
XX
XX AC ADE57092;
XX
XX 29-JAN-2004 (first entry)
XX
XX Rat Protein Q07439, SEQ ID NO 2952.
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
XX Rattus norvegicus.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO) GEN HOSPITAL CORP.
XX PA (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX

DR WPI; 2003-268312/26.
 XX GENBANK; Q07439.
 PT New composition comprising two or more isolated polypeptides, useful for
 XX preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 641 AA;
 Query Match 95.7%; Score 1258; DB 7; Length 641;
 Best Local Similarity 95.3%; Pred. No. 4.1e-96;
 Matches 246; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 QY 1 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTIPTKTQTFITYSDNQGVLIQVY 60
 DB 384 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTIPTKTQTFITYSDNQGVLIQVY 443
 QY 61 EGERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 444 EGERAMTRDNNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 180
 DB 504 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 563
 QY 181 EADKKVLDKCOEIVSWLDANTLAEKDFEHRKELEQVCNPIISGLYQAGGPGGFG 240
 DB 564 EADKKVLDKCOEIVSWLDNTLAKEEFVHKREELERVCNPIISGLYQAGAGPGAGGFG 623
 QY 241 AQPKPGSGSGPTIEVD 258
 DB 624 AQAPKGGSGSGPTIEVD 641
 RESULT 29
 ID ADD45046
 XX ADD45046 standard; protein; 641 AA.
 AC ADD45046;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Rat Protein Q07439, SEQ ID NO 10478.
 XX

Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 Rattus norvegicus.
 OS
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; Q07439.
 XX
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 641 AA;
 Query Match 95.7%; Score 1258; DB 7; Length 641;
 Best Local Similarity 95.3%; Pred. No. 4.1e-96;
 Matches 246; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 QY 1 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTIPTKTQTFITYSDNQGVLIQVY 60
 DB 384 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTIPTKTQTFITYSDNQGVLIQVY 443
 QY 61 EGERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 444 EGERAMTRDNNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 180
 DB 504 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 563
 QY 181 EADKKVLDKCOEIVSWLDANTLAEKDFEHRKELEQVCNPIISGLYQAGGPGGFG 240
 DB 564 EADKKVLDKCOEIVSWLDNTLAKEEFVHKREELERVCNPIISGLYQAGAGPGAGGFG 623
 QY 241 AQPKPGSGSGPTIEVD 258
 DB 624 AQAPKGGSGSGPTIEVD 641
 RESULT 29
 ID ADD45046
 XX ADD45046 standard; protein; 641 AA.
 AC ADD45046;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Rat Protein Q07439, SEQ ID NO 10478.
 XX

181 EADKKVLDKQCVISWLDANTLAERKDEFEHKKELQVNCNPIISGLYQAGGPGGFG 240
 564 EADKKVLDKQCVISWLDNTLAERKEFEVHKRELERVNCNPIISGLYQAGGPGGFG 623

241 AQPKGGSGSGPTIEVD 258
 624 AQAPKGGSGSGPTIEVD 641

RESULT 30
 ADD47457
 ID ADD47457 standard; protein; 641 AA.
 XX AC ADD47457;
 XX 02-DEC-2004 (revised)
 DT 29-JAN-2004 (first entry)
 XX Rat Protein NP_114177, SEQ ID NO 13152.
 XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX Rattus norvegicus.
 OS Unidentified.
 XX W02003016475-A2.
 XX 27-FEB-2003.
 XX 14-AUG-2002; 2002WO-US025765.
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX Woolf C, D'urso D, Belfort K, Costigan M;
 PI WPI; 2003-268312/26.
 DR GENBANK; NP_114177.
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX Example 1; Page; 1017pp; English.
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung)), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (described in Table 3

CC of the specification) which is differentially expressed during pain.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 641 AA;

Query Match 95.7%; Score 1258; DB 7; Length 641;
 Best Local Similarity 95.3%; Pred. No. 4.1e-96;
 Matches 246; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 KSENVQDLLLLDVAPLSGLGLETAGGYMTALIKENSTIPTKQTQITFTTYSNQPGLVLIQVY 60
 Db 384 KSENVQDLLLLDVAPLSGLGLETAGGYMTALIKENSTIPTKQTQITFTTYSNQPGLVLIQVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPPPAGVQIEVTFDIDANGILNVTTATDKSTGKANKITI 120
 Db 444 EGERAMTRDNNLLGRFELSGIPPPAGVQIEVTFDIDANGILNVTTATDKSTGKANKITI 503
 QY 121 TNDKGRLSKBEIERVMQEAERKARDEVORERSAKNALESVAFNMKSAVEDGLGKGIS 180
 Db 504 TNDKGRLSKBEIERVMQEAERKARDEVORERSAKNALESVAFNMKSAVEDGLGKGIS 563
 QY 181 EADKKVLDKQCVISWLDANTLAERKDEFEHKKELQVNCNPIISGLYQAGGPGGFG 240
 Db 564 EADKKVLDKQCVISWLDNTLAERKEFEVHKRELERVNCNPIISGLYQAGGPGGFG 623
 QY 241 AQPKGGSGSGPTIEVD 258
 Db 624 AQAPKGGSGSGPTIEVD 641

RESULT 31

ADP30465
 ID ADP30465 standard; protein; 641 AA.

XX AC ADP30465;

XX 12-FEB-2004 (first entry)

XX Rat angiogenesis modulating protein #9.

XX rat; angiogenesis; angiogenesis modulating protein;
 KW retinal neovascularisation; choroidal neovascularisation;
 KW chronic inflammation; myocardial ischaemia; stroke;
 KW coronary artery disease; peripheral vascular disease.

XX Rattus norvegicus.

XX US2003162706-A1.

XX 28-AUG-2003.

XX 10-DEC-2002; 2002US-00316253.

XX 08-FEB-2002; 2002US-0355295P.

XX 26-JUN-2002; 2002US-0391758P.

XX (PROC) PROCTER & GAMBLE CO.

XX Peters KG, Thompson LJ, Wang F, Greis KD;

XX WPI; 2003-711557/67.

XX N-PSDB; ADP30464.

XX Treating angiogenesis-mediated disorder, e.g., retinal or choroidal
 PT neovascularization or diseases associated with chronic inflammation,
 PT myocardial ischemia, stroke, coronary artery disease or peripheral
 PT vascular disease.

XX Claim 2; SEQ ID NO 28; 26pp; English.

XX The invention relates to a method of treating an angiogenesis-mediated

CC disorder in a subject. The method is useful for treating angiogenesis-mediated disorder, e.g., retinal or choroidal neovascularisation or mediated disorder, e.g., retinal or choroidal neovascularisation or diseases associated with chronic inflammation, myocardial ischaemia, CC stroke, coronary artery disease or peripheral vascular disease. The CC present sequence is used in the exemplification of the invention.

XX SQ Sequence 641 AA;

Query Match 95.7%; Score 1258; DB 7; Length 641;
Best Local Similarity 95.3%; Pred. No. 4.1e-96;
Matches 246; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQIFTTYSNQPGLVLIQVY 60
DB 384 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQIFTTYSNQPGLVLIQVY 443

QY 61 EGERAMTKNNLLGRFELSGLGIPAPRGVPOIEVTFDIDANGILNVTTATDKSTGKANKITI 120
DB 444 EGERAMTRDNNLLGRFELSGLGIPAPRGVPOIEVTFDIDANGILNVTTATDKSTGKANKITI 503

QY 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 180
DB 504 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 563

QY 181 EADKKVLDKQEVISWLDANTLAEDFEHKKRKELEQVCNPIISGLYQAGGPGGFG 240
DB 564 EADKKVLDKQEVISWLDANTLAEDFEHKKRKELEQVCNPIISGLYQAGGPGGFG 623

QY 241 AQPKGGSGSGPTIEVD 258
DB 624 AQPKGGSGSGPTIEVD 641

RESULT 32

ADF30534

ID ADF30534 standard; protein; 641 AA.

XX AC ADF30534;

DT 12-FEB-2004 (first entry)

XX DE Rat angiogenesis modulating protein #56.

XX KW rat; angiogenesis; angiogenesis modulating protein;

XX KW retinal neovascularisation; choroidal neovascularisation;

XX KW chronic inflammation; myocardial ischaemia; stroke;

XX KW coronary artery disease; peripheral vascular disease.

XX OS Rattus norvegicus.

XX PN US2003162706-A1.

XX PD 28-AUG-2003.

XX PF 10-DEC-2002; 2002US-00316253.

XX PR 08-FEB-2002; 2002US-0355295P.

XX PR 26-JUN-2002; 2002US-0391758P.

XX PA (PROC) PROCTER & GAMBLE CO.

XX PI Peters KG, Thompson LJ, Wang F, Greis KD;

XX DR WPI; 2003-711557/67.

XX DR N-PSDB; ADF30533.

XX PT Treating angiogenesis-mediated disorder, e.g., retinal or choroidal neovascularization or diseases associated with chronic inflammation, PT myocardial ischemia, stroke, coronary artery disease or peripheral vascular disease.

XX PS Claim 2; SEQ ID NO 97; 26pp; English.

CC The invention relates to a method of treating an angiogenesis-mediated disorder in a subject. The method is useful for treating angiogenesis-mediated disorder, e.g., retinal or choroidal neovascularisation or diseases associated with chronic inflammation, myocardial ischaemia, CC stroke, coronary artery disease or peripheral vascular disease. The CC present sequence is used in the exemplification of the invention.

XX SQ Sequence 641 AA;

Query Match 95.7%; Score 1258; DB 7; Length 641;
Best Local Similarity 95.3%; Pred. No. 4.1e-96;
Matches 246; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQIFTTYSNQPGLVLIQVY 60
DB 384 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQIFTTYSNQPGLVLIQVY 443

QY 61 EGERAMTKNNLLGRFELSGLGIPAPRGVPOIEVTFDIDANGILNVTTATDKSTGKANKITI 120
DB 444 EGERAMTRDNNLLGRFELSGLGIPAPRGVPOIEVTFDIDANGILNVTTATDKSTGKANKITI 503

QY 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 180
DB 504 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 563

QY 181 EADKKVLDKQEVISWLDANTLAEDFEHKKRKELEQVCNPIISGLYQAGGPGGFG 240
DB 564 EADKKVLDKQEVISWLDANTLAEDFEHKKRKELEQVCNPIISGLYQAGGPGGFG 623

QY 241 AQPKGGSGSGPTIEVD 258
DB 624 AQPKGGSGSGPTIEVD 641

RESULT 33

AAB09886

ID AAB09886 standard; protein; 244 AA.

XX AC AAB09886;

DT 06-NOV-2000 (first entry)

XX DE Hsp70 C-terminal 244 amino acid polypeptide sequence.

XX KW Heat shock protein 70; Hsp70; NF-kappaB; transplant rejection;

XX KW autoimmune disease; inflammatory disease; cancer; vascular disease.

XX OS Homo sapiens.

XX PN W0200031113-A1.

XX PD 02-JUN-2000.

XX PF 17-NOV-1999; 99WO-US027244.

XX PR 24-NOV-1998; 98US-0109872P.

XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX PI Fujihara SM, Nadler SG;

XX DR WPI; 2000-400029/34.

XX PT Intracellular targeted delivery of compounds using the 70 kilodalton heat shock protein, useful in the treatment of transplant rejection,

XX PT autoimmune diseases and cancer.

XX PS Claim 6; Page 17; 37pp; English.

XX CC The present sequence is the C-terminal 244 amino acids of the 70kD heat shock protein (Hsp70). This sequence was used in a fusion protein with the p50 subunit of transcription factor NF-kappaB, the sequence of which is indicated in the specification as being SEQ ID NO: 1, but which is not

CC given. This fusion protein was created in order to determine the ability
 CC of the Hsp70 sequence to direct other proteins into the cell. It was
 CC shown that Hsp70 fragments are able to direct other proteins into the
 CC cell, a feature which can be used in the treatment of transplant
 CC rejection, autoimmune diseases such as rheumatoid arthritis, multiple
 CC sclerosis, diabetes, asthma, inflammatory bowel disease, psoriasis,
 CC hepatitis, Graves' disease and viteligo, inflammatory diseases including
 CC osteoarthritis, pancreatitis and adult respiratory distress syndrome,
 CC cancer, vascular diseases (such as restenosis and atherosclerosis) and
 CC DNA and RNA viral replication diseases (including herpes)

XX SQ Sequence 244 AA;

Query Match 95.1%; Score 1249; DB 3; Length 244;
 Best Local Similarity 100.0%; Pred. No. 6.7e-96;
 Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLSGLTAGVMTALIKRNSTIPTKTQITFTTYSNQPGLVIOVYEGRAMTKNNLLG 74

DB 1 PLSGLTAGVMTALIKRNSTIPTKTQITFTTYSNQPGLVIOVYEGRAMTKNNLLG 60

QY 75 RFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITITNDKGRLSKEIER 134

DB 61 RFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITITNDKGRLSKEIER 120

QY 135 MVQEAERYKAEDVQERVSAAKNALESYAFNMKSAVEDGLKGKISEADKKVLDKQEV 194

DB 121 MVQEAERYKAEDVQERVSAAKNALESYAFNMKSAVEDGLKGKISEADKKVLDKQEV 180

QY 195 ISWLDANTLAEKDFEHRKELKEQVNCNPIISGLYQAGGPGPGFGAQQGPKGSGSGPTI 254

DB 181 ISWLDANTLAEKDFEHRKELKEQVNCNPIISGLYQAGGPGPGFGAQQGPKGSGSGPTI 240

QY 255 EEVD 258

DB 241 EEVD 244

RESULT 34

AAR43004

ID AAR43004 standard; protein; 641 AA.

XX AC AAR43004;

DT 14-MAY-2003 (revised)

DT 25-MAR-2003 (revised)

DT 20-MAY-1994 (first entry)

XX DE Mature mouse sperm 70kD heat shock protein.

XX KW Sulphoglycolipid immobilising protein 1; sperm plasma membrane; HSC70B;

XX KW mammalian; infertility; mycoplasma; HSP70.

XX OS Mus musculus.

XX FH Key

XX FH Region

FT 1. .385 Location/Qualifiers

FT /label= 44kD ATPase fragment

FT /note= "peptides comprising an intact domain from the

FT ATPase fragment of hsp70 are claimed; the peptides are

FT homologous to sequences conserved between SLIP1 and

FT 74.5kD mycoplasma protein"

FT 1. .39

FT /label= IA

FT /note= "part"

FT 40. .115

FT /label= IB

FT 116. .188

FT /label= IA

FT /note= "part"

FT 189. .228

FT /label= IIA

FT /note= "part"

FT Domain 229. .306

FT /label= IIB

FT Domain 307. .385

FT /label= IIA

FT /note= "part"

PN WO9321954-A1.

XX 11-NOV-1993.

PD 22-APR-1993; 93WO-US003816.

XX 24-APR-1992; 92US-00873961.

XX (BERL-) BERLEX LAB INC.

PA (OTTA-) OTTAWA CIVIC HOSPITAL.

XX Paulds DH, Lingwood CA, Tanphaichitr N;

XX WPI; 1993-368422/46.

XX Mammalian fertilisation decrease for detecting and treating infertility -

PT using sulpho glyco lipid immobilising protein 1-sulphated-glyco moiety

PT interfering compsn., for mycoplasma infection treatment.

XX Claim 2, 17; Page 60-62; 77pp; English.

XX The likelihood of mammalian fertilisation is decreased by contacting a

CC gamete with a sulphoglycolipid immobilising protein 1 (SLIP1)/ sulphated

CC glyco-moiety interfering composition. The interfering compsn. is e.g. the

CC heat shock 70kD protein, SLIP1 (or analogues such as the mouse SLIP1

CC analogue "HSC70B" comprising the amino acid sequence AAR43002) or the

CC 74.5kD mycoplasma protein (AAR43003). (Updated on 25-MAR-2003 to correct

CC PN field.) (Updated on 14-MAY-2003 to correct PS field.)

XX SQ Sequence 641 AA;

Query Match 94.3%; Score 1239; DB 2; Length 641;

Best Local Similarity 93.4%; Pred. No. 1.6e-94;

Matches 241; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 KSENVODLLLDVAPLSGLTAGVMTALIKRNSTIPTKTQITFTTYSNQPGLVIOVY 60

DB 384 KSENVODLLLDVAPLSGLTAGVMTALIKRNSTIPTKTQITFTTYSNQPGLVIOVY 443

QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120

DB 444 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503

QY 121 TNDKGRLSKEIERMVQEAERYKAEDVQERVSAAKNALESYAFNMKSAVEDGLKGKIS 180

DB 504 TNDKGRLSKEIERMVQEAERYKAEDVQERVSAAKNALESYAFNMKSAVEDGLKGKIS 563

QY 181 EADKKVLDKQEVISWLDANTLAEKDFEHRKELKEQVNCNPIISGLYQAGGPGPGFG 240

DB 564 EADKKVLDKQEVISWLDANTLAEKDFEHRKELKEQVNCNPIISGLYQAGGPGPGFG 623

QY 241 AQGPKGSGSGPTIEVD 258

DB 624 AQGPKGSGSGPTIEVD 641

RESULT 35

ABR40397

ID ABR40397 standard; protein; 641 AA.

XX AC ABR40397;

XX 08-AUG-2003 (first entry)

DT Mouse Hsp70 protein.

XX heat shock protein; HSP; cytokine; CC chemokine; nitric oxide; cancer;

KW antimicrobial; virucide; cytostatic; microbial infection; anti-HIV;
 KW viral infection; immune system disorder; vaccine; HSP70; mouse.
 XX Mus sp.
 XX WO2003029289-A2.
 XX 10-APR-2003.
 XX 03-OCT-2002; 2002WO-GB004475.
 XX 03-OCT-2001; 2001GB-00023756.
 XX (UNLO) KINGS COLLEGE LONDON.
 XX Lehner T, Kelly CG, Singh M, Wang Y;
 XX WPI; 2003-430189/40.
 XX Novel heat shock protein fragment useful for treating microbial
 PT infection, viral infection or cancer, that can increase the level of
 PT cytokines and/or CC chemokines and/or nitric oxide produced by a cell.
 XX Example 3; Page 17-20; 30pp; English.
 XX The invention relates to a novel heat shock protein fragment (HSP) that
 CC can increase the level of one or more cytokines and/or one or more CC
 CC chemokines and/or nitric oxide produced by a cell, above that caused by
 CC the corresponding full length heat shock protein. The protein fragment of
 CC the invention has antimicrobial, virucide, and cytostatic activity. The
 CC protein fragment is useful in therapy, in treatment or prophylaxis of a
 CC disease and in the manufacture of a medicament for treatment or
 CC prophylaxis of a disease such as microbial infection, viral infection,
 CC disease of the immune system or cancer. The fragment is also useful as an
 CC adjuvant in vaccines, preferably, anti-HIV vaccines. The present sequence
 CC represents the mouse HSP70 protein
 XX
 SQ Sequence 641 AA;
 Query Match 94.3%; Score 1239; DB 6; Length 641;
 Best Local Similarity 93.4%; Pred. No. 1.6e-94;
 Matches 241; Conservative 11; Mismatches 6; Indels 0; Gaps 0;
 QY 1 KSENVQDLLLDVAPLSLGLTAGGVTALIKENSTIPTKQTQFTTYSNQGVLIQVY 60
 DB 384 KSENVQDLLLDVAPLSLGLTAGGVTALIKENSTIPTKQTQFTTYSNQGVLIQVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 444 EGERAMTRDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEEIERMVOEAEKYAEDEVQREVSAKNALESYAFNMKSAVEDGLKGKLS 180
 DB 504 TNDKGRLSKEEIERMVOEAEKYAEDEVQREVSAKNALESYAFNMKSAVEDGLKGKLS 563
 QY 181 EADKKVLDKQCVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGGFG 240
 DB 564 EADKKVLDKQCVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGGFG 623
 QY 241 AQPKGSGSGGPTIEVD 258
 DB 624 AQAPKGASGSGPTIEVD 641
 RESULT 36
 ADJ27277
 ID ADJ27277 standard; protein; 641 AA.
 XX
 AC ADJ27277;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Mouse HSP70.3.

XX heat shock protein-70; HSP70; HSP70.1; HSP70.3; inducible; induction;
 KW heat; tumour necrosis factor; TNF; interferon-gamma; tumour.
 XX Mus sp.
 XX WO2003061684-A2.
 XX 31-JUL-2003.
 XX 24-JAN-2003; 2003WO-BE000786.
 XX 24-JAN-2002; 2002EP-00075297.
 XX (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
 XX Libert C, Wielockx B, Van Molle W, Mahieu T;
 XX WPI; 2003-608168/57.
 DR N-PSDB; ADJ27276.
 XX New pharmaceutical composition comprising HSP70 that is endogenously
 PT induced by heat and TNF, useful for the manufacture of a medicament for
 PT treating systemic tumor.
 XX Disclosure; SEQ ID NO 4; 53pp; English.
 XX This sequence represents mouse heat shock protein-70.3 (HSP70.3). HSP70.1
 CC and HSP70.3 are inducible members of the HSP70 family of proteins. The
 CC heat shock proteins of the invention are endogenously induced by heat and
 CC tumour necrosis factor (TNF). This heat shock protein may be used in a
 CC composition which further comprises interferon-gamma, and/or a
 CC chemotherapeutic compound. The pharmaceutical composition is useful for
 CC the manufacture of a medicament for treating systemic tumour.
 XX
 SQ Sequence 641 AA;
 Query Match 94.3%; Score 1239; DB 7; Length 641;
 Best Local Similarity 93.4%; Pred. No. 1.6e-94;
 Matches 241; Conservative 11; Mismatches 6; Indels 0; Gaps 0;
 QY 1 KSENVQDLLLDVAPLSLGLTAGGVTALIKENSTIPTKQTQFTTYSNQGVLIQVY 60
 DB 384 KSENVQDLLLDVAPLSLGLTAGGVTALIKENSTIPTKQTQFTTYSNQGVLIQVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 444 EGERAMTRDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEEIERMVOEAEKYAEDEVQREVSAKNALESYAFNMKSAVEDGLKGKLS 180
 DB 504 TNDKGRLSKEEIERMVOEAEKYAEDEVQREVSAKNALESYAFNMKSAVEDGLKGKLS 563
 QY 181 EADKKVLDKQCVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGGFG 240
 DB 564 EADKKVLDKQCVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGGFG 623
 QY 241 AQPKGSGSGGPTIEVD 258
 DB 624 AQAPKGASGSGPTIEVD 641
 RESULT 37
 AAB23650
 ID AAB23650 standard; protein; 642 AA.
 XX
 AC AAB23650;
 XX
 DT 05-JAN-2001 (first entry)
 XX
 DE Rat heat shock protein Hsp70.1 protein sequence SEQ ID NO:2.
 XX
 KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;

immune response; infectious disease; malaria; cytotoxic T cell; cytostatic; immunostimulant; cellular immune response inducer; protozoacide; leukaemia; cancer.

Rattus sp.
WO200049041-A1.
24-AUG-2000.

18-FEB-2000; 2000WO-JP000941.
19-FEB-1999; 99JP-00041535.

(SUME) SUMITOMO ELECTRIC IND CO.
Shinbara N, Udono H, Yui K;
WPI; 2000-543748/49.

Fused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer.

Claim 3; Page 39-42; 72pp; Japanese.

The present invention describes a fused protein (I) prepared from a peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by cytotoxic T cells and a protein containing the Afpase domain of a heat shock protein. Also described are: (1) a drug composition containing (I) as active ingredient; (2) a DNA encoding (I); (3) an expression vector containing the DNA of (2); and (4) a transformant which can retain the expression vector of (3). (I) has cytostatic, immunostimulant and protozoacide activities, and can be used as a cellular immune response inducer. The protein is useful as an active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer e.g. to provide systemic immunity against leukaemia. The present sequence represents a specifically claimed heat shock protein for use in a fused protein of the present invention

Query Match 93.5%; Score 1228.5; DB 3; Length 642;
Best Local Similarity 93.1%; Pred. No. 1.2e-93;
Matches 241; Conservative 11; Mismatches 6; Indels 1; Gaps 1;

Qy 1 KSENVQDLLLLDVAPLSIGLETAGGVMTALIKRNSITPTKQTQIFTTYSNQPGLIQVY 60
Db 384 KSENVQDLLLLDVAPLSIGLETAGGVMTALIKRNSITPTKQTQIFTTYSNQPGLIQVY 443

Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTRDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 503

Qy 121 TNDKGRLSKEEIERMVOEAEKYKAEDVORERSAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 504 TNDKGRLSKEEIERMVOEAEKYKAEDVORERSAKNALESYAFNMKSAVEDEGLKGKIS 563

Qy 181 EADKKVKLDKQCVISWLDANTLAERKDEFEHKKRKELEQVNCNPIISGLYQAGAGPGGFG 240
Db 564 EADKKVKLDKQCVISWLDNSNTLADKEEFVHKREELERVCSPIISGLYQAGAGPGGFG 623

Qy 241 AQG-PKGGSGSGPTIEVD 258
Db 624 AQAPPKGASGSGPTIEVD 642

RESULT 38
ADJ27275
ID ADJ27275 standard; protein; 642 AA.
XX AC ADJ27275;
XX

20-MAY-2004 (first entry)
Mouse HSP70.1.
heat shock protein-70; HSP70; HSP70.1; HSP70.3; inducible; induction; heat; tumour necrosis factor; TNF; interferon-gamma; tumour.
Mus sp.
WO2003061684-A2.
31-JUL-2003.
24-JAN-2003; 2003WO-BP000786.
24-JAN-2002; 2002EP-00075297.
(VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
Libert C, Wielockx B, Van Molle W, Mahieu T;
WPI; 2003-608168/57.
N-PSDB; ADJ27274.

New pharmaceutical composition comprising HSP70 that is endogenously induced by heat and TNF, useful for the manufacture of a medicament for treating systemic tumor.

Disclosure; SEQ ID NO 2; 53pp; English.

This sequence represents mouse heat shock protein-70.1 (HSP70.1). HSP70.1 and HSP70.3 are inducible members of the HSP70 family of proteins. The heat shock proteins of the invention are endogenously induced by heat and tumour necrosis factor (TNF). This heat shock protein may be used in a composition which further comprises interferon-gamma, and/or a chemotherapeutic compound. The pharmaceutical composition is useful for the manufacture of a medicament for treating systemic tumour.

Query Match 93.5%; Score 1228.5; DB 7; Length 642;
Best Local Similarity 93.1%; Pred. No. 1.2e-93;
Matches 241; Conservative 11; Mismatches 6; Indels 1; Gaps 1;

Qy 1 KSENVQDLLLLDVAPLSIGLETAGGVMTALIKRNSITPTKQTQIFTTYSNQPGLIQVY 60
Db 384 KSENVQDLLLLDVAPLSIGLETAGGVMTALIKRNSITPTKQTQIFTTYSNQPGLIQVY 443

Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTRDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 503

Qy 121 TNDKGRLSKEEIERMVOEAEKYKAEDVORERSAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 504 TNDKGRLSKEEIERMVOEAEKYKAEDVORERSAKNALESYAFNMKSAVEDEGLKGKIS 563

Qy 181 EADKKVKLDKQCVISWLDANTLAERKDEFEHKKRKELEQVNCNPIISGLYQAGAGPGGFG 240
Db 564 EADKKVKLDKQCVISWLDNSNTLADKEEFVHKREELERVCSPIISGLYQAGAGPGGFG 623

Qy 241 AQG-PKGGSGSGPTIEVD 258
Db 624 AQAPPKGASGSGPTIEVD 642

RESULT 39
AAB23252
ID AAB23252 standard; protein; 624 AA.
XX AC AAB23252;
XX DT 29-JAN-2001 (first entry)
XX

DE Human Hsp72 (heat shock protein 72).

XX Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor;

XX expression modulator; JNK phosphatase inhibitor; antiproliferative;

KW drug screening; cancer; leukemia; lymphoma; solid tumour; sarcoma;

KW carcinoma; breast cancer; prostate cancer; premalignant condition.

XX Homo sapiens.

XX WO200054814-A1.

XX 21-SEP-2000.

XX 17-MAR-2000; 2000WO-US007350.

XX 18-MAR-1999; 99US-0125046P.

XX (PHYL-) PHYLOGENY INC.

XX Volloch VZ, Sherman M;

XX WPI: 2000-647056/62.

XX N-PSDB; AAA97541.

XX Identifying compounds that inhibit proliferation of cells and capable of

PT modulating the expression of heat shock protein 72 gene and/or activity

PT of Hsp72 useful for treating cancers such as leukemia, lymphoma.

XX Example; Fig 16B; 77pp; English.

XX The invention relates to a novel method of identifying compounds that

CC inhibit proliferation of cells comprising contacting a test compound with

CC a cell which overexpresses Hsp72 (heat shock protein 72), and determining

CC if the test compound inhibits activity or expression of Hsp72.

CC Optionally, Hsp72 is contacted with the test compound under optimum

CC conditions to allow the two components to interact and bind, forming a

CC complex which is detected. The invention also relates to a method of

CC identifying compounds that inhibit Hsp72-mediated JNK phosphatase

CC activation, comprising contacting a test compound with a cell which

CC expresses Hsp72, exposing the cell to a heat induced stress and

CC determining if the compound inhibits JNK phosphatase activity. The

CC invention additionally encompasses compositions comprising an inhibitor

CC of Hsp72 or JNK phosphatase activity. The compounds identified as

CC inhibitors of Hsp72 or JNK phosphatase activity are useful for inhibiting

CC the proliferation of cells. Modulation of the activity of the JNK

CC phosphatase or Hsp72 is used to treat a proliferative disorder such as

CC cancers (e.g., leukaemia, lymphoma, solid tumours such as sarcomas and

CC carcinomas, breast cancer, prostate cancer). The compounds that inhibit

CC Hsp72 activity can also be administered to treat premalignant conditions

CC and to prevent progression to a neoplastic or malignant state. The

CC compounds that inhibit Hsp72 function are administered to a patient

CC having a disease or disorder mediated by an increase of Hsp72 expression

CC or activity relative to normal levels. The present sequence represents

CC human Hsp72 used in the exemplifications of the invention

XX

SQ Sequence 624 AA;

Query Match 93.1%; Score 1223; DB 3; Length 624;

Best Local Similarity 100.0%; Pred. No. 3.3e-93;

Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSENVQDLLLDVAPLSGLTAGGVMTALIKENSTIPTKQTQIFTTSDNQGVLIQVY 60

DB 384 KSENVQDLLLDVAPLSGLTAGGVMTALIKENSTIPTKQTQIFTTSDNQGVLIQVY 443

QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120

DB 444 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503

QY 121 TNDKGRLSKEEIERMWQEAKEYKAEDVQERVSAKNALESYAFNMKSAVEDSGLGKIS 180

DB 504 TNDKGRLSKEEIERMWQEAKEYKAEDVQERVSAKNALESYAFNMKSAVEDSGLGKIS 563

QY 181 EADKKVKLDKQCVISWLDANTLAEKDFEHHKKELEQVCNPIISGLYQAGGPGGFG 240

DB 564 EADKKVKLDKQCVISWLDANTLAEKDFEHHKKELEQVCNPIISGLYQAGGPGGFG 623

QY 241 A 241

DB 624 A 624

RESULT 40

AA88413

ID AAY88413 standard; protein; 554 AA.

XX AAY88413;

XX 31-JUL-2000 (first entry)

XX Human heat shock protein SHSP70 amino acid sequence.

XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;

KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;

KW depression; nephrotic syndrome; SHSP70.

XX Homo sapiens.

OS JP2000069999-A.

PN 07-MAR-2000.

PD 01-JUN-1995; 99JP-00257146.

PF 01-JUN-1995; 95JP-00158581.

PR (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX WPI: 2000-264458/23.

XX Abnormal transcription of intracellular HSP70mRNA under acute and chronic

PT continuous load of stress in a human being and its application.

XX Disclosure; Fig 6; 11pp; Japanese.

XX This sequence represents the human heat shock protein SHSP70 amino acid

CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22

CC and 14q22-24. The invention relates to the abnormal transcription of

CC intracellular HSP70mRNA under acute and chronic stress load in a human.

CC The abnormal transcription of HSP70 can be used in the improvement of

CC stress and response and diagnosis of stress diseases including

CC rheumatism, schizophrenia, depression and nephrotic syndrome

XX Sequence 554 AA;

Query Match 92.7%; Score 1217.5; DB 3; Length 554;

Best Local Similarity 95.3%; Pred. No. 8.2e-93;

Matches 246; Conservative 3; Mismatches 8; Indels 1; Gaps 1;

QY 1 KSENVQDLLLDVAPLSGLTAGGVMTALIKENSTIPTKQTQIFTTSDNQGVLIQVY 60

DB 298 KSENVQDLLLDVAPLSGLTAGGVMTALIKENSTIPTKQTQIFTTSDNQGVLIQVY 357

QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120

DB 358 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 416

QY 121 TNDKGRLSKEEIERMWQEAKEYKAEDVQERVSAKNALESYAFNMKSAVEDSGLGKIS 180

DB 417 TNDKGRLSKEEIERMWQEAKEYKAEDVQERVSAKNALESYAFNMKSAVEDSGLGKIS 476

QY 181 EADKKVKLDKQCVISWLDANTLAEKDFEHHKKELEQVCNPIISGLYQAGGPGGFG 240

DB 477 EADKKVKLDKQCVISWLDANTLAEKDFEHHKKELEQVCNPIISGLYQAGGPGGFG 536

QY 241 AQGPKGGSGSGPTIEVD 258

Db 537 AQPCKGGSGGPTIEYD 554
|||||
RESULT 41
AA98412
ID AAY8412 standard; protein; 554 AA.
XX AC AAY8412;
XX 31-JUL-2000 (first entry)
XX Human heat shock protein SHSP70 amino acid sequence.
DE Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;
KW depression; nephrotic syndrome; SHSP70.
XX Homo sapiens.
OS JP2000069999-A.
PN 07-MAR-2000.
PD 01-JUN-1995; 99JP-00257146.
PF 01-JUN-1995; 95JP-00158581.
PR (HOK-) HOKEN KAGAKU KENKUSHO KK.
PA WPI; 2000-264458/23.
XX Abnormal transcription of intracellular HSP70mRNA under acute and chronic
XX continuous load of stress in a human being and its application.
XX Disclosure; Fig 5; 11pp; Japanese.
PS This sequence represents the human heat shock protein SHSP70 amino acid
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
CC and 14q22-24. The invention relates to the abnormal transcription of
CC intracellular HSP70mRNA under acute and chronic stress load in a human.
CC The abnormal transcription of HSP70 can be used in the improvement of
CC stress and response and diagnosis of stress diseases including
CC rheumatism, schizophrenia, depression and nephrotic syndrome
XX Sequence 554 AA;
SQ Query Match 91.1%; Score 1196.5; DB 3; Length 554;
Best Local Similarity 94.6%; Pred. No. 4.6e-91;
Matches 244; Conservative 3; Mismatches 10; Indels 1; Gaps 1;
QY 1 KSENVODLLDVLAPLSGLTAGGVTALIKENSTIPTKQTQIIFTYSDNQGVLIQVY 60
Db 298 KSENVODLLDVLAPLSGLTAGGVTALIKENSTIPTKQTQIIFTYSDNQGVLIQVY 357
QY 61 EGERAMTKNNLLGRFELSGLTAPRGVQIETVFDIDANGILNVTATDKSTGKANKITI 120
Db 358 EGERAMTKNNLLGRFELSGLTAPRGVQIETVFDIDANGILNVTATDKSTGKANKITI 416
QY 121 TNDKGRLSKEIEIRMQEAKYAEDEVQERVSNAKNALESYAFNMKSAVEDSGLGKGIS 180
Db 417 TNDKGRLSKEIEIRMQEAKYAEDEVQERVSNAKNALESYAFNMKSAVEDSGLGKGIS 476
QY 181 EADKKVLDKQCVISWLDANTLAEKDFEKKKELEBOVCNPIISGLYQAGGPGGFG 240
Db 477 EADKKVLDKQCVISWLDANTLAEKDFEKKKELEBOVCNPIISGLYQAGGPGGFG 536
QY 241 AQPCKGGSGGPTIEYD 258
Db 537 AQPCKGGSGGPTIEYD 554
RESULT 42

ADJ69869
ID ADJ69869 standard; protein; 641 AA.
XX AC ADJ69869;
XX 06-MAY-2004 (first entry)
XX Human heat mitochondrial protein as a therapeutic target SeqID1675.
DE mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX Homo sapiens.
OS WO2003087768-A2.
PN 23-OCT-2003.
PD 04-APR-2003; 2003WO-US010870.
PF 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX WPI; 2003-845369/78.
XX Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX Claim 1; SEQ ID NO 1675; 180pp; English.
PS This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, neurotropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX Sequence 641 AA;
SQ Query Match 83.9%; Score 1103; DB 7; Length 641;
Best Local Similarity 82.3%; Pred. No. 3.5e-83;
Matches 218; Conservative 16; Mismatches 15; Indels 16; Gaps 2;
QY 1 KSENVODLLDVLAPLSGLTAGGVTALIKENSTIPTKQTQIIFTYSDNQGVLIQVY 60
Db 386 KSENVODLLDVLAPLSGLTAGGVTALIKENSTIPTKQTQIIFTYSDNQGVLIQVY 445
QY 61 EGERAMTKNNLLGRFELSGLTAPRGVQIETVFDIDANGILNVTATDKSTGKANKITI 120
Db 446 EGERAMTKNNLLGRFELSGLTAPRGVQIETVFDIDANGILNVTATDKSTGKANKITI 505

QY 121 TNDKRLSKKEIERMVOEAKYKAEDVQERVSANNALESYAFNMKSAVEDGLGKIS 180
 DB 506 TNDKRLSKKEIERMVOEAKYKAEDVQERVSANNALESYAFNMKSAVEDGLGKIS 565
 QY 181 EADKKVLDKCOEIVSWLDANTLAEDKDEFEHKEKELEQVNCNPIISGLYQAGGPGGFC 240
 DB 566 ESKDKILDKCNELLSWLEVNQLAEDKDEFEHKEKELEQVNCNPIITKLYQG-----G 616
 QY 241 AQQPKGGSG-----SGPTIEVD 258
 DB 617 CTGPACGTGVVGRPATGPTIEVD 641

RESULT 43
 AAY17408
 ID AAY17408 standard; protein; 646 AA.
 AC AAY17408;
 DT 26-JUL-1999 (first entry)
 DE Mouse heat shock cognate 73.
 XX
 KW Heat shock cognate 73; HSC73; cancer gene; diagnosis; neoplasia;
 KW detection; carcinoma; breast; tumour.
 XX
 OS Mus musculus.
 XX
 PN WO9923252-A1.
 XX
 PD 14-MAY-1999.
 XX
 PF 05-NOV-1998; 98WO-GB003375.
 XX
 PR 05-NOV-1997; 97GB-00023412.
 PR 19-AUG-1998; 98GB-00018118.
 XX
 PA (ISIS-) ISIS INNOVATION LTD.
 XX
 PI Bakkenist CJ, Koreth J, Mcgee JO;
 XX
 DR WI; 1999-337489/28.
 DR N-PSDB; AAX56458.
 XX
 PT Method for diagnosis of cancer by detecting aberrant expression of gene.
 XX
 PS Disclosure; Fig 6; 49pp; English.
 XX

CC A method of diagnosis performed on a biological sample has been developed
 CC comprising detecting the aberrant expression of a gene at the heat shock
 CC cognate 73 (HSC73) locus, or detecting a mutation at the HSC73 locus. The
 CC method is used for diagnosing neoplasia or a susceptibility to neoplasia
 CC especially malignant neoplasia, and carcinomas of the breast. Gene or
 CC protein therapy of mutated HSC73 is performed by administration of native
 CC HSC73, and the transgenic mammal is useful as an experimental model for
 CC technical development of gene therapy. The HSC73 gene was transfected
 CC into cell lines, which were introduced into test animals. These animals
 CC were injected with untransfected cells of a breast cancer line.
 CC Expression of wild type HSC73 prevented breast cancer cells forming
 CC tumours in the mice. The present sequence represents mouse HSC73 from the
 CC present invention
 XX
 SQ Sequence 646 AA;

Query Match 83.8%; Score 1100.5; DB 2; Length 646;
 Best Local Similarity 81.7%; Pred. No. 5.8e-83;
 Matches 215; Conservative 23; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVODLLLDVAPLSGLHETAGGVMTALIKENSTIPTKQTQFTTYSNQPGLIQVY 60
 DB 384 KSENVODLLLDVTPUSLGIETAGGVMTLVKRNNTTPTKQTQFTTYSNQPGLIQVY 443

QY 61 EGERAMTKNNLLGRFELSGIPPAKGVQIEVTFDIDANGILNVTTATDKSTGKANKITI 120
 DB 444 EGERAMTKNNLLGKFEFGTIPPAKGVQIEVTFDIDANGILNVSAVDKSTGKANKITI 503
 QY 121 TNDKRLSKKEIERMVOEAKYKAEDVQERVSANNALESYAFNMKSAVEDGLGKIS 180
 DB 504 TNDKRLSKKEIERMVOEAKYKAEDKQDKVSSKNSLESYAFNMKATVEDKLOKIN 563
 QY 181 EADKKVLDKCOEIVSWLDANTLAEDKDEFEHKEKELEQVNCNPIISGLYQAGG-PG--PG 237
 DB 564 DEBKQKILDKCNEIISWLDKNOTAEKEFEHQKLEKVCNPIITKLYQSAGGMPGMPG 623
 QY 238 GP--GAQPKGGSGSGPTIEVD 258
 DB 624 GPPGGGAPPSPGSGSGPTIEVD 646

RESULT 44
 AAB23649
 ID AAB23649 standard; protein; 646 AA.
 AC AAB23649;
 DT 05-JAN-2001 (first entry)
 DE Mouse heat shock protein Hsc70 protein sequence SEQ ID NO:1.
 XX
 KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;
 KW immune response; infectious disease; malaria; cytotoxic T cell;
 KW cytostatic; immunostimulant; cellular immune response inducer;
 KW protozoacide; leukaemia; cancer.
 XX
 OS Mus sp.
 XX
 PN WO200049041-A1.
 XX
 PD 24-AUG-2000.
 XX
 PF 18-FEB-2000; 2000WO-JP000941.
 XX
 PR 19-FEB-1999; 99JP-00041535.
 XX
 PA (SUME) SUMITOMO ELECTRIC IND CO.
 XX
 PI Shinbara N, Udono H, Yui K;
 DR WPI; 2000-543748/49.
 XX

PT Fused protein capable of inducing cellular immune response, useful as
 PT active ingredient for drug compositions in preventing and/or treating
 PT infectious diseases such as malaria or cancer.
 XX
 PS Claim 3; Page 36-39; 72pp; Japanese.

CC The present invention describes a fused protein (I) prepared from a
 CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by
 CC cytotoxic T cells and a protein containing the ATPase domain of a heat
 CC shock protein. Also described are: (1) a drug composition containing (I)
 CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector
 CC containing the DNA of (2); and (4) a transformant which can retain the
 CC expression vector of (3). (I) has cytostatic, immunostimulant and
 CC protozoacide activities, and can be used as a cellular immune response
 CC inducer. The protein is useful as an active ingredient for drug
 CC compositions in preventing and/or treating infectious diseases such as
 CC malaria or cancer e.g. to provide systemic immunity against leukaemia.
 CC The present sequence represents a specifically claimed heat shock protein
 CC for use in a fused protein of the present invention
 XX
 SQ Sequence 646 AA;

Query Match 83.8%; Score 1100.5; DB 3; Length 646;
 Best Local Similarity 81.7%; Pred. No. 5.8e-83;
 Matches 215; Conservative 23; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVQDLLLLLDVAPLSGLTETAGGVTALIKRNSIPTKQTOIFTTYSNQPGLVIOVY 60
 DB 384 KSENVQDLLLLLDVTPLSGLTETAGGVTALIKRNTTPTKQTOFTTYSNQPGLVIOVY 443
 QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 444 EGERAMTKDNLLGKFELSGIPAPRGVPOIEVTFDIDANGILNVSADVKSTGKANKITI 503
 QY 121 TNDKRLSKKEEIERMVQAEKYKAEDVQREVRSKNALESYAFNMKSAVEDGLKGKIS 180
 DB 504 TNDKRLSKKEEIERMVQAEKYKAEDQKQDVSKNSLESYAFNMKATVEDEKLQCKIN 563
 QY 181 EADKKVKLDKQCEVSWLDANTLAEKDFEHRKELEOVCPNIIISGLYQAGG-PG--PG 237
 DB 564 DEDQKILDKCNEIISWLDKXNTAEKEFEHQKELEKVCNPIITIKLYQAGGMPGMPG 623
 QY 238 GF--GAQGPKGSGSGPTIEVD 258
 DB 624 GPFGGGAPPSGSGSGPTIEVD 646

RESULT 45
 ADD18652
 ID ADD18652 standard; protein; 646 AA.
 AC ADD18652;
 AC ADD18652;
 DT 22-SEP-2003 (first entry)
 DE Rat heat shock cognate protein 70.
 DE spinal cord; neuropathic pain; central sensitisation pain; pain;
 KW analgesic; gene therapy.
 KW Rattus norvegicus.
 OS EPI284298-A2.
 PN 19-FEB-2003.
 PD 26-JUL-2002; 2002EP-0025229.
 PF 27-JUL-2001; 2001GB-00018354.
 PR 07-FEB-2002; 2002GB-00002883.
 PR (WARN) WARNER LAMBERT CO.
 FA Brooksbank RA, Dixon AK, Lee K, Pinnock RD;
 FI WPI; 2003-543489/52.
 DR N-PSDB; ACF25380.
 DR Use of an isolated gene sequence in the screening of compounds for
 PT diagnosing or treating pain.
 PT Claim 1; Page 170-172; 188pp; English.

The invention relates to a novel isolated gene sequence that is
 downregulated in the spinal cord of a mammal in response to mechanically
 distinct first and second models of neuropathic or central sensitisation
 pain, useful in the screening of compounds for diagnosing or treating
 pain. A protein encoded by a gene of the invention has analgesic
 activity. A polynucleotide of the invention may have a use in gene
 therapy. The gene sequence is useful for preparing a composition for
 diagnosing or treating pain. The present sequence represents a protein
 encoded by a gene of the invention

Query Match 83.8%; Score 1100.5; DB 6; Length 646;
 Best Local Similarity 81.7%; Pred. No. 5.8e-83;
 Matches 215; Conservative 23; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVQDLLLLLDVAPLSGLTETAGGVTALIKRNSIPTKQTOIFTTYSNQPGLVIOVY 60
 DB 384 KSENVQDLLLLLDVTPLSGLTETAGGVTALIKRNTTPTKQTOFTTYSNQPGLVIOVY 443
 QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 444 EGERAMTKDNLLGKFELSGIPAPRGVPOIEVTFDIDANGILNVSADVKSTGKANKITI 503
 QY 121 TNDKRLSKKEEIERMVQAEKYKAEDVQREVRSKNALESYAFNMKSAVEDGLKGKIS 180
 DB 504 TNDKRLSKKEEIERMVQAEKYKAEDQKQDVSKNSLESYAFNMKATVEDEKLQCKIN 563
 QY 181 EADKKVKLDKQCEVSWLDANTLAEKDFEHRKELEOVCPNIIISGLYQAGG-PG--PG 237
 DB 564 DEDQKILDKCNEIISWLDKXNTAEKEFEHQKELEKVCNPIITIKLYQAGGMPGMPG 623
 QY 238 GF--GAQGPKGSGSGPTIEVD 258
 DB 624 GPFGGGAPPSGSGSGPTIEVD 646

RESULT 46
 ADD18652
 ID ADD18652 standard; protein; 641 AA.
 AC ADD18652;
 AC ADD18652;
 DT 15-JAN-2004 (first entry)
 DE Human disease related protein SeqID83.
 DE human; disease state; cytostatic; antiinflammatory; ophthalmological;
 KW antiarteriosclerotic; vulnary; gene therapy;
 KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
 KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
 KW glucose transport; catecholamine synthesis; iron transport;
 KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
 KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
 KW inflammatory condition; wound healing.
 OS Homo sapiens.
 OS WO2003018621-A2.
 PN 06-MAR-2003.
 PD 23-AUG-2002; 2002WO-GB003892.
 PF 23-AUG-2001; 2001GB-00020558.
 PR 05-OCT-2001; 2001GB-00024037.
 PR (OXFO-) OXFORD BIOMEDICA UK LTD.
 PA Kingman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
 PI WPI; 2003-290046/28.
 DR N-PSDB; ADD18653.
 DR New substantially purified polypeptide, useful for diagnosing or treating
 PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
 PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
 PT wound healing.
 PS Claim 25; SEQ ID NO 83; 424pp; English.
 PS This invention relates to novel human genes and gene product which are
 CC implicated in certain disease states. Compounds which modulate the
 CC proteins of the invention may have cytostatic, antiinflammatory, or
 CC ophthalmological, antiarteriosclerotic or vulnary activities. The
 CC sequences of the invention may be useful for gene therapy. The invention
 CC may be useful for diagnosing or treating a hypoxia-regulated condition,
 CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,

CC erythropoiesis, or the biological response to hypoxia conditions
 CC including processes such as glycolysis, gluconeogenesis, glucose
 CC transportation, catecholamine synthesis, iron transport or nitric oxide
 CC synthesis. The disease includes cancer, ischemic conditions, reperfusion
 CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
 CC inflammatory conditions or wound healing. The present sequence is that of
 CC a disease related protein of the invention.
 XX
 SQ Sequence 641 AA;
 Query Match 83.6%; Score 1099; DB 7; Length 641;
 Best Local Similarity 81.9%; Pred. No. 7.6e-83;
 Matches 217; Conservative 16; Mismatches 16; Indels 16; Gaps 2;
 QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQIFTTYSNQPGLVLIQVY 60
 DB 386 KSEKVDLLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQIFTTYSNQPGLVLIQVY 445
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTTATDKSTGKANKITI 120
 DB 446 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTTATDKSTGKANKITI 505
 QY 121 TNDKGLSKSEIEIRVMQEAKEYKAEDVQERVSAAKNALESYAFNMKSAVEDGLGKGIS 180
 DB 506 TNDKGLSKSEIEIRVMQEAKEYKAEDVQERVSAAKNALESYAFNMKSAVEDGLGKGIS 565
 QY 181 EADKKVKLDKCOEIVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGGFG 240
 DB 566 ESDNKILDKCNELLSWLVNQLAEDFEHKKRKELEQVNCNPIITKLYQG-----G 616
 QY 241 AQSPKGGSG-----SGPTIEEVD 258
 DB 617 CTGPACGTGYVPGRPATGPTIEEVD 641
 RESULT 47
 ADA50750
 ID ADA50750 standard; protein; 586 AA.
 XX
 AC ADA50750;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human heat shock cognate protein-71 (FOXc2-interacting) protein (HSC71).
 XX
 KW protein kinase stimulator; protein kinase inhibitor; human; FOXc2;
 KW FOXc2-interacting protein; FOXc2 protein complex; obesity;
 KW hypertriglyceridemia; diet-induced insulin resistance; type 2 diabetes;
 KW anorexia; HSC71; heat shock cognate protein-71.
 XX
 OS Homo sapiens.
 XX
 PN WO2003064467-A1.
 XX
 PD 07-AUG-2003.
 XX
 PF 28-JAN-2003; 2003WO-SR000139.
 XX
 PR 29-JAN-2002; 2002SE-00000265.
 PR 30-APR-2002; 2002US-0377349P.
 XX
 PA (BIOV-) BIOVITRUM AB.
 XX
 PI Climent-Johansson I, Enerbaeck S;
 XX
 DR WPI; 2003-663466/62.
 XX
 PT New substantially pure FOXc2 protein complex, useful for treating or
 PT preventing a medical condition treatable by modulated FOXc2 activity,
 PT e.g. obesity, hypertriglyceridemia, diet-induced insulin resistance or
 PT anorexia.
 XX
 PS Claim 1; Page 27-29; 46pp; English.

XX
 CC The invention comprises a protein complex of human FOXc2 protein and a
 CC FOXc2-interacting protein. The FOXc2 protein complex is useful for
 CC treating or preventing a medical condition treatable by modulated FOXc2
 CC activity, such as: obesity, hypertriglyceridemia, diet-induced insulin
 CC resistance, type 2 diabetes, and anorexia. The present amino acid
 CC sequence represents a human FOXc2-interacting protein of the invention.
 XX
 SQ Sequence 586 AA;
 Query Match 83.5%; Score 1097.5; DB 6; Length 586;
 Best Local Similarity 81.4%; Pred. No. 9.1e-83;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQIFTTYSNQPGLVLIQVY 60
 DB 324 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQIFTTYSNQPGLVLIQVY 383
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTTATDKSTGKANKITI 120
 DB 384 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTTATDKSTGKANKITI 443
 QY 121 TNDKGLSKSEIEIRVMQEAKEYKAEDVQERVSAAKNALESYAFNMKSAVEDGLGKGIS 180
 DB 444 TNDKGLSKSEIEIRVMQEAKEYKAEDVQERVSAAKNALESYAFNMKSAVEDGLGKGIS 503
 QY 181 EADKKVKLDKCOEIVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGG-PG--PG 237
 DB 504 DEDKQKILDKCNELINWLDKNQTAKEEFHQKKELEKVCNPIITKLYQSAGGMPGMPG 563
 QY 238 GF--GAQSPKGGSGSGPTIEEVD 258
 DB 564 GPPGGAGPPSGGASGPTIEEVD 586
 RESULT 48
 ADJ69947
 ID ADJ69947 standard; protein; 586 AA.
 XX
 AC ADJ69947;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human heat mitochondrial protein as a therapeutic target SeqID1753.
 XX
 KW mitochondrial; human; screening assay; diabetes mellitus;
 KW Huntington's disease; osteoarthritis;
 KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO2003087768-A2.
 XX
 PD 23-OCT-2003.
 XX
 PF 04-APR-2003; 2003WO-US010870.
 XX
 PR 12-APR-2002; 2002US-0372843P.
 PR 17-JUN-2002; 2002US-0389987P.
 PR 20-SEP-2002; 2002US-0412418P.
 XX
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 XX
 PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 PI Warnock DE;
 XX
 DR WPI; 2003-845369/78.
 XX

PT Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function.
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.

XX Claim 1; SEQ ID NO 1753; 180pp; English.

XX This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, neurotropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytoskeletal activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.

XX Sequence 586 AA;

Query Match 83.5%; Score 1097.5; DB 7; Length 586;
Best Local Similarity 81.4%; Pred. No. 9.1e-83;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVMTALIKRNTIPTKTQITFTTYSNQPGLVLIQY 60
DB 324 KSENVQDLLLLDVTPLSGLGLETAGGVMTVLIKRNTIPTKTQITFTTYSNQPGLVLIQY 383
QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 384 EGERAMTKDNLLGKFLTGIPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 443
QY 121 TNDKGRLSKEEIERMVQAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 180
DB 444 TNDKGRLSKEDIERMVQAEKYKAEDKQDKVSSKNLSLEYAFNMKATVEDEKLQKIN 503
QY 181 EADKKVLDKQEVISWLDANTLAEKDPEHKKRKELEQVNCNPIISGLYQAGG-PG--PG 237
DB 504 DEDKQILDKCNEIINWLDKNQTAKEEFHQKELEKVCNPIITKLYQAGGMPGMPG 563
QY 238 GF--GAQGPKGSGSGPTIEVD 258
DB 564 GPPGGAPPSSGGSGSGPTIEVD 586

RESULT 49
AAW54364
ID AAW54364 standard; protein; 646 AA.

XX AAW54364;
AC AAW54364;
DT 14-AUG-1998 (first entry)
DE Heat shock cognate 71 kD protein.
XX Endometrium; hyperplasia; adenocarcinoma; proliferative phase;
XX 2D gel electrophoresis; detection.
XX Homo sapiens.
XX WO9810291-A1.
XX 12-MAR-1998.
XX 05-SEP-1997; 97WO-GB002394.
XX 06-SEP-1996; 96GB-00018600.
PR 08-APR-1997; 97GB-00007132.

XX (CLIN-) CENT CLINICAL & BASIC RES.
XX Byrjalsen I, Larsen P, Fey SJ;
XX WPI; 1998-207057/18.
XX Biochemical markers of human endometrium - useful for, e.g. diagnosis of
PT hyperplasia and adenocarcinoma.
XX Disclosure; Page 23; 77pp; English.
XX Proteins AAW54349-W54364 are examples of proteins produced in the
CC endometrium during the hyperplasia, adenocarcinoma or proliferative phase
CC of the endometrium. The presence and quantities of these proteins can be
CC detected using 2D gel electrophoresis comparison of cell lysates. The
CC proteins can be used as biochemical markers to detect the phase of the
CC endometrium and can be measured in body fluids, obviating the need for
CC endometrial biopsies
XX Sequence 646 AA;

Query Match 83.5%; Score 1097.5; DB 2; Length 646;
Best Local Similarity 81.4%; Pred. No. 1e-82;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVMTALIKRNTIPTKTQITFTTYSNQPGLVLIQY 60
DB 384 KSENVQDLLLLDVTPLSGLGLETAGGVMTVLIKRNTIPTKTQITFTTYSNQPGLVLIQY 443
QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 444 EGERAMTKDNLLGKFLTGIPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVQAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 180
DB 504 TNDKGRLSKEDIERMVQAEKYKAEDKQDKVSSKNLSLEYAFNMKATVEDEKLQKIN 563
QY 181 EADKKVLDKQEVISWLDANTLAEKDPEHKKRKELEQVNCNPIISGLYQAGG-PG--PG 237
DB 564 DEDKQILDKCNEIINWLDKNQTAKEEFHQKELEKVCNPIITKLYQAGGMPGMPG 623
QY 238 GF--GAQGPKGSGSGPTIEVD 258
DB 624 GPPGGAPPSSGGSGSGPTIEVD 646

RESULT 50
AAV17407
ID AAV17407 standard; protein; 646 AA.

XX AAV17407;
AC AAV17407;
DT 26-JUL-1999 (first entry)
DE Human heat shock cognate 73.
XX Heat shock cognate 73; HSC73; cancer gene; diagnosis; neoplasia;
XX detection; carcinoma; breast; tumour.
XX Homo sapiens.
XX WO9923252-A1.
XX 14-MAY-1999.
XX 05-NOV-1998; 98WO-GB003375.
XX 05-NOV-1997; 97GB-00023412.
PR 19-AUG-1998; 98GB-00018118.
XX (ISIS-) ISIS INNOVATION LTD.

PI Bakkenist CJ, Koreth J, Mcgee JO;
 XX WPI; 1999-337489/28.
 XX DR N-PSDB; AAX56457.
 XX Method for diagnosis of cancer by detecting aberrant expression of gene.
 XX PT Disclosure; Fig 5; 49pp; English.
 XX PS
 CC A method of diagnosis performed on a biological sample has been developed
 CC comprising detecting the aberrant expression of a gene at the heat shock
 CC cognate 73 (HSC73) locus, or detecting a mutation at the HSC73 locus. The
 CC method is used for diagnosing neoplasia or a susceptibility to neoplasia
 CC especially malignant neoplasia, and carcinomas of the breast. Gene or
 CC protein therapy of mutated HSC73 is performed by administration of native
 CC HSC73, and the transgenic mammal is useful as an experimental model for
 CC technical development of gene therapy. The HSC73 gene was transfected
 CC into cell lines, which were introduced into test animals. These animals
 CC were injected with untransfected cells of a breast cancer line.
 CC Expression of wild type HSC73 prevented breast cancer cells forming
 CC tumours in the mice. The present sequence represents human HSC73 from the
 CC present invention
 XX SQ
 SQ Sequence 646 AA;
 Query Match 83.5%; Score 1097.5; DB 2; Length 646;
 Best Local Similarity 81.4%; Pred. No. 1e-82;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVODLLDVLAPLSGLTAGGVTALIKENSTPTKQTQFTTYSNQGVLIOVY 60
 DB 384 KSENVODLLDVLAPLSGLTAGGVTALIKENSTPTKQTQFTTYSNQGVLIOVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 444 EGERAMTKNNLLGKELTGIPIAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503
 QY 121 TNDKGRLSKEIERMVOEAEKYKAEDVQERVSAKNVALESYAFNMKSAVEDGLKGKIS 180
 DB 504 TNDKGRLSKEDIERMVOEAEKYKAEDKQKRDVSKNSLESYAFNMKATVEDEKLQCKIN 563
 QY 181 EADKKVLDKCOEIVSWLDANTLAEKDFEHEKKELEOVNPIISGLYQAGG-PG--PG 237
 DB 564 DEDKQKILDKCNEIINWLDKNOTAEKEEFHQOKELEKVCNPIITTKLYSAGGMPGMPG 623
 QY 238 GF--GAQGPKGSGSGPTIEVD 258
 DB 624 GPPGGAPPSSGASSGPTIEVD 646
 RESULT 51
 AAB23651
 ID AAB23651 standard; protein; 646 AA.
 XX AAB23651;
 AC AAB23651;
 XX 05-JAN-2001 (first entry)
 XX Human heat shock protein Hsc70 protein sequence SEQ ID NO:3.
 XX ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;
 KW immune response; infectious disease; malaria; cytotoxic T cell;
 KW cytosolic; immunostimulant; cellular immune response inducer;
 KW protozoicide; leukaemia; cancer.
 XX Homo sapiens.
 OS
 PN WO200049041-A1.
 XX 24-AUG-2000.
 PD
 XX 18-FEB-2000; 2000WO-JP000941.
 PF
 XX

PR 19-FEB-1999; 99JP-00041535.
 XX (SUME) SUMITOMO ELECTRIC IND CO.
 PA Shinbara N, Udono H, Yui K;
 XX WPI; 2000-543748/49.
 DR
 XX Fused protein capable of inducing cellular immune response, useful as
 PT active ingredient for drug compositions in preventing and/or treating
 PT infectious diseases such as malaria or cancer.
 XX
 PS Claim 3; Page 42-45; 72pp; Japanese.
 XX
 CC The present invention describes a fused protein (I) prepared from a
 CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by
 CC cytotoxic T cells and a protein containing the ATPase domain of a heat
 CC shock protein. Also described are: (1) a drug composition containing (I)
 CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector
 CC containing the DNA of (2); and (4) a transformant which can retain the
 CC expression vector of (3). (I) has cytostatic, immunostimulant and
 CC protozoicide activities, and can be used as a cellular immune response
 CC inducer. The protein is useful as an active ingredient for drug
 CC compositions in preventing and/or treating infectious diseases such as
 CC malaria or cancer e.g. to provide systemic immunity against leukaemia.
 CC The present sequence represents a specifically claimed heat shock protein
 CC for use in a fused protein of the present invention
 XX SQ
 SQ Sequence 646 AA;
 Query Match 83.5%; Score 1097.5; DB 3; Length 646;
 Best Local Similarity 81.4%; Pred. No. 1e-82;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVODLLDVLAPLSGLTAGGVTALIKENSTPTKQTQFTTYSNQGVLIOVY 60
 DB 384 KSENVODLLDVLAPLSGLTAGGVTALIKENSTPTKQTQFTTYSNQGVLIOVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 444 EGERAMTKNNLLGKELTGIPIAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503
 QY 121 TNDKGRLSKEIERMVOEAEKYKAEDVQERVSAKNVALESYAFNMKSAVEDGLKGKIS 180
 DB 504 TNDKGRLSKEDIERMVOEAEKYKAEDKQKRDVSKNSLESYAFNMKATVEDEKLQCKIN 563
 QY 181 EADKKVLDKCOEIVSWLDANTLAEKDFEHEKKELEOVNPIISGLYQAGG-PG--PG 237
 DB 564 DEDKQKILDKCNEIINWLDKNOTAEKEEFHQOKELEKVCNPIITTKLYSAGGMPGMPG 623
 QY 238 GF--GAQGPKGSGSGPTIEVD 258
 DB 624 GPPGGAPPSSGASSGPTIEVD 646
 RESULT 52
 AAB82535
 ID AAB82535 standard; protein; 646 AA.
 XX AAB82535;
 AC AAB82535;
 XX 17-SEP-2001 (first entry)
 XX Human heat shock protein Hsc70.
 XX Hsc70; human; heat shock protein; immunotherapy; therapy; cancer;
 KW infection; vaccine.
 XX Homo sapiens.
 OS
 PH Key Location/Qualifiers
 Binding-site 391..615
 FT /note= "peptide-binding domain"

QY 61 EGERAMTKONNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
 DB 444 EGERAMTKONNLLGKFKELTGIPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503
 QY 121 TNDKGRLSKEEIERMWQAEKYKAEDVQVORERYSAKNALESYAFNMKSAYEDSLGKGIS 180
 DB 504 TNDKGRLSKEDIERMWQAEKYKAEDKQDKVSSKNSLESYAFNMKATVEDEKLQSKIN 563
 QY 181 EADKKVLDKQEVISWLDANTLAEDFEHFKRKELEBOVCNPIISGLYQAGG-PG--PG 237
 DB 564 DEDKQKILDKCNEIINWLDKNQTAKEEFHQQKELEKVCNPIITKLYQAGGMPGMPG 623
 QY 238 GF--GAQPGKGGSGGPTIEVD 258
 DB 624 GPPGGGAPPSSGSGGPTIEVD 646

RESULT 54
 AAU75102 ID AAU75102 standard; protein; 646 AA.
 AC AAU75102;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Heat shock protein 8 (Hsp8).
 XX
 KW MAPKAP-K3; AP-3 delta; APP-695; amyloid A4; Hsp8; heat shock protein 8;
 KW L130; NY-REN-58; P38 Beta; ERK3; KIAA0934; CDK9;
 KW cell cycle dependent kinase 9; CLK; C-NAP-1; clathrin heavy chain;
 KW amphiphysin; PN9109; KIAA1106; neurodegenerative disorder;
 KW non-insulin dependent diabetes mellitus; NIDDM; Alzheimer's disease;
 KW inflammatory disease; rheumatoid arthritis; inflammatory bowel disorder;
 KW atherosclerosis; cardiac hypertrophy; hypoxic brain injury;
 KW yeast two-hybrid; signal transduction pathway; human;
 KW mitogen activated protein kinase.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 260..533
 FT /note="This region binds the mitogen activated protein
 FT kinase (MAPK) AP-K3 (see ABK13301), the bait protein in a
 FT yeast two-hybrid assay, producing a complex claimed in
 FT claim 1"
 FT
 XX
 PN WO200198524-A2.
 XX
 PD 27-DEC-2001.
 XX
 XX 21-JUN-2001; 2001WO-US019762.
 XX
 XX 22-JUN-2000; 2000US-0213245P.
 XX
 XX (MYRI-) MYRIAD GENETICS INC.
 XX
 XX Heichman K, Bartel PL;
 XX
 XX WPI; 2002-122287/16.
 XX
 FT New protein complexes comprising protein-protein interactions (e.g.
 FT MAPKAP-K3/AP-3 delta or C-NAP-1/clathrin HC), useful for diagnosing
 FT physiological generative disorders or screening drugs for these diseases.
 XX
 PS Example 4; Page; 60pp; English.
 XX
 CC The invention describes an isolated protein complex, comprising two
 CC proteins. The protein complex comprises: protein kinase MAPKAP-K3 and AP-
 CC 3 adaptor complex delta sub-unit; MAPKAP-K3 and amyloid A4 precursor
 CC protein, APP-695; MAPKAP-K3 and heat shock protein (Hsp) 8; leucine rich
 CC L130 and NY-REN-58; P38 Alpha and P38 Beta; protein kinase ERK3 and
 CC KIAA0934 (unknown function); ERK3 and cell cycle dependent kinase (CDK) 9
 CC ; ERK3 and protein kinase CLK; C-NAP-1 and Clathrin heavy chain; C-NAP-1

CC and Amphiphysin; C-NAP-1 and novel protein PN9109 or C-NAP-1 and KIAA1106
 CC (unknown function) interactions. The protein complexes are useful for
 CC diagnosing physiological generative disorders, drug screening for agents
 CC that modulate the interaction of the proteins (thus identify drug
 CC targets), and identifying additional proteins in the pathway common to
 CC the proteins. These physiological disorders include non-insulin dependent
 CC diabetes mellitus (NIDDM), neurodegenerative disorders (e.g. Alzheimer's
 CC disease), inflammatory diseases (e.g. rheumatoid arthritis and
 CC atherosclerosis, cardiac hypertrophy and hypoxic brain injury. This
 CC sequence represents heat shock protein 8 (Hsp8) residues 260-533 of which
 CC binds to the bait protein MAPKAP-K3 (see ABK13301 for nucleotide
 CC sequence) in a yeast two-hybrid assay for determining components of
 CC signal transduction pathways and forms an interaction claimed in claim 1
 CC of the invention. Note: This sequence does not appear in the
 CC specification but has been obtained from a reference given in the
 XX invention
 XX
 SQ Sequence 646 AA;
 Query Match 83.5%; Score 1097.5; DB 5; Length 646;
 Best Local Similarity 81.4%; Pred. No. 1e-82;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVQDLLLLDVAPLSGLGTFAGGVTALIKKNSIPTKQTOIFTTYSNQPGVLIQVY 60
 DB 384 KSENVQDLLLLDVTPLSGLGTFAGGVTMLIKRNTTPTKQTFTTYSNQPGVLIQVY 443
 QY 61 EGERAMTKONNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
 DB 444 EGERAMTKONNLLGKFKELTGIPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503
 QY 121 TNDKGRLSKEEIERMWQAEKYKAEDVQVORERYSAKNALESYAFNMKSAYEDSLGKGIS 180
 DB 504 TNDKGRLSKEDIERMWQAEKYKAEDKQDKVSSKNSLESYAFNMKATVEDEKLQSKIN 563
 QY 181 EADKKVLDKQEVISWLDANTLAEDFEHFKRKELEBOVCNPIISGLYQAGG-PG--PG 237
 DB 564 DEDKQKILDKCNEIINWLDKNQTAKEEFHQQKELEKVCNPIITKLYQAGGMPGMPG 623
 QY 238 GF--GAQPGKGGSGGPTIEVD 258
 DB 624 GPPGGGAPPSSGSGGPTIEVD 646

RESULT 55
 ABU69612 ID ABU69612 standard; protein; 646 AA.
 XX
 AC ABU69612;
 XX
 DT 05-JUN-2003 (first entry)
 XX
 DE Human NF-kappaB associated polypeptide sequence #15.
 XX
 KW Human; nuclear factor-kappaB; NF-kappaB; immune disorder; cancer;
 KW inflammatory disorder; apoptosis; hepatic disorder; Hodgkin's lymphoma;
 KW haematopoietic tumour; hyper-IGM syndrome; viral infection; asthma;
 KW hypohidrotic ectodermal dysplasia; human immunodeficiency virus; HIV;
 KW X-linked anhidrotic ectodermal dysplasia; al incontinentia pigmenti;
 KW influenza; rheumatoid arthritis; inflammatory bowel disease; colitis;
 KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
 KW experimental allergic encephalomyelitis; autoimmune disorder; wound;
 KW hyper immune activity; acute phase response; hypercongenital condition;
 KW birth defect; necrotic lesion; organ transplant rejection; pancreas;
 KW signal transduction; hyperproliferative disorder; diabetes mellitus;
 KW vitamin B12 malabsorption; neurological disorder; Huntington's chorea;
 KW Turner's syndrome; bacterial infection; cardiovascular disorder;
 KW infertility; psoriasis; haemolytic anaemia; antiinflammatory; anti-HIV;
 KW cytostatic; hepatotropic; virucide; antirheumatic; antiarthritic;
 KW antiasthmatic; immunomodulator; antidiabetic; antiallergic;
 KW neuroprotective; immunosuppressive; vulnerary; antibacterial;
 KW antiinfertility; antianaemic; antipsoriatic; cerebroprotective; cardiant;

KW antiarteriosclerotic.

XX Homo sapiens.

XX WO200286076-A2.

XX 31-OCT-2002.

XX 19-APR-2002; 2002WO-US012636.

XX 19-APR-2001; 2001US-0284962P.

XX 26-APR-2001; 2001US-0286645P.

XX 09-JAN-2002; 2002US-0346986P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Carman J, Feder J, Nadler S;

XX WPI; 2003-093119/08.

XX N-PSDB; ACA54673.

XX Novel NF-kappaB-associated polypeptides and polynucleotides useful for

XX diagnosing, treating and preventing cancer, hepatic disorders, aberrant

XX apoptosis, viral infections, autoimmune disorders, asthma and stroke.

XX Claim 6; Fig 10F; 608pp; English.

XX The present invention relates to the isolation of human nuclear factor-

XX kappaB (NF-kappaB) associated polypeptides and polynucleotides. The NF-

XX kappaB associated polypeptide and polynucleotide sequences are useful for

XX preventing, treating or ameliorating various disorders including immune

XX disorders, inflammatory disorders, cancers, disorders relating to

XX aberrant apoptosis, hepatic disorders, Hodgkin's lymphomas,

XX haematopoietic tumours, hyper-IGM syndromes, hypohidrotic ectodermal

XX dysplasia, X-linked anhidrotic ectodermal dysplasia, immunodeficiency, al

XX inconitencia pigmenti, viral infections (e.g. those caused by human

XX immunodeficiency virus (HIV), human T-cell lymphotropic virus (HTLV),

XX hepatitis B, hepatitis C, Epstein Barr virus (EBV), influenza),

XX rheumatoid arthritis, inflammatory bowel disease, colitis, asthma,

XX atherosclerosis, cachexia, euthyroid sick syndrome, stroke, experimental

XX allergic encephalomyelitis (EAE), autoimmune disorders, disorders related

XX to hyper immune activity, disorders related to aberrant acute phase

XX responses, hypercongenital conditions, birth defects, necrotic lesions,

XX wounds, organ transplant rejection, disorders related to aberrant signal

XX transduction, hyperproliferative disorders, diseases of the pancreas

XX (e.g. diabetes mellitus, vitamin B12 malabsorption), neurological

XX disorders (e.g. Huntington's chorea), Turner's syndrome, bacterial

XX infections, cardiovascular disorders, infertility, psoriasis and

XX haemolytic anaemia. The present sequence represents a human NF-kappaB

XX associated polypeptide of the invention

XX Sequence 646 AA;

Query Match 83.5%; Score 1097.5; DB 6; Length 646;

Best Local Similarity 81.4%; Pred. NO. 1e-82;

Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVQDILLDVAFLSLGLETAGGVMTALIKENSTIPTKOTQFTTYSNDQPGVLIQVY 60

DB 384 KSENVQDILLDVTPLSLGLETAGGVMTVLKRNRTIPTKOTQFTTYSNDQPGVLIQVY 443

QY 61 EGERAMTKDNLLGRFSLSGIPPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120

DB 444 EGERAMTKDNLLGKFLGTGIPPPAPRGVPQIEVTFDIDANGILNVSADVKTGKANKITI 503

QY 121 TNDKRLSKBEETRMVQAEKKADEQVQERVSXNALESYAFNMKSAVEDGLKKGKIS 180

DB 504 TNDKRLSKBEDTRMVQAEKKADEKQKRDVSSKNSLESYAFNMKATVDEKLGQKIN 563

QY 181 EADKKVLDKCOEVLISLDANTLAKEDEFEHKKKELEQVCPNIIISGLYQGAGG-PG--PG 237

DB 564 DEDKQKILDKCNEIINWLDKNQTAKEEPEHQKELEKVCNPIITKLQVSAGMPGMPG 623

QY 238 GF--GAQGPKGGSGSGPTIEEVD 258

DB 624 GPPGGAPPSSGASSGPTIEEVD 646

RESULT 56

ID ABR64224

XX ABR64224 standard; protein; 646 AA.

XX AC ABR64224;

XX DT 15-OCT-2003 (first entry)

XX DE Angiogenesis protein BNO128.

XX KW Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;

XX KW antipsoriatic; antiarteriosclerotic; cardiant; vasotropic; angiogenesis;

XX KW gene therapy; vasculature; cancer; rheumatoid arthritis; psoriasis;

XX KW diabetic retinopathy; cardiovascular disease; atherosclerosis;

XX KW ischemic limb disease; coronary artery disease.

XX OS Homo sapiens.

XX WO2003027285-A1.

XX 03-APR-2003.

XX 19-SEP-2002; 2002WO-AU001282.

XX 27-SEP-2001; 2001AU-00007973.

XX 27-SEP-2001; 2001AU-00007974.

XX 11-OCT-2001; 2001AU-00008210.

XX 29-OCT-2001; 2001AU-00008532.

XX 13-NOV-2001; 2001AU-00008838.

XX 28-AUG-2002; 2002AU-00951032.

XX (BION-) BIONOMICS LTD.

XX Gamble JR, Hahn CN, Vadas MA;

XX WPI; 2003-354655/33.

XX N-PSDB; ACF34439.

XX New angiogenic genes and polypeptides, useful for diagnosing,

XX prognosticating or treating an angiogenesis-related disorder, e.g.

XX cancer, rheumatoid arthritis, diabetic retinopathy, psoriasis or

XX cardiovascular diseases.

XX Claim 15; SEQ ID NO 159; 90pp; English.

XX The invention relates to the isolation of novel genes (ACF34446-ACF34559)

XX encoding proteins (ABR64180-ABR64281) involved in the process of

XX angiogenesis. The nucleic acid molecules are useful in identifying and/or

XX obtaining full-length human genes involved in an angiogenic process. The

XX nucleic acid molecule, polypeptides or complexes encoded, cells or

XX genetically modified non-human animals derived from these are useful for

XX the screening of candidate pharmaceutical compounds used in treating,

XX angiogenesis-related disorders. They are also useful for diagnosing,

XX prognosticating or treating an angiogenesis-related disorder, which

XX involves uncontrolled or enhanced angiogenesis or is a disorder in which

XX a decreased vasculature is of benefit (e.g. cancer, rheumatoid arthritis,

XX diabetic retinopathy, psoriasis or cardiovascular diseases such as

XX atherosclerosis), or involves inappropriately arrested or decreased

XX angiogenesis or is a disorder in which an expanding vasculature is of

XX benefit (e.g. ischemic limb disease or coronary artery disease). The

XX modulator of expression or activity of the polypeptide encoded by the

XX nucleic acid sequence is useful for manufacturing a medicament for the

XX treatment of an angiogenesis-related disorder. This sequence corresponds

XX to one of the novel angiogenic protein

XX Sequence 646 AA;

Query Match 83.5%; Score 1097.5; DB 6; Length 646;

Best Local Similarity 81.4%; Pred. No. 1e-82;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVQDLLLLDVAPLSIGLETAGGVMTALIKRNSITPTKQTQITFTTYSNQPGLVQVY 60
DB 384 KSENVQDLLLLDVTPSLGSETAGGVMTVLKRNITPTKQTQITFTTYSNQPGLVQVY 443

QY 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIETFTDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKNNLLGKFLTGIPPPAPRGVPOIETFTDANGILNVSADVSTGKANKITI 503

QY 121 TNDKGRLSKEIEIRMVQEAKEYKAEDVQERVSANVALESYAFNMKSAYEDELKKGKIS 180
DB 504 TNDKGRLSKEDIERMVQEAKEYKAEDKQKRDVSSKNLSLEYAFNMKATVEDEKLQKIN 563

QY 181 EADKKVLDKQCVISWLDANTLAEKDFEHRKLEQVNCNPIISGLYQAGG--PG--PG 237
DB 564 DEDQKILDKCNELIINWLDKNQTAKEEPEHQKELEKVCNPIITKLYQAGGPGGMPG 623

QY 238 GF--GAQPKGGSGSGPTIEVD 258
DB 624 GFGGAGPPSGGSGSGPTIEVD 646

RESULT 57
ID ABU79083
AC ABU79083 standard; protein; 646 AA.
XX ABU79083;
XX 18-JUN-2003 (first entry)
XX Staphylococcal heat shock protein 70, HSP-70, protein.
XX Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis;
KW gene therapy; mammalian cell receptor; cytostatic;
KW tumour associated lipid; energy; T cell; antigen presenting cell; APC;
KW tumouricidal immunocyte; antitumour.
XX Staphylococcus sp.
XX US2002177551-A1.
XX 28-NOV-2002.
XX 30-MAY-2001; 2001US-00870759.
XX 31-MAY-2000; 2000US-0208128P.
XX (TERM/) TERMAN D S.
XX Terman DS;
XX WPI; 2003-361759/34.
XX N-PSDB; ACA64714.
XX A mammalian cell receptor, useful in the treatment of cancer by binding
PT to tumour associated lipids where the binding induces energy or apoptosis
PT in T cells and antigen presenting cells..
XX Disclosure; Page; 167pp; English.
XX The invention relates to a mammalian cell receptor, useful in the
XX treatment of cancer, which binds to tumour associated lipids and induces
XX energy or apoptosis in the T cells and antigen presenting cells (APCs).
XX Also included are a mammalian cell useful in the treatment of cancer
XX where the receptor which binds tumour associated lipids and induces
XX cellular inactivation or death is deleted or functionally deactivated,
XX producing (M1) a tumouricidal immunocyte population in vivo in a mammal
XX (by allowing tumour associated lipids to contact immunocytes in which
XX receptors for immunosuppressive fatty acids, ceramides, glycolipids,
XX sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
XX sialylated glycans, lipopeptides and proteoglycolipids are inactivated or

deleted), a construct useful in the treatment of cancer comprising a
superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
inhibits T cell activation by tumour associated antigens is deleted or
functionally deactivated), a composition useful in the treatment of
cancer (comprising a lipid raft conjugated to a superantigen), producing
(M2) a tumouricidal immunocyte population ex vivo in a mammal (by
allowing tumour associated lipids to contact immunocytes, in which
receptors for the lipids are inactivated or deleted to produce a
tumouricidal immunocyte population, and administering the tumouricidal
activated immunocytes to the host), producing (M3) a tumouricidal APC
population ex vivo in a mammal (by allowing a tumour associated lipid to
contact APCs, in which receptors for the tumour associated lipids are
inactivated or deleted to produce a tumouricidal activated population,
and administering APCs to the host), producing a tumouricidal T cell
population ex vivo in a mammal) by allowing a tumour associated lipids to
contact T cells, in which adaptor proteins which inhibit T cell
activation by tumour associated antigens, are deleted or functionally
deactivated to produce a tumouricidal population of T cells, and
administering the tumouricidal activated T cells to the host, or
allowing a superantigen-lipid raft to contact T cells ex vivo, and
administering the tumouricidal activated T cells to the host), treating
(M5) cancer in a mammal (by administering a lipid binding molecule which
binds immunosuppressive tumour associated lipids in vivo), producing (M6)
a tumouricidal T cell population in vivo in a mammal (by allowing a
tumour associated antigen to contact immunocytes in which adaptor
proteins which inhibit T cell activation by tumour associated antigens
are deleted or functionally deactivated) and producing (M7) a
tumouricidal T cell population ex vivo in a mammal comprising allowing a
superantigen-lipid raft conjugate to contact immunocytes in vivo. The
receptors, methods and compositions are useful for treating cancers and
tumours. Bacterial superantigens are co-administered or administered as
fusion constructs with anti-tumour proteins or motifs. The present
sequence represents an anti-tumour protein which is co-administered with
or incorporated into a fusion construct with a superantigen. Note: The
sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format from the US patent
office website at "seqdata.uspto.gov/sequence.html?docID=20020177551"

XX SQ Sequence 646 AA;

Query Match 83.5%; Score 1097.5; DB 6; Length 646;
Best Local Similarity 81.4%; Pred. No. 1e-82;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVQDLLLLDVAPLSIGLETAGGVMTALIKRNSITPTKQTQITFTTYSNQPGLVQVY 60
DB 384 KSENVQDLLLLDVTPSLGSETAGGVMTVLKRNITPTKQTQITFTTYSNQPGLVQVY 443

QY 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIETFTDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKNNLLGKFLTGIPPPAPRGVPOIETFTDANGILNVSADVSTGKANKITI 503

QY 121 TNDKGRLSKEIEIRMVQEAKEYKAEDVQERVSANVALESYAFNMKSAYEDELKKGKIS 180
DB 504 TNDKGRLSKEDIERMVQEAKEYKAEDKQKRDVSSKNLSLEYAFNMKATVEDEKLQKIN 563

QY 181 EADKKVLDKQCVISWLDANTLAEKDFEHRKLEQVNCNPIISGLYQAGG--PG--PG 237
DB 564 DEDQKILDKCNELIINWLDKNQTAKEEPEHQKELEKVCNPIITKLYQAGGPGGMPG 623

QY 238 GF--GAQPKGGSGSGPTIEVD 258
DB 624 GFGGAGPPSGGSGSGPTIEVD 646

RESULT 58
ADD22402
ID ADD22402 standard; protein; 646 AA.
XX ADD22402;
XX AC ADD22402;
XX 15-JAN-2004 (first entry)

XX HLA-B46 T cell recognised tumour antigenic polypeptide, SEQ NO 52.
DE tumour antigenic peptide; cancer; vaccine; cytostatic; cytotoxic T cell;
KW colon; mouth; lung; prostatic; gynecological; human.
XX Homo sapiens.
XX JF2003111595-A.
XX 15-APR-2003.
XX 24-JUN-2002; 2002JP-00183603.
XX 25-JUN-2001; 2001JP-00191974.
XX (ITOY/) ITO Y.
XX WPI; 2003-611129/58.
XX Novel tumor antigenic peptide or polypeptide useful for inducing
PT cytotoxic T cells or for treating cancer such as colon, mouth, lung,
PT prostatic or gynecological cancer.
XX
XX Claim 2; SEQ ID NO 52; 98pp; Japanese.
XX The invention relates to a novel tumour antigenic peptide or polypeptide
CC comprising a sequence selected from 99 sequences fully defined in the
CC specification. The tumour antigenic peptide or polypeptide comprises a
CC sequence selected from 99 sequences fully defined in the specification,
CC where the tumour antigenic peptide preferably has a sequence of Glu-Pro-
CC Pro-Leu-Ser-Gln-Glu-Thr-Phe, and the polypeptide preferably has a
CC sequence comprising 393 amino acids fully defined in the specification.
CC The invention further provides a cancer vaccine comprising a tumour
CC antigenic peptide or polypeptide, which has cytostatic activity. A tumour
CC antigenic peptide, polypeptide, its encoding polynucleotide, a
CC hybridising polynucleotide, a recombinant vector containing the
CC polynucleotide, a host transformed with the vector or an antibody are
CC useful for screening for compounds that interact with the tumour
CC antigenic peptide, the polypeptide or its encoding polynucleotide and
CC increases the expression of the tumour antigenic peptide, the polypeptide
CC or polynucleotide. The tumour antigenic peptide or the polypeptide is
CC useful for inducing cytotoxic T cells. The tumour antigenic peptide
CC vaccine is useful for treating cancer such as colon, mouth, lung,
CC prostatic or gynecological cancer. The invention also provides a
CC pharmaceutical composition useful for treating cancer. The tumour
CC antigenic peptide or the polypeptide is useful as an antigen to create
CC antibodies. This sequence represents one of the tumour antigenic
CC polypeptides of the invention.

Sequence 646 AA;

Query Match 83.5%; Score 1097.5; DB 7; Length 646;
Best Local Similarity 81.4%; Pred. No. 1e-82;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
QY 1 KSENVQDILLDDVAPLSGLGTAGGVTALIKRNTIPTKTQTOFTTYSNQPGVLIQVY 60
DB 384 KSENVQDILLDDVAPLSGLGTAGGVTALIKRNTIPTKTQTOFTTYSNQPGVLIQVY 443
QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
DB 444 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 503
QY 121 TNDKGRLSKEIEIRMWQEAKEYKAEDVQREVSVAKNALESYAFNMKSAVEDGLKGGKIS 180
DB 504 TNDKGRLSKEIEIRMWQEAKEYKAEDVQREVSVAKNALESYAFNMKSAVEDGLKGGKIN 563
QY 181 EADKKVLDKQCVISWLDANTLAEKDFEKKKELEQVNCNPIISGLYQAGG-PG--PG 237
DB 564 DEDKQKILDKCNEIINWLDKNQTAKEEFHQKELEKVCNPIITKLYQAGGMPGMPG 623
QY 238 GF--GAQGPKGSGSGPTIEVD 258

DB 624 GPFPGGAPSPGGAGSGPTIEVD 646
RESULT 59
ADF43323
ID ADF43323 standard; protein; 646 AA.
XX ADF43323;
AC ADF43323;
XX 12-FEB-2004 (first entry)
XX Superantigen associated protein seq id 43.
XX receptor; lipid-based tumour associated antigen; cytostatic;
KW antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
KW infectious disease.
XX Unidentified.
OS US2003157113-A1.
PN 21-AUG-2003.
PD 28-DEC-2000; 2000US-00751708.
XX 28-DEC-1999; 99US-0173371P.
PR (TERM/) TERMAN D S.
XX Terman DS;
PI WPI; 2003-787326/74.
XX New receptor in a mammalian cell that inhibits regular activation by
PT receptors specific for lipid-based tumor associated antigens, useful for
PT treating a neoplastic disease or tumor, and infectious diseases.
XX Disclosure; SEQ ID NO 43; 151pp; English.
XX The invention describes a receptor in a mammalian cell that inhibits
CC regular activation by receptors specific for lipid-based tumour
CC associated antigen. The receptor has cytostatic and antimicrobial
CC properties and is suitable for use in gene therapy. The receptors,
CC methods and compositions are useful for treating a neoplastic disease or
CC tumour (cancer), and infectious diseases. This sequence represents a
CC protein associated with superantigens used to generate antitumour
CC immunity.

Sequence 646 AA;

Query Match 83.5%; Score 1097.5; DB 7; Length 646;
Best Local Similarity 81.4%; Pred. No. 1e-82;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
QY 1 KSENVQDILLDDVAPLSGLGTAGGVTALIKRNTIPTKTQTOFTTYSNQPGVLIQVY 60
DB 384 KSENVQDILLDDVAPLSGLGTAGGVTALIKRNTIPTKTQTOFTTYSNQPGVLIQVY 443
QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
DB 444 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 503
QY 121 TNDKGRLSKEIEIRMWQEAKEYKAEDVQREVSVAKNALESYAFNMKSAVEDGLKGGKIS 180
DB 504 TNDKGRLSKEIEIRMWQEAKEYKAEDVQREVSVAKNALESYAFNMKSAVEDGLKGGKIN 563
QY 181 EADKKVLDKQCVISWLDANTLAEKDFEKKKELEQVNCNPIISGLYQAGG-PG--PG 237
DB 564 DEDKQKILDKCNEIINWLDKNQTAKEEFHQKELEKVCNPIITKLYQAGGMPGMPG 623
QY 238 GF--GAQGPKGSGSGPTIEVD 258

Db 624 GFFGGGAPPSGASSGPTIEVD 646

RESULT 60

AD120103
ID AD120103 standard; protein; 646 AA.

XX AC AD120103;

XX DT 22-APR-2004 (first entry)

XX DE Hsc70.

XX KW inducible heat shock protein; Hsp70; constitutive heat shock protein;
XX KM Hsc70; human leukocyte antigen; HLA.

XX OS Unidentified.

XX XX WO2003029288-A2.

PN PD 10-APR-2003.

XX XX 26-SEP-2002; 2002WO-EP010821.

XX XX 27-SEP-2001; 2001EP-00402496.

XX PA (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.

XX PA (INSR) INST ROUSSY GUSTAVE.

XX PA (INRM) INSERM.

XX PI Faure O, Kosmatopoulos K;

XX DR WPI; 2003-449139/42.

XX PT Novel peptide derived from inducible heat shock protein Hsp70, useful for
XX PT inducing cytotoxic T lymphocyte response that targets cells expressing
XX PT inducible Hsp70, and for preparing drugs for treating cancer.

XX PS Disclosure; SEQ ID NO 2; 49pp; English.

XX CC The present invention relates to a peptide comprising a sequence of at
XX CC least 8 contiguous amino acids, having at least 65 % identity to a
XX CC portion inducible heat shock protein (Hsp)-70 sequence, differing from a
XX CC sequence of constitutive heat shock protein Hsc70 by at least one amino
XX CC acid, and capable of inducing cytotoxic T lymphocytes that specifically
XX CC recognize cells naturally producing inducible Hsp70, in vitro or in vivo.
XX CC The peptides are stable, and has high affinity for human leukocyte
XX CC antigen (HLA) class I molecules. The present sequence represents Hsc 70.

XX SQ Sequence 646 AA;

Query Match 83.5%; Score 1097.5; DB 7; Length 646;

Best Local Similarity 81.4%; Pred. No. 1e-82;

Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVODLLLDVAPISLGLTAGGVTALIKRNTIPTKTQTFTTYSNQPGLVIOY 60

Db 384 KSENVODLLLDVAPISLGLTAGGVTALIKRNTIPTKTQTFTTYSNQPGLVIOY 443

QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120

Db 444 EGERAMTKNNLLGKFLTGIPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503

QY 121 TNDKGRLSKEEIERMWQAEKYAEDEVQERYSAKNALSYAFNMKSAVEDGLGKIS 180

Db 504 TNDKGRLSKEDIERMWQAEKYAEDEVQERYSAKNALSYAFNMKATVEDGLGKIN 563

QY 181 EADKKVLDKQCEVISWLDANTLAEDKDFEHRKELEFQVCNPIISGLYQAGG-PG--PG 237

Db 564 DEDKQILDKCNELINWLDKNQTAKEEFHQKELEKVCNPIITKLYQAGGMPGMPG 623

QY 238 GP--GAQGPKGSGSGPTIEVD 258

Db 384 KSENVODLLLDVAPISLGLTAGGVTALIKRNTIPTKTQTFTTYSNQPGLVIOY 443

Db 624 GFFGGGAPPSGASSGPTIEVD 646

RESULT 61

ADJ68897
ID ADJ68897 standard; protein; 646 AA.

XX AC ADJ68897;

XX DT 06-MAY-2004 (first entry)

XX DE Human heat mitochondrial protein as a therapeutic target SeqID703.

XX KW mitochondrial; human; screening assay; diabetes mellitus;
XX KM Huntington's disease; osteoarthritis;
XX KW Leber's hereditary optic neuropathy; LHON;
XX KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
XX KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
XX KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
XX KW osteopathic; ophthalmological; cytostatic.

XX OS Homo sapiens.

XX PN WO2003087768-A2.

XX XX 23-OCT-2003.

XX PF 04-APR-2003; 2003WO-US010870.

XX PR 12-APR-2002; 2002US-0372843P.

XX PR 17-JUN-2002; 2002US-0389987P.

XX PR 20-SEP-2002; 2002US-0412418P.

XX XX (MITO-) MITOKOR.

XX PA (BUCK-) BUCK INST AGE RES.

XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;

XX PI Warnock DE;

XX XX WPI; 2003-845369/78.

XX PT Identifying a mitochondrial target for drug screening assays and for
XX PT treating diseases associated with altered mitochondrial function,
XX PT comprises detecting a modified polypeptide in a sample and correlating
XX PT with the disease.

XX PS Claim 1; SEQ ID NO 703; 180pp; English.

XX CC This invention relates to novel mitochondrial targets that can be used
XX CC for therapeutic intervention in treating a disease associated with
XX CC altered mitochondrial function. Specifically, it refers to a method for
XX CC identifying proteins of the human heart mitochondrial proteome that are
XX CC useful for drug screening assays, as well as therapeutic targets. The
XX CC present invention describes a method for identifying such proteins that
XX CC can be used in the treatment of various diseases associated with altered
XX CC mitochondrial function including diabetes mellitus, Huntington's disease,
XX CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
XX CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
XX CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
XX CC compositions have neuroprotective, nootropic, antidiabetic,
XX CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
XX CC cytostatic activities. This polypeptide sequence is a human heart
XX CC mitochondrial protein of the invention.

XX SQ Sequence 646 AA;

Query Match 83.5%; Score 1097.5; DB 7; Length 646;

Best Local Similarity 81.4%; Pred. No. 1e-82;

Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVODLLLDVAPISLGLTAGGVTALIKRNTIPTKTQTFTTYSNQPGLVIOY 60

Db 384 KSENVODLLLDVAPISLGLTAGGVTALIKRNTIPTKTQTFTTYSNQPGLVIOY 443

Query Match	83.5%;	Score 1097.5;	DB 8;	Length 646;
Best Local Similarity	81.4%;	Pred. No. 1e-82;		
Matches 214;	Conservative	24;	Mismatches 20;	Indels 5; Gaps 3

QY	1	KSENVQDLILLDDVAPLSIGLETAGGVMTALIKRNSTIPTKOTQIFTTYSNDNQPGVLIQVY	60
DB	384	KSENVQDLILLDDVTPLSIGLETAGGVMTVLIKRNSTIPTKOTQIFTTYSNDNQPGVLIQVY	443
QY	61	EGERAMTKNNLLGRFELSGIPPAAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI	120
DB	444	EGERAMTKNNLLGKPELTGIPPAAPRGVPOIEVTFDIDANGILNVSAVDKSTGKENKITI	503
QY	121	TNDKGRLSKEIEIEMVQEAKEYKAEDVQRRERVSQAKNALESYAFNMKSAVEDEGLKGKIS	180
DB	504	TNDKGRLSKEDIEMVQEAKEYKAEDKQDKVSKNSLESYAFNMKATVDEKIQGKIN	563
QY	181	EADKKKVLDKCOEVIWLDANTLAEKDEFEHKKRKELEOVNCNPIISGLYQAGG-PG--PG	237
DB	564	DEDKQKILDKCNEIINWLDKQTAKEFEFHQQKELEKVCNPIITKLQASAGMPGPG	623
QY	238	GF--GAQGPKGSGSGPTIEVD	258
DB	624	GFGGGAPPSSGASSGPTIEVD	646

RESULT 64	
ADQ91627	
ID	ADQ91627 standard; protein; 646 AA.
XX	
AC	ADQ91627;
XX	
DT	07-OCT-2004 (first entry)
DE	Human heat shock cognate protein 70 (HSC70).
XX	
KW	Human; heat shock cognate protein 70; HSC70; multidrug resistance;
KW	cytostatic; cancer; vaccine; gene therapy.
XX	
OS	Homo sapiens.
XX	
PN	WO2004061458-A2.
XX	
PD	22-JUL-2004.
XX	
PF	15-DEC-2003; 2003WO-IB006416.
XX	
PR	03-JAN-2003; 2003US-0438012P.
XX	
PA	(AURE-) AURELIUM BIOPHARMA INC.
XX	
PI	Georges E, Serfass L, Bonneau A, Dallaire F;
XX	
DR	WPI; 2004-553396/53.
DR	N-PSDB; ADQ91628.
XX	GENBANK; AAK17898.
XX	
PT	Detecting multidrug resistance/multidrug resistance potential in test
PT	neoplastic cell, by measuring heat shock cognate 70 protein level in test
PT	cell, comparing level of protein expression in test cell and non-
PT	resistant neoplastic cell.
XX	
PS	Claim 44; SEQ ID NO 1; 166pp; English.
XX	
CC	The present sequence is the protein sequence of human heat shock cognate
CC	protein 70 (HSC70). The invention is based on the discovery that HSC70, a
CC	normally intracellular protein, is expressed in full length on the cell
CC	surface of neoplastic cells and damaged cells, and is expressed more
CC	abundantly on the cell surfaces of multidrug resistant (MDR) neoplastic
CC	cells and MDR damaged cells. Although lower levels of HSC70 are expressed
CC	on the cell surface of drug-sensitive neoplastic cells, in contrast to
CC	other cell surface MDR markers such as P-glycoprotein, HSC70 is expressed
CC	in only negligible amounts on the cell surface of normal cells of the
CC	body. Thus, the invention provides a method for detecting multidrug

CC	resistance in a test neoplastic cell by measuring the level of cell
CC	surface-expressed HSC70 protein. The neoplastic cell is especially a
CC	breast cancer, ovarian cancer, myeloma, lymphoma, melanoma, sarcoma,
CC	leukaemia, retinoblastoma, hepatoma, glioma, mesothelioma or carcinoma,
CC	cancer cell, or from a tissue selected from blood, bone marrow, spleen,
CC	lymph node, liver, thymus, kidney, brain, skin, gastrointestinal tract,
CC	eye, breast, prostate and ovary. The invention also provides a cell
CC	surface HSC70-targeted agent for treatment or prevention of an MDR
CC	neoplasm. This may include an HSC70 binding component and a therapeutic
CC	component such as a chemotherapeutic agent or radioisotope. Vaccines for
CC	treating or preventing MDR neoplasms comprise a HSC70 polypeptide or, in
CC	the case of DNA vaccines, a nucleic acid sequence encoding HSC70.
XX	
SQ	Sequence 646 AA;
	Query Match 83.5%; Score 1097.5; DB 8; Length 646;
	Best Local Similarity 81.4%; Pred. No. le-82;
	Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps
Qy	1 KSNVODLLLDLVAPLSLGLETAGGVMTALIKRNTIPTKQTQIPTTYSNDQPGLVIQVY 60
Dd	384 KSENVQDLLLDVTPLSLGIETAGGVMTVLIKRNTIPTKQTQETTTYSNDQPGLVIQVY 44
Qy	61 EGERAMTKDNNLLGRFELSGIPPARPGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 12
Dd	444 EGERAMTKDNNLLGKFELTGIPPARPGVPQIEVTFDIDANGILNVSVDKSTGKENKITI 10
Qy	121 TNDKGRLSKKEIERVMVOEAEKYKAEDVQRERVSARNALLESYAFNMKSADVEGLKGKIS 18
Dd	504 TNDKGRLSKEDIERVMVOEAEKYKADEKQKDVKSSKNSLESYAFNMKATVEDEKLQGIN 56
Qy	181 EADKKVKL DKOEIVSWLDANTLAKDBFEHKRKELEVCNPIISGLYQGAGG-PG--PG 23
Dd	564 DEDQKILDKCNEIIINWLDKNQTAEBBFEHQOKELEKVCNPIITKLYQSAGMPGGMGP 62
Qy	238 GP--GAQGPKGSGSGPTIEEYD 258
Dd	624 GFPGGGAPPFGSAGSGPTIEEYD 646
RESULT 65	
ADQ89812	
ID	ADQ89812 standard; protein; 646 AA.
XX	
AC	ADQ89812;
XX	
DT	21-OCT-2004 (first entry)
XX	
DE	Antagonist of cell cycle progression polypeptide #121.
XX	
KW	Cytostatic; cancer; cell division cycle; mitosis; meiosis;
KW	cell cycle progression.
XX	
OS	Homo sapiens.
XX	
PN	WO2004063362-A2.
XX	
PD	29-JUL-2004.
XX	
PF	31-DEC-2003; 2003WO-GB005635.
XX	
PR	10-JAN-2003; 2003US-0439123P.
PR	06-MAY-2003; 2003US-0468402P.
XX	
PA	(CYCL-) CYCLACEL LTD.
XX	
PI	Glover D, Bell G, Frenz L, Midgley C;
XX	
DR	WPI; 2004-544089/52.
DR	N-PSDB; ADQ89811.
XX	
PT	New cell cycle progression genes and proteins for modulating cell cycle
PT	progression in cells, for preventing, treating or diagnosing cell

PT proliferative diseases (e.g. cancer) or for identifying modulators of
PT mitosis or meiosis.
PS Claim 2; SEQ ID NO 242; 461pp; English.
XX
CC The present invention relates to a polynucleotide for preventing,
CC treating or diagnosing a disease in an individual. The composition or the
CC polypeptide, polynucleotide or RNA precursor, or antibody is useful for
CC diagnosing, preventing or treating diseases (e.g. cell proliferative
CC diseases such as cancer) in an individual. These may also be used for
CC identifying substances capable of binding to or modulating the function
CC of the polypeptide, capable of affecting the function of the
CC corresponding gene, or capable of inhibiting the cell division cycle or
CC cell cycle progression, preferably mitosis and/or meiosis. The present
CC sequence represents an antagonist of cell cycle progression protein
CC sequence.
XX
SQ Sequence 646 AA;
Query Match 83.5%; Score 1097.5; DB 8; Length 646;
Best Local Similarity 81.4%; Pred. No. 1e-82;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
QY 1 KSENVQDLLLDVAPLSGLGTAGGVTALIKRNSTIPTKQTQFTTYSNQPGLIQVY 60
Db 384 KSENVQDLLLDVTPLSGLGTAGGVTALIKRNTIPTKQTQFTTYSNQPGLIQVY 443
QY 61 EGERAMTKDNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTKDNLLGKFLTGIPAPRGVQIEVTFDIDANGILNVSAVDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVQEAKEYKAEDQKDVSSKNLSLEYAFNMKSAVEDGLKGKIS 180
Db 504 TNDKGRLSKEDIERMVQEAKEYKAEDQKDVSSKNLSLEYAFNMKATVEDEKLOGKIN 563
QY 181 EADKKVLDKQEVISWLDANTLAEKDFEHHKKELEQVCNPIISGLYQAGG-PG--PG 237
Db 564 DEDQKILDKCNEIINWLDKNQTAKEEFHQKELEKVCNPIITKLYQSAGGMPGMPG 623
QY 238 GF--GAQGPKGSGSGPTIEEVD 258
Db 624 GPPGGAPPSSGSGSGPTIEEVD 646
RESULT 66
ADQ89798
XX AC ADQ89798;
XX DT 21-OCT-2004 (first entry)
XX DE Antagonist of cell cycle progression polypeptide #114.
XX KW Cytostatic; cancer; cell division cycle; mitosis; meiosis;
XX KW cell cycle progression.
XX OS Homo sapiens.
XX PN WO2004063362-A2.
XX PD 29-JUL-2004.
XX PF 31-DEC-2003; 2003WO-GB005635.
XX PR 10-JAN-2003; 2003US-0439123P.
XX PR 06-MAY-2003; 2003US-0468402P.
XX PA (CYCL-) CYCLACEL LTD.
XX PI Glover D; Bell G, Frenz L, Midgley C;
XX WP1; 2004-544089/52.

DR N-PSDB; ADQ89797.
XX
PT New cell cycle progression genes and proteins for modulating cell cycle
PT progression in cells, for preventing, treating or diagnosing cell
PT proliferative diseases (e.g. cancer) or for identifying modulators of
PT mitosis or meiosis.
XX
XX Claim 2; SEQ ID NO 228; 461pp; English.
XX
CC The present invention relates to a polynucleotide for preventing,
CC treating or diagnosing a disease in an individual. The composition or the
CC polypeptide, polynucleotide or RNA precursor, or antibody is useful for
CC diagnosing, preventing or treating diseases (e.g. cell proliferative
CC diseases such as cancer) in an individual. These may also be used for
CC identifying substances capable of binding to or modulating the function
CC of the polypeptide, capable of affecting the function of the
CC corresponding gene, or capable of inhibiting the cell division cycle or
CC cell cycle progression, preferably mitosis and/or meiosis. The present
CC sequence represents an antagonist of cell cycle progression protein
CC sequence.
XX
SQ Sequence 646 AA;
Query Match 83.5%; Score 1097.5; DB 8; Length 646;
Best Local Similarity 81.4%; Pred. No. 1e-82;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
QY 1 KSENVQDLLLDVAPLSGLGTAGGVTALIKRNSTIPTKQTQFTTYSNQPGLIQVY 60
Db 384 KSENVQDLLLDVTPLSGLGTAGGVTALIKRNTIPTKQTQFTTYSNQPGLIQVY 443
QY 61 EGERAMTKDNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTKDNLLGKFLTGIPAPRGVQIEVTFDIDANGILNVSAVDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVQEAKEYKAEDQKDVSSKNLSLEYAFNMKSAVEDGLKGKIS 180
Db 504 TNDKGRLSKEDIERMVQEAKEYKAEDQKDVSSKNLSLEYAFNMKATVEDEKLOGKIN 563
QY 181 EADKKVLDKQEVISWLDANTLAEKDFEHHKKELEQVCNPIISGLYQAGG-PG--PG 237
Db 564 DEDQKILDKCNEIINWLDKNQTAKEEFHQKELEKVCNPIITKLYQSAGGMPGMPG 623
QY 238 GF--GAQGPKGSGSGPTIEEVD 258
Db 624 GPPGGAPPSSGSGSGPTIEEVD 646
RESULT 67
ADP54908
XX ID ADP54908 standard; protein; 646 AA.
XX AC ADP54908;
XX DT 18-NOV-2004 (first entry)
XX DE Human PRO protein sequence SEQ ID NO:884.
XX KW human; PRO; immune related disease; inflammatory immune response;
XX KW immune response stimulation; antiallergic; antianemic; antiarthritic;
XX KW antisthmatic; antidiabetic; antiinflammatory; antipsoriatic;
XX KW antirheumatic; antithyroid; CNS; dermatological; gastrointestinal;
XX KW haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;
XX KW nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
XX KW virucide; gene therapy.
XX OS Homo sapiens.
XX PN WO2004039956-A2.
XX PD 13-MAY-2004.
XX PF 28-OCT-2003; 2003WO-US034381.

XX 29-OCT-2002; 2002US-0422472P.
XX (GETH) GENENTECH INC.
XX Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;
XX Wood WI, Wu TD;
XX N-PSDB; ADP54907.
XX WPI; 2004-376182/35.
XX DR N-PSDB; ADP54907.
XX PT New PRO polynucleotides and polypeptides, useful in useful in diagnosing
XX and treating an immune related disease, e.g. systemic lupus
XX erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
XX stimulating an immune response.
XX Claim 1; SEQ ID NO 884; 3009pp; English.
XX The present invention describes an isolated PRO nucleic acid (1). Also
XX described: (1) a vector comprising (1); (2) a host cell comprising the
XX vector of (1); (3) a process for producing a PRO polypeptides; (4) an
XX isolated PRO polypeptide; (5) a chimeric molecule comprising the
XX polypeptide of (4) fused to a heterologous amino acid sequence; (6) an
XX antibody which specifically binds to a polypeptide of (4); (7) a
XX composition of matter comprising a polypeptide of (4), an agonist or
XX antagonist of the polypeptide or an antibody that binds to the
XX polypeptide in combination with a carrier; (8) an article of manufacture
XX comprising a container, a label on the container and a composition of
XX matter of (7); (9) a method of treating an immune related disease in a
XX mammal; (10) a method for determining the presence of a PRO polypeptide
XX in a sample suspected of having the polypeptide; (11) a method of
XX diagnosing an immune related disease or an inflammatory immune response
XX in a mammal; (12) a method of identifying a compound that inhibits or
XX mimics the activity of or expression of a gene encoding a PRO polypeptide
XX, and (13) a method of stimulating the immune response in a mammal. The
XX PRO sequences have anti-allergic, anti-inflammatory, antiarthritic,
XX antiasthmatic, antidiabetic, antihypertensive, antipsoriatic,
XX antirheumatic, antithyroid, CNS, dermatological, gastrointestinal,
XX haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,
XX nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and
XX virucide activities, and can be used in gene therapy. The nucleic acid
XX (1) and the encoded polypeptides, compositions, kits and methods are
XX useful in diagnosing and treating an immune related disease and in
XX stimulating an immune response. The present sequence represents a human
XX PRO protein from the present invention.
XX Sequence 646 AA;

Query Match 83.5%; Score 1097.5; DB 8; Length 646;
Best Local Similarity 81.4%; Pred. No. 1e-82;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
QY 1 KSENVQDILLVAPISLIGTAGGVTALIKNSTIPTKTQITFTYSNQPGLIÖVY 60
DB 384 KSENVQDILLVAPISLIGTAGGVTALIKNSTIPTKTQITFTYSNQPGLIÖVY 443
QY 61 EGERAMTKDNNLLGRPELSGIPAPRGVPOIETVFDIDANGILNVATDKSTGKANKITI 120
DB 444 EGERAMTKDNNLLGRPELSGIPAPRGVPOIETVFDIDANGILNVATDKSTGKANKITI 503
QY 121 TNDKRLSKKEIERWQAEKYKAEDVQRERYSAKNALESYAFNMKSAVEDGLKGKIS 180
DB 504 TNDKRLSKKEIERWQAEKYKAEDVQRERYSAKNALESYAFNMKSAVEDGLKGKIN 563
QY 181 EADKKVLDKQEVISWLDANTLAEDKFEHKELEQVNCNPIISGLYQAGG-PG--PG 237
DB 564 DEDKQKILDKCNRIINWLDKXNTAEKEEFHQKELEKVCNPIITKLQYAGGMPGMPG 623
QY 238 GF--GAQGPKGSGSGPTIEVD 258
DB 624 GFFGGAGPPSGGASSGPTIEVD 646

RESULT 68
ADP24120
ID ADP24120 standard; protein; 646 AA.
XX AC ADP24120;
XX DT 18-NOV-2004 (first entry)
XX DE PRO polypeptide SEQ ID NO:1298.
XX KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
XX osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
XX antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
XX OS Unidentified.
XX PN WQ2004041170-A2.
XX PD 21-MAY-2004.
XX PF 30-OCT-2003; 2003WO-US034312.
XX PR 01-NOV-2002; 2002US-0423394P.
XX PA (GETH) GENENTECH INC.
XX PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
XX Wu TD;
XX WPI; 2004-419628/39.
XX N-PSDB; ADP24119.
XX New PRO polypeptides and polynucleotides, useful for treating e.g.
XX erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated
XX renal disease, or demyelinating diseases of the central or peripheral
XX nervous system.
XX Claim 7; SEQ ID NO 1298; 2940pp; English.
XX The invention relates to a novel isolated nucleic acid and the PRO
XX polypeptide encoded by it. A protein of the invention has
XX antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
XX osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
XX antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
XX of the invention may have a use in gene therapy. The PRO polypeptide, its
XX agonist, antagonist, or antibody that specifically binds to the
XX polypeptide is useful for treating an immune related disorder such as
XX systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
XX juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
XX idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
XX vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
XX thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
XX disease, a demyelinating disease of the central or peripheral nervous
XX system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
XX a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
XX disease, infectious or autoimmune chronic active hepatitis, primary
XX biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
XX inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
XX disease, an autoimmune or immune-mediated skin disease, a bullous skin
XX disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
XX disease, asthma, allergic rhinitis, atopic dermatitis, food
XX hypersensitivity, urticaria, an immunologic disease of the lung,
XX eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
XX pneumonitis, a transplantation associated disease, graft rejection or
XX graft-versus-host disease. The present sequence represents a PRO protein
XX of the invention.
XX Sequence 646 AA;

Query Match 83.5%; Score 1097.5; DB 8; Length 646;
Best Local Similarity 81.4%; Pred. No. 1e-82;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVODLLLDVAPISLGLTETAGGVTALIKRNSIPTKQTQITFTTYSNQPGLVLIQVY 60
 DB 384 KSENVODLLLDVTPISLGLTETAGGVTALIKRNTIPTKQTQITFTTYSNQPGLVLIQVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVQIETVTFDIDANGILNVATDKSTGKANKITI 120
 DB 444 EGERAMTKNNLLGKPELTGIPAPRGVQIETVTFDIDANGILNVSAVDKSTGKANKITI 503
 QY 121 TNDKGRLSKEIERMVOEAEKYKAEDVQERVSAKNALLESYAFNMKSAAVEDGLKQKIS 180
 DB 504 TNDKGRLSKEDIERMVOEAEKYKAEDKQDKVSSKNLSLESYAFNMKATVEDEKLQKIN 563
 QY 181 EADKKVLDKQCFVSWLDANTLAEDRFEHKEKELEQVNCNPIISGLYQAGG-PG--PG 237
 DB 564 DEDKQKILDKNCNEIINWLDKQNTAEKEEFHQKELEKVCNPIITKLYQAGGMPGMPG 623
 QY 238 GF--GAQGPKGSGSGPTIEVD 258
 DB 624 GFPGGGAPPSSGSGSGPTIEVD 646
 RESULT 69
 ADT66611
 ID ADT66611 standard; protein; 646 AA.
 AC ADT66611;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Human chaperone Hsc70 protein.
 XX
 KW pain regulation; screening; LuzP; PEP-19; phosphatidylinositol synthase;
 KW valosin; interleukin 6 receptor subunit beta; aspartate aminotransferase;
 KW neuronal immediate early gene; heat shock protein 27; HSC70; calmodulin;
 KW syntaxin binding protein 1; spliceosomal protein SAP 155; neurodap 1;
 KW bamacan; leukotriene A4 hydrolase; chondromodulin 1;
 KW Msa4/phosphatidylinositol-4-phosphate 5 kinase; 26S proteasome UE p112;
 KW UE Z; UE p44.5; ingensin; 3-hydroxy-3-methylglutaryl-Co A synthase;
 KW phosphoglycerate kinase; RNA polymerase II TF SIII p18 UE;
 KW protein phosphatase EF hands-1; RAB21;
 KW TNF receptor-associated factor 6-binding protein; spagheetti protein;
 KW HSKM-B; calnexin-t; nexin 3; glia-derived nexin precursor;
 KW microtubuli-associated protein 4; CDC10;
 KW transcription co-activator CRSP150; JERKY; SOUL protein;
 KW RNA intron-encoded homing endonuclease;
 KW epithelial cell growth inhibitor; glutathione transferase A4; CGI-69;
 KW differential display; chronic pain; gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX W02004070383-A2.
 XX
 PD 19-AUG-2004.
 XX
 XX 02-DEC-2003; 2003MO-EP013597.
 XX
 XX 05-FEB-2003; 2003DE-01004680.
 XX
 XX (CHEF) GRUENENTHAL GMBH.
 XX
 XX Weihe E, Bieller A, Schaefer MK;
 XX
 XX WPI; 2004-604492/58.
 XX
 XX N-PSDB; ADT66610.
 XX
 XX New polynucleotides and polypeptides involved in pain regulation, useful
 PT in screening for pain-regulating compounds for therapy and diagnosis.
 XX
 XX Claim 1; Fig 27b; 241pp; German.
 XX
 XX This invention describes novel polynucleotides and polypeptides involved
 CC in pain regulation which are useful in screening for pain-regulating
 CC compounds for therapy and diagnosis. Identifying pain-regulating

CC substances comprises incubating a test compound with a cell, and/or
 CC preparation of a cell, that synthesises at least one specific peptide or
 CC protein, then measuring either binding of test compound to the protein or
 CC a functional parameter that is altered by the binding. The protein is one
 CC or more of any of LuzP, PEP-19, phosphatidylinositol synthase, valosin-
 CC containing protein, interleukin 6 receptor subunit beta, aspartate
 CC aminotransferase, neuronal immediate early gene, heat shock protein 27,
 CC HSC70, calmodulin, syntaxin binding protein 1, spliceosomal protein SAP
 CC 155, neurodap 1, bamacan, leukotriene A4 hydrolase, chondromodulin 1
 CC Msa4/phosphatidylinositol-4-phosphate 5 kinase, 26S proteasome UE p112 or
 CC UE Z or UE p44.5, ingensin, 3-hydroxy-3-methylglutaryl-Co A synthase,
 CC phosphoglycerate kinase, RNA polymerase II TF SIII p18 UE, protein
 CC phosphatase EF hands-1, RAB21, TNF receptor-associated factor 6-binding
 CC protein, ortholog of the Drosophila gene 'spagheetti', protein with 4-
 CC transmembrane domains member 3, vacuolar protein sorting protein, HSKM-B,
 CC calnexin-t, sorting nexin 3, glia-derived nexin precursor, microtubuli-
 CC associated protein 4, CDC 10, transcription co-activator CRSP150, JERKY,
 CC XW-209528, TF SOX10, SOUL protein, RNA intron-encoded homing
 CC endonuclease, epithelial cell growth inhibitor, glutathione transferase
 CC A4 and/or CGI-69; The specified nucleic acids and proteins have been
 CC identified using the restriction fragment differential display PCR method
 CC (Biochem. Biophys. Res. Commun., 234 (1997) 16), applied to rats in which
 CC arthritis has been induced by injection of Complete Freund's adjuvant.
 CC Compounds identified by the new method, also specified polynucleotides,
 CC their antisense sequences, encoded proteins and peptides, vectors,
 CC antibodies and cells, are useful as therapeutic and diagnostic agents,
 CC particularly for treatment of chronic pain, including by in vivo or in
 CC vitro gene therapy. This sequence represents the human chaperone Hsc70
 CC protein.
 XX
 XX Sequence 646 AA;

Query Match 83.5%; Score 1097.5; DB 8; Length 646;
 Best Local Similarity 81.4%; Pred. No. 1e-82;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVODLLLDVAPISLGLTETAGGVTALIKRNSIPTKQTQITFTTYSNQPGLVLIQVY 60
 DB 384 KSENVODLLLDVTPISLGLTETAGGVTALIKRNTIPTKQTQITFTTYSNQPGLVLIQVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVQIETVTFDIDANGILNVATDKSTGKANKITI 120
 DB 444 EGERAMTKNNLLGKPELTGIPAPRGVQIETVTFDIDANGILNVSAVDKSTGKANKITI 503
 QY 121 TNDKGRLSKEIERMVOEAEKYKAEDVQERVSAKNALLESYAFNMKSAAVEDGLKQKIS 180
 DB 504 TNDKGRLSKEDIERMVOEAEKYKAEDKQDKVSSKNLSLESYAFNMKATVEDEKLQKIN 563
 QY 181 EADKKVLDKQCFVSWLDANTLAEDRFEHKEKELEQVNCNPIISGLYQAGG-PG--PG 237
 DB 564 DEDKQKILDKNCNEIINWLDKQNTAEKEEFHQKELEKVCNPIITKLYQAGGMPGMPG 623
 QY 238 GF--GAQGPKGSGSGPTIEVD 258
 DB 624 GFPGGGAPPSSGSGSGPTIEVD 646

RESULT 70

AAB22938
 ID AAB22938 standard; protein; 890 AA.
 XX
 XX AAB22938;
 XX
 XX 12-SEP-2003 (revised)
 DT 10-JAN-2001 (first entry)
 XX
 XX GFP-HSC70 fusion protein, SEQ ID NO:174.

XX Bioreceptor protein; fusion protein; recognition site;
 KW cellular targeting sequence; cellular localisation; fluorescent protein;
 KW protease activity detection; toxin detection; cellular stress detection;
 KW drug discovery; cell based screening.

OS Aequorea victoria.
OS Mammalia.
OS Chimeric.
XX WO2000050872-A2.
XX 31-AUG-2000.
XX 25-FEB-2000; 2000WO-US004794.
XX 26-FEB-1999; 99US-0122152P.
PR 08-MAR-1999; 99US-0123399P.
PR 12-JUL-1999; 99US-00352171.
XX (CELL-) CELLOMICS INC.
XX Giuliano KA, Kapur R;
XX WPI; 2000-594086/56.
DR N-PSDB; AAA93443.
XX Automated cell-based characterization of toxin by contacting cells
PT containing luminescent reporter molecules with test substance and
PT analyzing optically.
XX Example 11; Page 315-318; 336pp; English.
XX The invention relates to systems, methods and reagents for cell-based
CC screening or detection of compounds which affect particular biological
CC functions. The methods of the invention utilise fluorescent bioreactor
CC molecules which, when acted on by a compound of interest, cause an
CC alteration in the cellular distribution of at least the fluorescent
CC moiety. In one embodiment, the biosensors comprise heat shock proteins
CC (HSPs) fused to a fluorescent protein (e.g., jellyfish green fluorescent
CC protein (GFP), or derivatives thereof). Such biosensors are located in
CC the cytoplasm, but on stress activation translocate to the nucleus. In
CC another embodiment bioreactor proteins can be used to detect protease
CC activity. Such protease bioreactor fusion proteins comprise one or more
CC fluorescent proteins; a recognition signal which is cleaved by the
CC protease; and at least one cellular localisation signal. The latter two
CC components may be components of a single protein which is acted upon by
CC the protease, or may be from heterologous sources. Due to the
CC localisation signal, the bioreactor protein is localised to a particular
CC region of the cell. Once acted on by the protease of interest, the
CC fluorescent protein is cleaved from the localisation sequence, and is
CC free to migrate to other locations within the cell. The presence of a
CC second localisation signal attached to the fluorescent protein enables
CC the fluorescent protein to be directed to a different cellular
CC compartment after cleavage of the protease recognition sequence. The
CC change in distribution of the fluorescent protein can be detected using
CC imaging methods with a high degree of spatial resolution. The methods and
CC biosensors of the invention can be used to investigate a wide range of
CC cellular activities and to screen compounds which modulate these
CC activities. Biosensors containing a recognition site for caspase, for
CC example, may be used for the screening of compounds which modulate
CC apoptosis, while biosensors containing other protease recognition sites
CC may be used for the detection of proteolytic toxins (such as anthrax
CC lethal factor). The method provides improved target validation and
CC candidate compound optimisation by combining many cell screening formats
CC with fluorescence-based molecular reagents and computer-based feature
CC extraction, data analysis and automation, resulting in increased quantity
CC and speed of data collection and faster evaluation of drug candidates.
CC Sequences AAB22860-B22876 and AAB22936-B22941 represent biosensor fusion
CC proteins produced in an exemplification of the invention. (Updated on 12-
CC SEP-2003 to standardise OS field)
XX Sequence 890 AA;
SQ Query Match 83.5%; Score 1097.5; DB 3; Length 890;
Best Local Similarity 81.4%; Pred. No. 1.6e-82;
Matches 214; Conservative
3;
1 KSENVQDLLLDDVTPSLGLETAGGVMTLKRNTIPTKTQTFTTYSNQPGVLQVY 60

Db 628 KSENVQDLLLDDVTPSLGLETAGGVMTLKRNTIPTKTQTFTTYSNQPGVLQVY 687
Qy 61 EGERAMTKONNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 688 EGERAMTKONNLLGKFLTGIPPPAPRGVPOIEVTFDIDANGILNVSADVSTGKANKITI 747
Qy 121 TNDKRLSKKEIERMVOEAKYKAEDVQERVSQAKNALESYAFNMKSAVEDEGLKQKIS 180
Db 748 TNDKRLSKKEDIERMVOEAKYKAEDKQDKVSSKNSLESYAFNMKATVEDEKLQKGIN 807
Qy 181 EADKKVLDKQCVISWLDANTLAEDKDFEHKKELEOVNPIISGLYQAGG-PG--PG 237
Db 808 DEDKQKILDKCNELIINWLDKQNTAEKEEFHQKLEKVCNPIITKLYQAGGMPGMPG 867
Qy 238 GF--GAQPGKSGSGPTIEVD 258
Db 868 GFGGGAGPPSGGASSGPTIEVD 890
RESULT 71
ABG94501
ID ABG94501 standard; protein; 890 AA.
XX AC ABG94501;
XX DT 27-NOV-2002 (first entry)
XX DE Protease biosensor related biosensor #3.
XX KW Detection; classification; identification; toxin detection; protease;
KW ADP-ribosylating toxin; cytotoxic phospholipase; exfoliative toxin;
XX OS Synthetic.
XX PN US6416959-B1.
XX PD 09-JUL-2002.
XX PF 25-FEB-2000; 2000US-00513783.
XX PR 27-FEB-1997; 97US-00810983.
PR 27-FEB-1998; 98US-00031271.
PR 26-FEB-1999; 99US-0122152P.
PR 08-MAR-1999; 99US-0123399P.
PR 12-JUL-1999; 99US-00352171.
PR 31-AUG-1999; 99US-0151797P.
PR 17-SEP-1999; 99US-00398965.
PR 29-OCT-1999; 99US-00430656.
PR 01-DEC-1999; 99US-0168408P.
PA (GIUL/) GIULIANO K.
PA (KAPU/) KAPUR R.
XX Giuliano K, Kapur R;
XX WPI; 2002-634730/68.
DR N-PSDB; ABS71562.
XX Automated cell-based toxin detection, classification, and/or
PT identification by treating cells involves use of three classes of
PT luminescent reporter molecules such as detectors, classifiers or
PT identifiers.
XX Example 11; Col 291-296; 214pp; English.
XX The invention describes methods of automated detection, classification
CC and identification comprising treating cells containing luminescent
CC reporter molecules (I) in array of locations with a test substance, where
CC (I) are detectors, classifiers or identifiers, imaging cells in each
CC location to obtain luminescent signals and converting optical information
CC into digital data to interpret presence of toxins in the test substance.

CC The method are useful for detection of toxins chosen from proteases, ADP-
 CC ribosylating toxins, cytotoxic phospholipases, and exfoliative toxins.
 CC Three classes of cell-based luminescent reporter molecules such as
 CC detectors, classifiers and identifiers are described and serve as
 CC reporters of toxic threat agents. The first two levels of
 CC characterisation ensure a rapid readout of toxin class without
 CC sacrificing the ability to detect many new mutant toxins or dissect
 CC several complex mixtures of known toxins. This is the amino acid sequence
 CC of a biosensor associated with the protease biosensor of the invention
 XX
 SQ Sequence 890 AA;

Query Match 83.5%; Score 1097.5; DB 5; Length 890;
 Best Local Similarity 81.4%; Pred. No. 1.6e-82;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVQDLLLDVAPISLGLTETAGGVTALIKRNSIPIPTKQIQIPTYSDNQPGVLIQVY 60
 DB 628 KSENVQDLLLDVTPISLGIETAGGVTMLIKRNTIPIPTKQIQIPTYSDNQPGVLIQVY 687
 QY 61 EGERAMTKONNLGRPELSGIPPPAPRGVPOIEVTFDIDANGIILNVTATDKSTGKANKITI 120
 DB 688 EGERAMTKONNLGKLFELTGIPPPAPRGVPOIEVTFDIDANGIILNVAVDKSTGKANKITI 747
 QY 121 TNDKGRLSKEEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDGLKKGKIS 180
 DB 748 TNDKGRLSKEDIERMVQAEKYKAEDKQDKVSSKNLSYAFNMKATVEDEKLQKIN 807
 QY 181 EADKKVLDKQEVISWLDANTLAEDKFEHKELEBOVCNPIISGLYQAGG-PG--PG 237
 DB 808 DEBKQKLDKCNRIINWLDKNQTAKEEPEHQKELEKVCNPIITKLYQAGGMPGMPG 867
 QY 238 GF--GAQGPKGSGSGPTIEVD 258
 DB 868 GPFQGGAPPSGGSGPTIEVD 890

RESULT 72
 ADM05456
 ID ADM05456 standard; protein; 250 AA.
 AC ADM05456;
 XX
 XX 20-MAY-2004 (first entry)
 XX
 XX Human protein of the invention SEQ ID NO:4141.
 XX human; gene therapy; diagnostic marker; pharmaceutical.
 XX Homo sapiens.
 XX
 XX EPI347046-A1.
 XX
 XX 24-SEP-2003.
 XX
 XX 12-APR-2002; 2002EP-00008400.
 XX
 XX 22-MAR-2002; 2002JP-00137785.
 XX
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 XX Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Tamechika I;
 XX Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 XX WPI; 2003-723558/69.
 XX N-PSDB; ADM03013.
 XX
 XX New polynucleotides and polypeptides are useful in gene therapy, for
 XX developing a diagnostic marker or medicines for regulating their
 XX expression and activity, or as a target of gene therapy.
 XX
 XX Claim 1; SEQ ID NO 4141; 305pp; English.

XX The invention relates to a novel human polynucleotide and the encoded
 CC polypeptide. A polynucleotide of the invention may have a use in gene
 CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
 CC as a primer for synthesizing the polynucleotide or as a probe for
 CC detecting the polynucleotide. The polynucleotides ADM0316-ADM03158 are
 CC useful in gene therapy, for developing a diagnostic marker or medicines
 CC for regulating their expression and activity, or as a target of gene
 CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
 CC are useful as pharmaceutical agents. The present sequence represents a
 CC protein sequence of the invention.
 XX
 SQ Sequence 250 AA;

Query Match 83.5%; Score 1097; DB 7; Length 250;
 Best Local Similarity 100.0%; Pred. No. 3.3e-83;
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 46 TTYSDNQPGVLIQVYGERAMTKONNLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNV 105
 DB 38 TTYSDNQPGVLIQVYGERAMTKONNLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNV 97
 QY 106 TATDKSTGKANKITITNDKGRLSKEEIERMVQAEKYKAEDVQRRVSAKNALESYAFN 165
 DB 98 TATDKSTGKANKITITNDKGRLSKEEIERMVQAEKYKAEDVQRRVSAKNALESYAFN 157
 QY 166 MKSAVEDGLKKGKISADKKVLDKQEVISWLDANTLAEDKFEHKELEBOVCNPIIS 225
 DB 158 MKSAVEDGLKKGKISADKKVLDKQEVISWLDANTLAEDKFEHKELEBOVCNPIIS 217
 QY 226 GLYQAGGPGPGFGAQQPKGSGSGPTIEVD 258
 DB 218 GLYQAGGPGPGFGAQQPKGSGSGPTIEVD 250

RESULT 73
 ADS85121
 ID ADS85121 standard; protein; 646 AA.
 XX
 XX ADS85121;
 XX
 XX 18-NOV-2004 (first entry)
 XX
 XX Mouse atopic dermatitis-related protein sequence SeqID123.
 XX atopic dermatitis; gene expression level; skin; inflammation; rash;
 XX dermatological; antiinflammatory; antipsoriatic; psoriasis; mouse;
 XX murine.
 XX Mus musculus.
 XX
 XX WO2004031386-A1.
 XX
 XX 15-APR-2004.
 XX
 XX 01-AUG-2003; 2003WO-JP009808.
 XX
 XX 06-AUG-2002; 2002JP-00229318.
 XX 14-MAY-2003; 2003JP-00136543.
 XX
 XX (GENO-) GENOX RES INC.
 XX (UYJU-) UNIV JUNTENDO.
 XX
 XX Itoh M, Ogawa K, Shinagawa A, Sudo H, Ogawa H, Ra C;
 XX Mitsuishi K;
 XX WPI; 2004-330185/30.
 XX N-PSDB; ADS85120.
 XX
 XX Determination of difference in expression level of specified genes in
 XX inflamed and non-inflamed skin sites for diagnosis and examination of
 XX atopic dermatitis and psoriasis.

PS	Example 1; SEQ ID NO 123; 61pp; Japanese.	PT	treated human C3A liver cell cultures, useful for treating liver disorders.
XX		XX	
CC	This invention relates to a novel method for the examination of atopic dermatitis in which the expression level of specified genes in specimens of skin taken from inflamed (rash) areas and non-inflamed areas is compared and the presence of increased or reduced expression in the inflamed areas determined. The invention may be useful for the development of compounds with a dermatological, antiinflammatory or antipsoriatic activity acting as inhibitors and stimulators of genes involved in atopic dermatitis and psoriasis. The invention may be useful for treatment, prevention, diagnosis and assessment of atopic dermatitis and psoriasis. The present sequence is that of an atopic dermatitis-related protein which was used in the exemplification of the invention.	CC	The invention relates to a composition comprising several cDNAs that are differentially expressed in a liver disorder. The composition is useful for treating liver disorder such as hyperlipidaemia, hypertension, type II diabetes, tumours of the liver and disorders of the inflammatory and immune response. The composition is useful for a high-throughput method of screening several cDNAs. A protein encoded by the cDNA is useful for specifically binds a cDNA. A protein encoded by the cDNA is useful for a high-throughput method for using a protein to screen several molecules or compounds to identify at least one ligand which specifically binds the protein which involves combining the protein encoded by the cDNA with several of molecules or compounds under conditions to allow specific binding, and detecting specific binding between the protein and a molecule or compound, therefore identifying a ligand which specifically binds the protein. The composition is useful for detecting and quantifying differential gene expression, can be used in gene therapy, to formulate prognosis and to design a treatment regimen and to monitor the efficacy of treatment. The present sequence represents the amino acid sequence of a protein encoded by a cDNA differentially expressed in a liver disorder.
XX		XX	
SQ	Sequence 646 AA;	SQ	Sequence 641 AA;
	Query Match 83.3%; Score 1094.5; DB 8; Length 646;		Query Match 83.2%; Score 1093; DB 8; Length 641;
	Best Local Similarity 81.4%; Pred. No. 1.8e-82;		Best Local Similarity 81.5%; Pred. No. 2.4e-82;
	Matches 214; Conservative 23; Mismatches 21; Indels 5; Gaps 3;		Matches 216; Conservative 16; Mismatches 17; Indels 16; Gaps 2;
QY	1 KSENVQDLLLDVAPLSGLGLETAGGVTALIKRNSTIPTKQITFTTYSNPGVLIQY 60	QY	1 KSENVQDLLLDVAPLSGLGLETAGGVTALIKRNSTIPTKQITFTTYSNPGVLIQY 60
DB	384 KSENVQDLLLDVAPLSGLGLETAGGVTALIKRNSTIPTKQITFTTYSNPGVLIQY 443	DB	386 KSENVQDLLLDVAPLSGLGLETAGGVTALIKRNSTIPTKQITFTTYSNPGVLIQY 445
QY	61 EGERAMTKDNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVATDKSTGKANKITI 120	QY	61 EGERAMTKDNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVATDKSTGKANKITI 120
DB	444 EGERAMTKDNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVATDKSTGKANKITI 503	DB	446 EGERAMTKDNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVATDKSTGKANKITI 505
QY	121 TNDKGRLSKEETERMVQAEKYKAEDVQERVSNAKNALESYAFNMKSADVEBGLGKIS 180	QY	121 TNDKGRLSKEETERMVQAEKYKAEDVQERVSNAKNALESYAFNMKSADVEBGLGKIS 180
DB	504 TNDKGRLSKEETERMVQAEKYKAEDVQERVSNAKNALESYAFNMKSADVEBGLGKIN 563	DB	506 TNDKGRLSKEETERMVQAEKYKAEDVQERVSNAKNALESYAFNMKSADVEBGLGKIS 565
QY	181 EADKKKVLKDCQEVISWLDANTLAERKDEFEHKKRKELEQVNCNPIISGLYQAGG-PG--PG 237	QY	181 EADKKKVLKDCQEVISWLDANTLAERKDEFEHKKRKELEQVNCNPIISGLYQAGGPG 240
DB	564 DEDQKILDKNEIISWLDKNCQAEKEEFHQKLEKVCNPIITKLYQSGAGGMPG 623	DB	566 ESDKNKILDKNELLSWLEVNQAEKDEPDHKKRKELEQVNCNPIITKLYQG-----G 616
QY	238 GP--GAQPGKGGSGPTIEVD 258	QY	241 AOGPKGGSG-----SGPTIEVD 258
DB	624 GPPGGGAPPSSGSGPTIEVD 646	DB	617 CTGPACGTGYVPGRPATGPTIEVD 641
RESULT 74		RESULT 75	
AD76908		ADD18948	
ID	ADE76908 standard; protein; 641 AA.	ID	ADD18948 standard; protein; 650 AA.
AC	AC	AC	AC
XX	ADE76908;	XX	ADD18948;
XX		XX	
DT	29-JAN-2004 (first entry)	DT	15-JAN-2004 (first entry)
DE	Human protein expressed in a liver disorder #22.	DE	Human disease related protein SeqID437.
XX	human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;	XX	human; disease state; cytostatic; antiinflammatory; ophthalmological;
KW	tumour; liver; inflammatory disorder; immune response disorder;	KW	antiartherosclerotic; vulnary; gene therapy;
KW	high-throughput screening; differential gene expression; gene therapy.	KW	hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
OS	Homo sapiens.	KW	inflammation; erythropoiesis; glycolysis; gluconeogenesis;
PN	US2003108871-A1.	KW	glucose transport; catecholamine synthesis; iron transport;
XX		KW	nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
PD	12-JUN-2003.	KW	retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
XX		XX	inflammatory condition; wound healing.
PF	30-JUL-2001; 2001US-00919039.	OS	Homo sapiens.
PR	28-JUL-2000; 2000US-0222113P.	XX	
XX	(KASE/) KASER M R.	XX	
PA		XX	
XX	Kaser MR;	XX	
PI		XX	
XX	WPI; 2004-031227/03.	XX	
DR	N-PSDB; ADE76907.	XX	
XX		XX	
FT	Composition comprising several cDNAs that are differentially expressed in		

CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 641 AA;
Query Match 82.7%; Score 1087; DB 7; Length 641;
Best Local Similarity 83.5%; Pred. No. 7.7e-82;
Matches 218; Conservative 17; Mismatches 18; Indels 8; Gaps 3;
QY 1 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSIPTKQTOIFTTYSNDQPGVLIQY 60
DB 386 KSEKVDLLLLDVAPLSGLGTAGGVTALIKRNSIPTKQTOIFTTYSNDQPGVLIQY 445
QY 61 EGERAMTKDNLGRFELSGIPAPRGVQIETVFDIDANGILNVATDSTGKANKITI 120
DB 446 EGERAMTRDNLGRFDLTGIPAPRGVQIETVFDIDANGILNVATDSTGKANKITI 505
QY 121 TNDKGRLSKEEIERMVQEAERYKAEDVQREVRSKNALESYAFNMKSADVEGLKDKITS 180
DB 506 TNDKGRLSKEEIERMVQEAERYKAEDVQREVRSKNALESYAFNMKSADVEGLKDKITS 565
QY 181 EADKKVLDKQCVISWLDANTLAEKDFEHRKKELEQVCNPIISGLYQ-GAGGP--GPG 237
DB 566 ESDKKKILDKCEVLSWLEAQAEKDFHKKKELENMNCNPIITKLYSGGCTGPTCAPG 625
QY 238 GFCAQGPKGSGSGPTIEVD 258
DB 626 -----YTPGRARTGPTIEVD 641
RESULT 79
ID ADD48986
XX ADD48986 standard; protein; 641 AA.
AC ADD48986;
XX
XX 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
XX Rat Protein P55063, SEQ ID NO 14698.
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
XX Rattus norvegicus.
XX Unidentified.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX
XX (GEO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
XX GENBANK; P55063.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Example 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell

comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (described in Table 3 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Query Match 82.7%; Score 1087; DB 7; Length 641;
Best Local Similarity 83.5%; Pred. No. 7.7e-82;
Matches 218; Conservative 17; Mismatches 18; Indels 8; Gaps 3;
QY 1 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSIPTKQTOIFTTYSNDQPGVLIQY 60
DB 386 KSEKVDLLLLDVAPLSGLGTAGGVTALIKRNSIPTKQTOIFTTYSNDQPGVLIQY 445
QY 61 EGERAMTKDNLGRFELSGIPAPRGVQIETVFDIDANGILNVATDSTGKANKITI 120
DB 446 EGERAMTRDNLGRFDLTGIPAPRGVQIETVFDIDANGILNVATDSTGKANKITI 505
QY 121 TNDKGRLSKEEIERMVQEAERYKAEDVQREVRSKNALESYAFNMKSADVEGLKDKITS 180
DB 506 TNDKGRLSKEEIERMVQEAERYKAEDVQREVRSKNALESYAFNMKSADVEGLKDKITS 565
QY 181 EADKKVLDKQCVISWLDANTLAEKDFEHRKKELEQVCNPIISGLYQ-GAGGP--GPG 237
DB 566 ESDKKKILDKCEVLSWLEAQAEKDFHKKKELENMNCNPIITKLYSGGCTGPTCAPG 625
QY 238 GFCAQGPKGSGSGPTIEVD 258
DB 626 -----YTPGRARTGPTIEVD 641
RESULT 80
ID ADD48287
XX ADD48287 standard; protein; 641 AA.
AC ADD48287;
XX
XX 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
XX Rat Protein P55063, SEQ ID NO 13985.
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
XX Rattus norvegicus.
XX Unidentified.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.

14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
(GEO) GEN HOSPITAL CORP.
(FARB) BAYER AG.
Woelf C, D'urso D, Befort K, Costigan M;
WPI; 2003-268312/26.
GENBANK; P55063.
New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
Example 1; Page; 1017pp; English.
The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (described in Table 3 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
Sequence 641 AA;
Query Match 82.7%; Score 1087; DB 7; Length 641;
Best Local Similarity 83.5%; Pred. No. 7.7e-82;
Matches 218; Conservative 17; Mismatches 18; Indels 8; Gaps 3;
QY 1 KSENVQDLLLLDVAPLSGLTAGGVTALIKRNSTIPTKQTOIFTYSDNPGVLIQVY 60
DB 386 KSEKVDLLLLDVAPLSGLTAGGVTALIKRNSTIPTKQTOIFTYSDNPGVLIQVY 445
QY 61 EGERAMTKDNLLGRFELSGIPAPRGVQIETVFDIDANGILNVTATDKSTGKANKITI 120
DB 446 EGERAMTRDNNLLGRFDLGIPIAPRGVQIETVFDIDANGILNVTAMDKSTGKANKITI 505
QY 121 TNDKGRLSKEETRMVQEAERYKAEDVQQRVRSKNALESYAFNMKSAVEDSGLKDKIS 180
DB 506 TNDKGRLSKEETRMVQEAERYKAEDVQQRVRSKNALESYAFNMKSAVEDSGLKDKIS 565
QY 181 EADKKVLDKQCVISWLDANTLAEDPEHKELEQVCNPIISGLYQ-GAGGP--GPG 237
DB 566 ESDKKKILDKCSVLNLAELAEKEEFDRHKELENMNCNPIITKLYQSGCTGPTCAPG 625
QY 238 GFCAQPGKSGSGPTIEVD 258
DB 626 -----YTPGRARTGPTIEVD 641

RESULT 81
ADD45650
ID ADD45650 standard; protein; 641 AA.
XX
AC ADD45650;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein CAA54424, SEQ ID NO 11317.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury, CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woelf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; CAA54424.
XX
PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (described in Table 3 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
Sequence 641 AA;
Query Match 82.7%; Score 1087; DB 7; Length 641;
Best Local Similarity 83.5%; Pred. No. 7.7e-82;
Matches 218; Conservative 17; Mismatches 18; Indels 8; Gaps 3;
QY 1 KSENVQDLLLLDVAPLSGLTAGGVTALIKRNSTIPTKQTOIFTYSDNPGVLIQVY 60

QY 1 KSENVQDLLLLDVAPLSGLTAGGVTALIKRNSTIPTKQTOIFTYSDNPGVLIQVY 60


```

Db 386 KSEKVDLLLDVAPLSGLIETAGGVTMLIKNSTIPTKQITFTTSDNQPGLVLIQVY 445
QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATATDKSTGKANKITI 120
Db 446 EGERAMTRDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATATDKSTGKANKITI 505
QY 121 TNDKGRLSKEETIERMVQEAERYKAEDQREKTAANKNALESYAFNMKSASVDEGLKGLIS 180
Db 506 TNDKGRLSKEETIERMVQEAERYKAEDQREKTAANKNALESYAFNMKSASVDEGLKGLIS 565
QY 181 EADKKVLDKQCEVSWLDANTLAERKDEFEHKKRKELEQVNCNPIISGLYQ--GAGP 237
Db 566 ESDKKILDKCEVSWLQANLAEKEEFDHKKRKELENCNPIITKLYQSGCTGPTCAPG 625
QY 238 GFQAQPKGGSGGPTIEVD 258
Db 626 -----YTPGRARTGPTIEVD 641

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RESULT 82
 AAR03927
 ID AAR03927 standard; protein; 646 AA.
 AC AAR03927;
 XX
 XX 27-AUG-2003 (revised)
 DT 30-AUG-1990 (first entry)
 XX
 XX Rat HSP (rathsp70).
 XX Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
 XX Rattus rattus.
 XX WO9002564-A.
 XX 22-MAR-1990.
 XX 12-SEP-1988; 88US-00243474.
 XX 12-SEP-1988; 88US-00243474.
 XX (CODON) CODON.
 XX Dragon E, Faulds D, Sias S;
 DR WPI; 1990-115820/15.

Proteins homologous to heat shock proteins of Trypanosoma cruzi - used in vaccines and diagnosis for species of e.g. muco-plasma or mycobacteria.
 PS Disclosure; Fig 2.1-2.14; 86pp; English.

Fig. 2 provides an alignment of heat shock proteins from a variety of organisms: 1. M. hyopneumoniae (Mhyhsp70 - AAR03922); 2. Bacillus megaterium (Bmeghsp70 - AAR03923); 3. E. coli (dnaK - AAR03924); 4. T. cruzi (tc70kd - AAR03925); 5. T. cruzi (AAR03926); 6. Rat rattus (rathsp70 - AAR03927); 7. Xenopus laevis (xl170 - AAR03928); 8. Homo sapiens (huhhsp70 - AAR03929); 9. Gallus gallus (chkhsp70 - AAR03930); 10. Zea mays (mzehsp70 - AAR03931); 11. Serratia marcescens (smahsp70 - AAR03932). The proteins having homology to hsp's of T. cruzi can be used in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and Mycobacteria species. (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 646 AA;
 Query Match 82.5%; Score 1084.5; DB 2; Length 646;
 Best Local Similarity 81.0%; Pred. No. 1.3e-81;
 Matches 213; Conservative 22; Mismatches 22; Indels 5; Gaps 3;

QY 1 KSENVQDLLLDVAPLSGLIETAGGVTMLIKNSTIPTKQITFTTSDNQPGLVLIQVY 60

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Db 384 KSENVQDLLLDVAPLSGLIETAGGVTMLIKNSTIPTKQITFTTSDNQPGLVLIQVY 443
QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATATDKSTGKANKITI 120
Db 444 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATATDKSTGKANKITI 503
QY 121 TNDKGRLSKEETIERMVQEAERYKAEDQREKTAANKNALESYAFNMKSASVDEGLKGLIS 180
Db 504 TNDKGRLSKEETIERMVQEAERYKAEDQREKTAANKNALESYAFNMKSASVDEGLKGLIS 563
QY 181 EADKKVLDKQCEVSWLDANTLAERKDEFEHKKRKELEQVNCNPIISGLYQAGG-PG 237
Db 564 ESDKKILDKCEVSWLQANLAEKEEFDHKKRKELENCNPIITKLYQSGAGMPGMPG 623
QY 238 GF--GAQPKGGSGGPTIEVD 258
Db 624 GFPGGAPPGSGGSGPTIEVD 646

```

RESULT 83
 ADM05931
 ID ADM05931 standard; protein; 413 AA.
 AC ADM05931;
 XX
 XX 20-MAY-2004 (first entry)
 DT Human protein of the invention SEQ ID NO:4616.
 DE human; gene therapy; diagnostic marker; pharmaceutical.
 XX Homo sapiens.
 XX EP1347046-A1.
 XX 24-SEP-2003.
 XX 12-APR-2002; 2002EP-00008400.
 XX 22-MAR-2002; 2002JP-00137785.
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.

Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 WPI; 2003-723558/69.
 DR N-PSDB; ADM03488.

New polynucleotides and polypeptides are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.

Claim 1; SEQ ID NO 4616; 305pp; English.

The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a protein sequence of the invention.

XX Sequence 413 AA;
 Query Match 80.6%; Score 1059.5; DB 7; Length 413;
 Best Local Similarity 79.1%; Pred. No. 8.6e-80;
 Matches 204; Conservative 24; Mismatches 25; Indels 5; Gaps 1;

QY 1 KSNVODLLLDVAPLSGLGLETAGGVTALIKNSTIPTKQTOIFTTYSNQPGVLIQVY 60
 DB 161 KSNVODLLLDVAPLSGLGLETAGGVTALIKNSTIPTKQTOIFTTYSNQPGVLIQVY 220
 QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 221 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 280
 QY 121 TNDKGRSLKEEIERMVOEAEKYKAEDVORERSAKNALESYAFNMKSAVEDGLGKGIS 180
 DB 281 TNDKGRSLKDDIDRMVQEAERYKSEDEANRDRVAANKNALESYTYNIKQTVDEKLGKIS 340
 QY 181 EADKKVLDKQCVISWLDANTLAEDKDEFEHKKKELEQVNCNPIISGLYQAGGPGPGGFG 240
 DB 341 EQDKNKILDKQCVINWLDNRQMAEKDEYEHKKKELEQVNCNPIISGLYQAGGPGGSGGGG 400
 QY 241 AQPGKGGSGGPTIEVD 258
 DB 401 S-----GASGGPTIEVD 413
 RESULT 84
 ID ADE63493 standard; protein; 639 AA.
 XX
 AC ADE63493;
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein P54652, SEQ ID NO 9437.
 XX
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 OS Homo sapiens.
 XX
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX
 DR WPI; 2003-268312/26.
 DR GENBANK; P54652.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the

CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 639 AA;
 Query Match 80.6%; Score 1059.5; DB 7; Length 639;
 Best Local Similarity 79.1%; Pred. No. 1.5e-79;
 Matches 204; Conservative 24; Mismatches 25; Indels 5; Gaps 1;
 QY 1 KSNVODLLLDVAPLSGLGLETAGGVTALIKNSTIPTKQTOIFTTYSNQPGVLIQVY 60
 DB 387 KSNVODLLLDVAPLSGLGLETAGGVTALIKNSTIPTKQTOIFTTYSNQPGVLIQVY 446
 QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 447 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 506
 QY 121 TNDKGRSLKEEIERMVOEAEKYKAEDVORERSAKNALESYAFNMKSAVEDGLGKGIS 180
 DB 507 TNDKGRSLKDDIDRMVQEAERYKSEDEANRDRVAANKNALESYTYNIKQTVDEKLGKIS 566
 QY 181 EADKKVLDKQCVISWLDANTLAEDKDEFEHKKKELEQVNCNPIISGLYQAGGPGPGGFG 240
 DB 567 EQDKNKILDKQCVINWLDNRQMAEKDEYEHKKKELEQVNCNPIISGLYQAGGPGGSGGGG 626
 QY 241 AQPGKGGSGGPTIEVD 258
 DB 627 S-----GASGGPTIEVD 639
 RESULT 85
 ID ADJ69917 standard; protein; 639 AA.
 XX
 AC ADJ69917;
 DT 06-MAY-2004 (first entry)
 XX
 DE Human heat mitochondrial protein as a therapeutic target SeqID1723.
 XX
 DE mitochondria; human; screening assay; diabetes mellitus;
 KW Huntington's disease; osteoarthritis;
 KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO2003087768-A2.
 XX
 PD 23-OCT-2003.
 XX
 PF 04-APR-2003; 2003WO-US010870.
 XX
 PR 12-APR-2002; 2002US-0372843P.
 PR 17-JUN-2002; 2002US-0389987P.
 PR 20-SEP-2002; 2002US-0412418P.
 XX
 PA (MITO-) MITOKOR.

PA (BUCK-) BUCK INST AGE RES.
 XX
 PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 PI Warnock DE;
 XX
 XX WPI; 2003-845369/78.
 XX
 XX Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function,
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.
 XX
 XX Claim 1; SEQ ID NO 1723; 180pp; English.
 XX
 XX This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, nootropic, antidiabetic,
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 CC cytotatic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.
 XX
 XX SQ Sequence 639 AA;
 XX
 XX Query Match 80.6%; Score 1059.5; DB 7; Length 639;
 XX Best Local Similarity 79.1%; Pred. No. 1.5e-79;
 XX Matches 204; Conservative 24; Mismatches 25; Indels 5; Gaps 1;
 XX
 XX 1 KSENVQDLLLLDVAPLSGLGLETAGGVMTALIKRNSTPTKQTQIFTTYSNQPGLVIOVY 60
 XX 387 KSENVQDLLLLDVTPLSGLGLETAGGVMTPLIKENTTPTKQTFTTYSNQSGLVQVY 446
 XX
 XX 61 EGERAMTKNNLLGRFELSGIPAPRGVQIETVFDIDANGILNVTAATKSTGKANKITI 120
 XX 447 EGERAMTKNNLLGKFDLTGIPAPRGVQIETVFDIDANGILNVTAADKSTGKANKITI 506
 XX
 XX 121 TNDKGRLSKEEIERMWQEAERYKAEDEVQERVSAAKNALSVAFNPKMSAVEDEGLKGIS 180
 XX 507 TNDKGRLSKDDIDRMVQEAERYKSEDEANDRVAANKNALESYTYNIKQTVDEKLRGIS 566
 XX
 XX 181 EADKKVLDKQCEVISWLDANTLAEKDEFHKKRKELEQVCNPIISGLYQAGGPGGPGF 240
 XX 567 EQDKNKILDKQCEVINWLDNRQMAEKDEYEHKQELERVNCNPIISKLYQGGPGGGGGG 626
 XX
 XX 241 AQPGKGGSGSGPTIEVD 258
 XX 627 S-----GASGGPTIEVD 639
 XX
 XX RESULT 86
 XX ADJ69887
 XX ID ADJ69887 standard; protein; 639 AA.
 XX
 XX AC ADJ69887;
 XX
 XX 06-MAY-2004 (first entry)
 XX
 XX Human heat mitochondrial protein as a therapeutic target SeqID1693.
 XX
 XX mitochondrial; human; screening assay; diabetes mellitus;
 XX Huntington's disease; osteoarthritis;
 XX Leber's hereditary optic neuropathy; LHON;
 XX mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 XX myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 XX neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;

KW osteopathic; ophthalmological; cytotatic.
 XX Homo sapiens.
 XX WO2003087768-A2.
 XX
 XX 23-OCT-2003.
 XX
 XX 04-APR-2003; 2003WO-US010870.
 XX
 XX 12-APR-2002; 2002US-0372843P.
 XX
 XX 17-JUN-2002; 2002US-0389987P.
 XX
 XX 20-SEP-2002; 2002US-0412418P.
 XX
 XX (MITO-) MITOKOR.
 XX (BUCK-) BUCK INST AGE RES.
 XX
 XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 XX Warnock DE;
 XX
 XX WPI; 2003-845369/78.
 XX
 XX Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function,
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.
 XX
 XX Claim 1; SEQ ID NO 1693; 180pp; English.
 XX
 XX This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, nootropic, antidiabetic,
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 CC cytotatic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.
 XX
 XX SQ Sequence 639 AA;
 XX
 XX Query Match 80.6%; Score 1059.5; DB 7; Length 639;
 XX Best Local Similarity 79.1%; Pred. No. 1.5e-79;
 XX Matches 204; Conservative 24; Mismatches 25; Indels 5; Gaps 1;
 XX
 XX 1 KSENVQDLLLLDVAPLSGLGLETAGGVMTALIKRNSTPTKQTQIFTTYSNQPGLVIOVY 60
 XX 387 KSENVQDLLLLDVTPLSGLGLETAGGVMTPLIKENTTPTKQTFTTYSNQSGLVQVY 446
 XX
 XX 61 EGERAMTKNNLLGRFELSGIPAPRGVQIETVFDIDANGILNVTAATKSTGKANKITI 120
 XX 447 EGERAMTKNNLLGKFDLTGIPAPRGVQIETVFDIDANGILNVTAADKSTGKANKITI 506
 XX
 XX 121 TNDKGRLSKEEIERMWQEAERYKAEDEVQERVSAAKNALSVAFNPKMSAVEDEGLKGIS 180
 XX 507 TNDKGRLSKDDIDRMVQEAERYKSEDEANDRVAANKNALESYTYNIKQTVDEKLRGIS 566
 XX
 XX 181 EADKKVLDKQCEVISWLDANTLAEKDEFHKKRKELEQVCNPIISGLYQAGGPGGPGF 240
 XX 567 EQDKNKILDKQCEVINWLDNRQMAEKDEYEHKQELERVNCNPIISKLYQGGPGGGGGG 626
 XX
 XX 241 AQPGKGGSGSGPTIEVD 258
 XX 627 S-----GASGGPTIEVD 639
 XX
 XX RESULT 87

ADN04525
 ID ADN04525 standard; protein; 639 AA.
 AC ADN04525;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Antipsoriatic protein sequence #455.
 XX
 KW antipsoriatic; gene therapy; psoriasis; diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO2004028479-A2.
 XX
 PD 08-APR-2004.
 XX
 PF 25-SEP-2003; 2003WO-US030907.
 XX
 PR 25-SEP-2002; 2002US-0414006P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood W;
 PI Wu TD;
 XX
 XX WPI; 2004-305105/28.
 DR N-PSDB; ADN04524.
 XX
 XX New PRO nucleic acid or polypeptide, useful for preparing a
 PT pharmaceutical composition for diagnosing or treating psoriasis in a
 PT mammal.
 XX
 PS Claim 9; SEQ ID NO 919; 3069pp; English.
 XX
 CC The invention relates to novel polynucleotide and polypeptides for
 CC treating psoriasis or a sequence having at least 80% identity to the
 CC above sequences. The nucleic acid is useful for preparing a composition
 CC for diagnosing or treating psoriasis in a mammal. This sequence
 CC corresponds to one of the polypeptides of the invention.
 XX
 SQ Sequence 639 AA;
 Query Match 80.6%; Score 1059.5; DB 8; Length 639;
 Best Local Similarity 79.1%; Pred. No. 1.5e-79;
 Matches 204; Conservative 24; Mismatches 25; Indels 5; Gaps 1;
 QY 1 KSENVQDLILLDVAPLSGLGTAGGVTALIKRNTIPTKQTQIFTTYSNQSGVLQVY 60
 DB 387 KSENVQDLILLDVTPLSGLGTAGGVTPLIKRNTIPTKQTQIFTTYSNQSGVLQVY 446
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 447 EGERAMTKNNLLGKFLDTGIPAPRGVPOIEVTFDIDANGILNVTAAADSTGKANKITI 506
 QY 121 TNDKGRLSKEIEIRMQEAEKKAEDVQRERVSANNALESYAFNMKMSAYEDELGKGKIS 180
 DB 507 TNDKGRLSKDDIDRMVQEAERYKSEDEANRDRVAANKNALESYTYNIQTVEDEKLRGKIS 566
 QY 181 EADKKVLDKQCVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQGAGPGPGGFG 240
 DB 567 EQDKNKILDKQCVINWLDNRNMAEKDEYHKKELERVCNPIISKLYQGPGGGGGGG 626
 QY 241 AQGPKGGSGSGPTIEVD 258
 DB 627 S-----GASGGPTIEVD 639
 RESULT 88
 AAR43002
 ID AAR43002 standard; protein; 633 AA.
 XX
 AC AAR43002;

XX
 DT 25-MAR-2003 (revised)
 DT 20-MAY-1994 (first entry)
 XX
 DE Mouse SLIP1 homologue HSC70B.
 XX
 KW Sulphoglycolipid immobilising protein 1; sperm plasma membrane;
 KW mouse homologue; HSC70B; mammalian; infertility; mycoplasma;
 KW anti-SLIP1 antibody.
 XX
 OS Mus musculus.
 XX
 PN WO9321954-A1.
 XX
 PD 11-NOV-1993.
 XX
 PF 22-APR-1993; 93WO-US003816.
 XX
 PR 24-APR-1992; 92US-00873961.
 XX
 PA (BERL-) BERLEX LAB INC.
 PA (OTTA-) OTTAWA CIVIC HOSPITAL.
 XX
 PI Paulde DH, Lingwood CA, Tanphaichitr N;
 XX
 XX WPI; 1993-368422/46.
 XX
 CC Mammalian fertilisation decrease for detecting and treating infertility -
 CC using sulpho glyco lipid immobilising protein 1-sulphated-glyco moiety
 CC interfering compsn., for mycoplasma infection treatment.
 XX
 PS Claim 2; Page 60-62; 77pp; English.
 XX
 CC The likelihood of mammalian fertilisation is decreased by contacting a
 CC gamete with a sulphoglycolipid immobilising protein 1 (SLIP1)/ sulphated
 CC glyco-moiety interfering composition. The interfering compsn. is e.g.
 CC SLIP1 (or analogues such as the mouse SLIP1 analogue "HSC70B" comprising
 CC the amino acid sequence AAR43002). SLIP1 binds to
 CC sulphogalactosylglycerolipid (SGG), a testicular glycolipid, and to
 CC sulphogalactosyl ceramide. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 633 AA;
 Query Match 80.3%; Score 1054.5; DB 2; Length 633;
 Best Local Similarity 79.1%; Pred. No. 3.9e-79;
 Matches 204; Conservative 23; Mismatches 20; Indels 11; Gaps 2;
 QY 1 KSENVQDLILLDVAPLSGLGTAGGVTALIKRNTIPTKQTQIFTTYSNQSGVLQVY 60
 DB 387 KSENVQDLILLDVTPLSGLGTAGGVTPLIKRNTIPTKQTQIFTTYSNQSGVLQVY 446
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 447 EGERAMTKNNLLGKFLDTGIPAPRGVPOIEVTFDIDANGILNVTAAADSTGKANKITI 506
 QY 121 TNDKGRLSKEIEIRMQEAEKKAEDVQRERVSANNALESYAFNMKMSAYEDELGKGKIS 180
 DB 507 TNDKGRLSKDDIDRMVQEAERYKSEDEANRDRVAANKNALESYTYNIQTVEDEKLRGKIS 566
 QY 181 EADKKVLDKQCVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQGAGPGPGGFG 240
 DB 567 EQDKNKILDKQCVINWLDNRNMAEKDEYHKKELERVCNPIISKLYQGPGGGGGGG 626
 QY 241 AQGPKGGSGSGPTIEVD 258
 DB 621 -----GSSGGPTIEVD 633
 RESULT 89
 ADE63491
 ID ADE63491 standard; protein; 633 AA.
 XX
 AC ADE63491;

QY 61 EGERAMTKDNLLGRFELSGIPPAQGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 445 EGERAMTKDNLLGRFELSGIPPAQGVPOIEVTFDIDANGILNVATDKSTGKANKITI 504
 QY 121 TNDKGRSLKKEIEIRMVQEAKEYKAEDVQQRERSAKNALESYAFNMKSAVEDEGLKGIS 180
 DB 505 TNDKGRSLKKEIEIRMVQEAKEYKAEDVQQRERSAKNALESYAFNMKSAVEDEGLKGIS 564
 QY 181 EADKKVLDKQEVISWLDANTLAEKDEFEHKEKELEQVCPNPIISGLYQAGAGPG--PGG 238
 DB 565 DEDKRTISEKCTQVSWLENNQLAEKEEYAFQOKLEKVKQPIITKLYQG-GVPGGVPGG 623
 QY 239 P-----GAQPKGSGSGPTIEVD 258
 DB 624 MPGSSGAQARQGN-SGPTIEVD 647
 RESULT 91
 AAR03930
 ID AAR03930 standard; protein; 634 AA.
 XX AC AAR03930;
 XX AC
 DT 30-AUG-1990 (first entry)
 XX DT
 DE Gallus gallus HSP (chkhsp70).
 XX DE
 KW Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
 XX KW
 OS Gallus gallus.
 XX OS
 FH Key Location/Qualifiers
 FT Misc-difference 634
 FT /note= "residue given as "O" in specification"
 XX FT
 XX WQ0902564-A.
 XX PN
 XX 22-MAR-1990.
 XX PD
 XX 12-SEP-1988; 88US-00243474.
 XX PF
 XX 12-SEP-1988; 88US-00243474.
 XX PR
 XX (CODON-) CODON.
 XX PA
 XX Dragon E, Faulds D, Sias S;
 XX PI
 XX WPI; 1990-115820/15.
 XX DR
 XX Proteins homologous to heat shock proteins of Trypanosoma cruzi - used in
 PT vaccines and diagnosis for species of e.g. muco-plasma or mycobacteria.
 PT
 XX Disclosure; Fig 2.1-2.14; 86pp; English.
 XX PS
 XX According to the legend of Fig 2, the G. gallus HSP sequence has 635
 CC amino acid residues, the sequence itself has only 634, including "O" (?)
 CC at position 634. Fig. 2 provides an alignment of heat shock proteins from
 CC a variety of organisms: 1. M.hypopneumoniae (Mhysp70 - AAR03922); 2.
 CC Bacillus megaterium (Bmehsp70 - AAR03923); 3. E. coli (dnaK - AAR03924);
 CC 4. T. cruzi (tc70kd - AAR03925); 5. T. cruzi (AAR03926); 6. Rat rattus
 CC (rathsp70 - AAR03927); 7. Xenopus laevis (xl170 - AAR03928); 8. Homo
 CC sapiens (humhsp70 - AAR03929); 9. Gallus gallus (chkhsp70 - AAR03930);
 CC 10. Zea mays (mzehsp70 - AAR03931); 11. Serratia marcescens (smahsp70 -
 CC AAR03932). The proteins having homology to hsp's of T. cruzi can be used
 CC in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
 CC Mycobacteria species
 XX CC
 SQ Sequence 634 AA;

Query Match 78.8%; Score 1035.5; DB 2; Length 634;
 Best Local Similarity 79.5%; Pred. No. 1.5e-77;
 Matches 205; Conservative 23; Mismatches 19; Indels 11; Gaps 3;

QY 1 KSENVQDLLLLDVAPISLGLETAGGVTALIKNSTIPTKQTOIFTTYSNQPGVLQVY 60
 DB 387 KSENVQDLLLLDVAPISLGLETAGGVTALIKNSTIPTKQTOIFTTYSNQSSVLQVY 446
 QY 61 EGERAMTKDNLLGRFELSGIPPAQGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 447 EGERAMTKDNLLGRFELSGIPPAQGVPOIEVTFDIDANGILNVATDKSTGKANKITI 506
 QY 121 TNDKGRSLKKEIEIRMVQEAKEYKAEDVQQRERSAKNALESYAFNMKSAVEDEGLKGIS 180
 DB 507 TNDKGRSLKKEIEIRMVQEAKEYKAEDVQQRERSAKNALESYAFNMKSAVEDEGLKGIS 566
 QY 181 EADKKVLDKQEVISWLDANTLAEKDEFEHKEKELEQVCPNPIISGLYQAGAGPGGPG 240
 DB 567 DQDKQKVLKQEVISWLDANTLAEKDEFEHKEKELEQVCPNPIISGLYQAGAGPGGPG 620
 QY 241 AQGPKGSGSGPTIEVD 258
 DB 621 A-----GGSG-GPTIEVD 633
 RESULT 92
 ADN23580
 ID ADN23580 standard; protein; 640 AA.
 XX AC ADN23580;
 XX AC
 DT 02-DEC-2004 (first entry)
 XX DT
 DE Bacterial polypeptide #6233.
 XX DE
 KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX KW
 OS Bacteria.
 XX OS
 XX US2003233675-A1.
 XX PN
 XX 18-DEC-2003.
 XX PD
 XX 20-FEB-2003; 2003US-00369493.
 XX PF
 XX 21-FEB-2002; 2002US-0360039P.
 XX PR
 XX (CAOY/) CAO Y.
 XX (HINK/) HINKLE G J.
 XX (SLAT/) SLATER S C.
 XX (CHEN/) CHEN X.
 XX (GOLD/) GOLDMAN B S.
 XX PA
 XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX PI
 XX WPI; 2004-061375/06.
 XX DR
 XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX PT
 XX Claim 1; SEQ ID NO 6233; 122pp; English.
 XX PS
 XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the

CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

SQ Sequence 640 AA;
 Query Match 78.7%; Score 1034; DB 8; Length 640;
 Best Local Similarity 77.9%; Pred. No. 2e-77;
 Matches 201; Conservative 21; Mismatches 34; Indels 2; Gaps 1;
 QY 1 KSNVODLLLDVAPLSGLTAGGVTALIKNSTIPTKQTIPTTYSNDQPGVLIQVY 60
 DB 385 KSEAVQDLLLLDVAPLSGLTAGGVTALIKNSTIPTKQTIPTTYSNDQPGVLIQVY 444
 QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 445 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 504
 QY 121 TNDKGRLSKEEIERMVQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDEGLKGLIS 180
 DB 505 TNDKGRLSKDDIERMVNEAEKYKADDEAQDRIGAKNGLESYAFNLKQTIEDKDKLIS 564
 QY 181 EADKKVLDKQEVISWLDANTLAEDKDEPHKKELEQVNCNPIISGLYQAGGPGG 240
 DB 565 PEDKKIEDKDEILKWLDSNQTAEKEEFHQKLEGLANPIISKLYSAGGAPPG--A 622
 QY 241 AQCPKGGSGSGPTIEVD 258
 DB 623 APCGAAGGAGGPTIEVD 640

RESULT 93
 AAR03928
 ID AAR03928 standard; protein; 647 AA.
 XX
 AC AAR03928;
 XX
 DT 30-AUG-1990 (first entry)
 XX
 DE Xenopus laevis HSP (xl70).
 XX
 KW Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
 XX
 OS Xenopus laevis.
 XX
 PN WO9002564-A.
 XX
 PD 22-MAR-1990.
 XX
 PF 12-SEP-1988; 88US-00243474.
 XX
 PR 12-SEP-1988; 88US-00243474.
 XX
 XX (CODON) CODON.
 PA
 XX Dragon E, Pauls D, Sias S;
 PI
 XX WPI; 1990-115820/15.
 DR
 XX Proteins homologous to heat shock proteins of Trypanosoma cruzi - used in

PT vaccines and diagnosis for species of e.g. muco-plasma or mycobacteria.
 XX Disclosure; Fig 2.1-2.14; 86pp; English.
 XX
 CC Fig. 2 provides an alignment of heat shock proteins from a variety of
 CC organisms: 1. M.hypneumonidae (Mhysp70 - AAR03922); 2. Bacillus
 CC megaterium (Bmehsp70 - AAR03923); 3. E. coli (dnaK - AAR03924); 4. T.
 CC cruzi (tc70kd - AAR03925); 5. T. cruzi (AAR03926); 6. Rat rattus
 CC (rathsp70 - AAR03927); 7. Xenopus laevis (xl70 - AAR03928); 8. Homo
 CC sapiens (humhsp70 - AAR03929); 9. Gallus gallus (chkhsp70 - AAR03930);
 CC 10. Zea mays (mzhsp70 - AAR03931); 11. Serratia marcescens (smahsp70 -
 CC AAR03932). The proteins having homology to hsp's of T. cruzi can be used
 CC in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
 CC Mycobacteria species
 XX
 SQ Sequence 647 AA;

Query Match 78.5%; Score 1031.5; DB 2; Length 647;
 Best Local Similarity 78.1%; Pred. No. 3.3e-77;
 Matches 207; Conservative 26; Mismatches 23; Indels 9; Gaps 4;
 QY 1 KSNVODLLLDVAPLSGLTAGGVTALIKNSTIPTKQTIPTTYSNDQPGVLIQVY 60
 DB 385 KSNVODLLLDVAPLSGLTAGGVTALIKNSTIPTKQTIPTTYSNDQPGVLIQVY 444
 QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 445 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 504
 QY 121 TNDKGRLSKEEIERMVQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDEGLKGLIS 180
 DB 505 TNDKGRLSKDDIERMVNEAEKYKADDEAQDRIGAKNGLESYAFNLKQTIEDKDKLIS 564
 QY 181 EADKKVLDKQEVISWLDANTLAEDKDEPHKKELEQVNCNPIISGLYQAGGPG--PGG 238
 DB 565 DEDKRTISKCTQVVISWLENNQLAEKEEYAFQKLEKVCQPIITKLYQG-GVPGGVP 623
 QY 239 F-----GAQCPKGGSGSGPTIEVD 258
 DB 624 MPGSSCGAQAQGGN-SGPTIEVD 647

RESULT 94
 ABB60514
 ID ABB60514 standard; protein; 651 AA.
 XX
 AC ABB60514;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 8334.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US009231.
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX
 XX (PEKE) PE CORP NY.
 PA
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI
 XX WPI; 2001-656860/75.
 DR
 XX N-PSDB; ABL04617.
 XX

PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.

PS Disclosure; SEQ ID NO 8334; 21pp + Sequence Listing; English.

XX

CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins (AB57737-
CC AB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at fip.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 651 AA;

Query Match 78.4%; Score 1030; DB 4; Length 651;
Best Local Similarity 74.3%; Pred. No. 4.5e-77;
Matches 199; Conservative 28; Mismatches 31; Indels 10; Gaps 2;

QY 1 KSENVQDLLLDVAPLSGLGLETAGGVTALIKRNSIPTTKQTQIFTTYSNQPGVLIQVY 60
DB 384 KSEVQDLLLLDVTPLSGLGLETAGGVTALIKRNTTPTTKQTQIFTTYSNQPGVLIQVY 443

QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 444 EGERAMTKNNLLGKLFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 503

QY 121 TNDKGRLSKEEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDGLKKGKIS 180
DB 504 TNDKGRLSKEDIERMVNEAEKYRNEDEKQETIAAKNGLESYCFNMKATLDEDNLTKIS 563

QY 181 EADKKVLDKQEVISWLDANTLAEKDFEHKKKELEQVCNPIISGLYQGA-----G 232
DB 564 DSDRTTILDKCNETIKWLDANLADKEEYEHKQKELEGVCNPIITKLYQAGFPFGMPG 623

QY 233 GPG--PGGFGAQPFGSGSGPTIEVD 258
DB 624 GPGMGGAAGAAGAGGAGPTIEVD 651

RESULT 96
ADQ89618
ID ADQ89618 standard; protein; 651 AA.
AC ADQ89618;
XX
XX 21-OCT-2004 (first entry)
DE Antagonist of cell cycle progression polypeptide #24.
XX
XX Cytostatic; cancer; cell division cycle; mitosis; meiosis;
KW cell cycle progression.
XX Drosophila melanogaster.
OS
XX WO2004063362-A2.
XX
XX 29-JUL-2004.
XX
XX 31-DEC-2003; 2003WO-GB005635.
XX
XX 10-JAN-2003; 2003US-0439123P.
PR 06-MAY-2003; 2003US-0468402P.
XX
XX (CYCL-) CYCLACEL LTD.
XX
XX Glover D, Bell G, Frenz L, Midgley C;
PI WPI; 2004-544089/52.
XX

DR N-PSDB; ADQ89617.
XX
PT New cell cycle progression genes and proteins for modulating cell cycle
PT progression in cells, for preventing, treating or diagnosing cell
PT proliferative diseases (e.g. cancer) or for identifying modulators of
PT mitosis or meiosis.
XX
XX Claim 2; SEQ ID NO 48; 461pp; English.
PS
XX The present invention relates to a polynucleotide for preventing,
XX treating or diagnosing a disease in an individual. The composition or the
CC polypeptide, polynucleotide or RNA precursor, or antibody is useful for
CC diagnosing, preventing or treating diseases (e.g. cell proliferative
CC diseases such as cancer) in an individual. These may also be used for
CC identifying substances capable of binding to or modulating the function
CC of the polypeptide, capable of affecting the function of the
CC corresponding gene, or capable of inhibiting the cell division cycle or
CC cell cycle progression, preferably mitosis and/or meiosis. The present
CC sequence represents an antagonist of cell cycle progression protein
XX sequence 651 AA;
SQ

Query Match 78.4%; Score 1030; DB 8; Length 651;
Best Local Similarity 74.3%; Pred. No. 4.5e-77;
Matches 199; Conservative 28; Mismatches 31; Indels 10; Gaps 2;

QY 1 KSENVQDLLLDVAPLSGLGLETAGGVTALIKRNSIPTTKQTQIFTTYSNQPGVLIQVY 60
DB 384 KSEVQDLLLLDVTPLSGLGLETAGGVTALIKRNTTPTTKQTQIFTTYSNQPGVLIQVY 443

QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 444 EGERAMTKNNLLGKLFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 503

QY 121 TNDKGRLSKEEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDGLKKGKIS 180
DB 504 TNDKGRLSKEDIERMVNEAEKYRNEDEKQETIAAKNGLESYCFNMKATLDEDNLTKIS 563

QY 181 EADKKVLDKQEVISWLDANTLAEKDFEHKKKELEQVCNPIISGLYQGA-----G 232
DB 564 DSDRTTILDKCNETIKWLDANLADKEEYEHKQKELEGVCNPIITKLYQAGFPFGMPG 623

QY 233 GPG--PGGFGAQPFGSGSGPTIEVD 258
DB 624 GPGMGGAAGAAGAGGAGPTIEVD 651

RESULT 96
AAM48711
ID AAM48711 standard; protein; 643 AA.
AC AAM48711;
XX
XX 21-MAR-2002 (first entry)
DT Human schizophrenia/SCZ associated protein HSP70B SEQ ID NO 2.
XX
XX Human; chromosome 1q22; SCZ; schizophrenia; in utero screening;
KW gene therapy; heat shock protein 70B; HSP70B.
XX
XX Homo sapiens.
OS
XX WO200190412-A1.
XX
XX 29-NOV-2001.
PD
XX 23-APR-2001; 2001WO-US013086.
PF
XX 21-APR-2000; 2000US-0198900P.
PR
XX (RUTP) UNIV RUTGERS STATE NEW JERSEY.
XX

XX AC ADE77039;
XX DT 29-JAN-2004 (first entry)
XX DE Human protein expressed in a liver disorder #57.
XX KW human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;
XX KW tumour; liver; inflammatory disorder; immune response disorder;
XX KW high-throughput screening; differential gene expression; gene therapy.
XX OS Homo sapiens.
XX PN US2003108871-A1.
XX PD 12-JUN-2003.
XX PF 30-JUL-2001; 2001US-00919039.
XX PR 28-JUL-2000; 2000US-0222113P.
XX PA (KASE/) KASER M R.
XX PI Kaser MR;
XX DR WPI; 2004-031227/03.
XX DR N-PSDB; ADE77038.
XX PT Composition comprising several cDNAs that are differentially expressed in
XX PT treated human C3A liver cell cultures, useful for treating liver
XX disorders.
XX PS Claim 1; SEQ ID NO 204; 41pp; English.
XX CC The invention relates to a composition comprising several cDNAs that are
XX CC differentially expressed in a liver disorder. The composition is useful
XX CC for treating liver disorder such as hyperlipidaemia, hypertension, type
XX CC II diabetes, tumours of the liver and disorders of the inflammatory and
XX CC immune response. The composition is useful for a high-throughput method
XX CC of screening several molecules or compounds to identify a ligand which
XX CC specifically binds a cDNA. A protein encoded by the cDNA is useful for a
XX CC high-throughput method for using a protein to screen several molecules or
XX CC compounds to identify at least one ligand which specifically binds the
XX CC protein which involves combining the protein encoded by the cDNA with
XX CC several of molecules or compounds under conditions to allow specific
XX CC binding, and detecting specific binding between the protein and a
XX CC molecule or compound, therefore identifying a ligand which specifically
XX CC binds the protein. The composition is useful for detecting and
XX CC quantifying differential gene expression, can be used in gene therapy, to
XX CC formulate prognosis and to design a treatment regimen and to monitor the
XX CC efficacy of treatment. The present sequence represents the amino acid
XX CC sequence of a protein encoded by a cDNA differentially expressed in a
XX CC liver disorder.
XX SQ Sequence 643 AA;
Query Match 77.0%; Score 1012; DB 8; Length 643;
Best Local Similarity 74.4%; Pred. No. 1.4e-75;
Matches 192; Conservative 33; Mismatches 33; Indels 0; Gaps 0;
QY 1 KSENVQDLLLLDVAPLSLGLTAGGVTALIKNSTIPTKTQITFTTYSNQGVLQVY 60
DB 386 KCEKVDLLLLDVAPLSLGLTAGGVTALIKNSTIPTKTQITFTTYSNQGVLQVY 445
QY 61 EGERAMTKNNLLGRFELSGIPAPRGVQIETFTDANGILNVATDSTKANKITI 120
DB 446 EGERAMTKNNLLGRFELSGIPAPRGVQIETFTDANGILNVATDSTKANKITI 505
QY 121 TNDKGRLSKEIEIRWVQEAQYKAEDVQREVSANNALESYAFNMKSAVEDGLKQKIS 180
DB 506 TNDKGRLSKEIEIRWVQEAQYKAEDVQREVSANNALESYAFNMKSAVEDGLKQKIP 565
QY 181 EADKKVLDKQCEVISWLDANTLAKEDEFEHKELEQVCNPIISGLYQAGGPGGFG 240

DB 566 BEDRRKXQDKCREVLAWLHNLAEYEHQRELEQICRPIFSRLYGGPGVPGSSCG 625
QY 241 AQGPKGSGSGGPTIREVD 258
DB 626 TQARQGDPTSGPIIEVD 643
RESULT 99
ADP12947
ID ADP12947 standard; protein; 643 AA.
XX AC ADP12947;
XX DT 12-AUG-2004 (first entry)
XX DE Protein encoding reference mRNA sequence #32.
XX KW transplant rejection; immune system; rheumatoid arthritis; lupus;
XX KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
XX OS Homo sapiens.
XX PN WO2004042346-A2.
XX PD 21-MAY-2004.
XX PF 24-APR-2003; 2003WO-US012946.
XX PR 24-APR-2002; 2002US-00131831.
XX PR 20-DEC-2002; 2002US-00325899.
XX PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX PI Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
XX PI Rosenberg S;
XX WPI; 2004-400724/37.
XX DT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
XX PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
XX PT rejection, in an individual, comprises detecting the expression level of
XX PT the genes.
XX PS Claim 65; SEQ ID NO 2956; 1762pp; English.
XX CC The present invention relates to diagnosing or monitoring transplant
XX CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
XX CC comprises detecting the expression level of one or more genes. The
XX CC methods, system and kits are useful in diagnosing or monitoring
XX CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
XX CC islet, lung, bone marrow or stem cell transplant rejection,
XX CC xenotransplant rejection or mechanical organ replacement rejection, in an
XX CC individual. The method is also useful in assessing the immune status of
XX CC an individual. The methods are also useful in diagnosing and monitoring
XX CC diseases that involve the immune system, e.g. rheumatoid arthritis,
XX CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
XX CC viral, bacterial or fungal infection. The present sequence represents a
XX CC protein encoded by an mRNA sequence of the invention which show altered
XX CC expression in renal transplantation and expression.
XX SQ Sequence 643 AA;
Query Match 77.0%; Score 1012; DB 8; Length 643;
Best Local Similarity 74.4%; Pred. No. 1.4e-75;
Matches 192; Conservative 33; Mismatches 33; Indels 0; Gaps 0;
QY 1 KSENVQDLLLLDVAPLSLGLTAGGVTALIKNSTIPTKTQITFTTYSNQGVLQVY 60
DB 386 KCEKVDLLLLDVAPLSLGLTAGGVTALIKNSTIPTKTQITFTTYSNQGVLQVY 445
QY 61 EGERAMTKNNLLGRFELSGIPAPRGVQIETFTDANGILNVATDSTKANKITI 120

Db 446 EGERAMTKNNLLGRFELSGIPAPRGVQIEVTFDIDANGILSVTATDRSTGKANKITI 505
 QY 121 TNDKGRLSKEEIERMVOEAKYKAEDVQERVSANKNALESYAFNMKSAVEDGLGKGIS 180
 Db 506 TNDKGRLSKEEVERMWEAEQYKAEDDAQRDRVAANKSLRAHVHVGSLQESLRDKIP 565
 QY 181 EADKKVLDRCQEVISWLDANTLAEDKDFPHRKELEQVCNPIISGLYQAGGPGPGFG 240
 Db 566 EEDRRKMQDKCREVLAWLHNLQAEKEEYEHQKRELEQICRPIFSRLYGGPGVPGGSSCG 625
 QY 241 AQGPKGGSGSGPTIEVD 258
 Db 626 TQARQGDPTSGPTIEVD 643

RESULT 100

ADRI4395
 ID ADRI4395 standard; protein; 643 AA.

XX AC ADRI4395;

XX DT 21-OCT-2004 (first entry)

XX DE Human NF-kappaB pathway-associated protein SeqID396.

XX KW NF-kappaB pathway; anti-inflammatory; cytostatic; hepatotropic; virucide;
 KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
 KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
 KW immunosuppressive; vulnerary; gene therapy; immune disorder;
 KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
 KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
 KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
 KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
 KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
 KW viral replication; host cell survival; evasion of immune response;
 KW rheumatoid arthritis; inflammatory bowel disease; colitis; ascuma;
 KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
 KW autoimmune disorder; hyper immune activity;
 KW aberrant acute phase response; hypercongenital condition; birth defect;
 KW necrotic lesion; wound; organ transplant rejection;
 KW aberrant signal transduction; proliferating disorder; cancer;
 KW HIV propagation; human.

XX OS Homo sapiens.

XX PN WO2004065577-A2.

XX PD 05-AUG-2004.

XX 13-JAN-2004; 2004WO-US000798.

XX 14-JAN-2003; 2003US-0440068P.

XX 12-MAY-2003; 2003US-0469757P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Nadler SG, Neubauer MG, Feder JN, Carman J;

XX WPI; 2004-562168/54.

XX N-PSDB; ADRI4394.

XX New isolated polynucleotides and polypeptides associated with NF-kappaB
 pathway, useful for diagnosing, treating, or preventing disorders or
 diseases associated with NF-kappaB pathway.

XX Claim 6; SEQ ID NO 396; 237pp; English.

XX This invention relates to the novel association of protein sequences (and
 the genes which encode them) to the NF-kappaB pathway. The invention may
 be useful for the production of compounds with an anti-inflammatory,
 cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,
 gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,
 immunomodulator, cerebroprotective, vasotropic, immunosuppressive or

CC vulnary activity or for gene therapy. The proteins and nucleotides are
 useful for diagnosing, preventing, treating, or ameliorating conditions
 or diseases associated with the NF-kappaB pathway. The condition is an
 immune disorder, an inflammatory disorder, an inflammatory disorder
 related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,
 hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM
 syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic
 ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
 hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell
 survival, evasion of immune responses, rheumatoid arthritis, inflammatory
 bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
 syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper
 immune activity, disorders related to aberrant acute phase responses,
 hypercongenital conditions, birth defects, necrotic lesions, wounds,
 organ transplant rejection, conditions related to organ transplant
 rejection, disorders related to aberrant signal transduction,
 proliferating disorders, cancers and HIV propagation in cells infected
 with other viruses. The present sequence is that of a human protein which
 is subject to the novel association with the NF-kappaB pathway of the
 invention. Note: This sequence does not appear in the specification but
 was obtained by the indexer from Genbank.

XX SQ Sequence 643 AA;

Query Match 77.0%; Score 1012; DB 8; Length 643;

Best Local Similarity 74.4%; Pred. No. 1.4e-75;

Matches 192; Conservative 33; Mismatches 33; Indels 0; Gaps 0;

QY 1 KSENVODLLLDVAPLSLGLTAGGVMATLKRNSIPTKQTIFTYSDNPGVLIQVY 60

Db 386 KCEKVODLLLDVAPLSLGLTAGGVMATLKRNSIPTKQTIFTYSDNPGVLIQVY 445

QY 61 EGERAMTKNNLLGRFELSGIPAPRGVQIEVTFDIDANGILSVTATDRSTGKANKITI 120

Db 446 EGERAMTKNNLLGRFELSGIPAPRGVQIEVTFDIDANGILSVTATDRSTGKANKITI 505

QY 121 TNDKGRLSKEEIERMVOEAKYKAEDVQERVSANKNALESYAFNMKSAVEDGLGKGIS 180

Db 506 TNDKGRLSKEEVERMWEAEQYKAEDDAQRDRVAANKSLRAHVHVGSLQESLRDKIP 565

QY 181 EADKKVLDRCQEVISWLDANTLAEDKDFPHRKELEQVCNPIISGLYQAGGPGPGFG 240

Db 566 EEDRRKMQDKCREVLAWLHNLQAEKEEYEHQKRELEQICRPIFSRLYGGPGVPGGSSCG 625

QY 241 AQGPKGGSGSGPTIEVD 258

Db 626 TQARQGDPTSGPTIEVD 643

Search completed: April 6, 2005, 17:20:53

Job time : 184 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 6, 2005, 17:16:54 ; Search time 43 Seconds
(without alignments)
447.894 Million cell updates/sec

Title: US-09-646-835-1_COPY_384_641

Perfect score: 1314

Sequence: 1 KSENVQDLLLDVAPLSLGL.....FGAQPKGSGSGSTIEEVD 258

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
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4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1314	100.0	641	4	US-09-919-039-146
2	1249	95.1	244	4	US-09-440-967-2
3	1097.5	83.5	646	4	US-09-919-039-11
4	1097.5	83.5	890	4	US-09-513-783A-174
5	1097.5	83.5	894	4	US-09-949-016-10605
6	1094.5	83.3	646	1	US-08-441-139-14
7	1093	83.2	641	4	US-09-919-039-73
8	1059.5	80.6	639	4	US-09-949-016-7028
9	1059.5	80.6	664	4	US-09-949-016-8177
10	1012	77.0	643	4	US-09-919-039-204
11	1009	76.8	643	3	US-08-797-358B-3
12	864.5	65.8	315	1	US-08-257-073-7
13	824	62.7	312	4	US-09-270-767-32060
14	824	62.7	312	4	US-09-270-767-47277
15	742.5	56.5	655	4	US-09-632-538C-36
16	724	55.1	666	1	US-08-441-139-16
17	717	54.6	654	1	US-08-441-139-11
18	717	54.6	654	4	US-09-919-172-54
19	717	54.6	654	4	US-09-919-039-260
20	716	54.5	692	4	US-09-248-796A-19789
21	705	53.7	682	1	US-08-441-139-2
22	703	53.5	253	4	US-09-581-001B-8
23	678	51.6	669	1	US-08-441-139-7
24	634	48.2	679	1	US-08-441-139-5
25	536.5	40.8	430	4	US-09-902-540-13248
26	531.5	40.4	625	4	US-09-501-097A-9
27	531.5	40.4	623	4	US-09-501-097A-20

28	531.5	40.4	724	4	US-09-613-303-45	Sequence 45, Appl
29	531.5	40.4	724	4	US-10-267-311-45	Sequence 45, Appl
30	530	40.3	618	4	US-09-603-208A-32	Sequence 32, Appl
31	526.5	40.1	618	4	US-09-603-208A-34	Sequence 34, Appl
32	525.5	40.0	711	4	US-09-613-303-41	Sequence 41, Appl
33	525.5	40.0	711	4	US-10-267-311-41	Sequence 41, Appl
34	524.5	39.9	539	4	US-09-710-279-888	Sequence 888, App
35	524.5	39.9	616	3	US-09-134-001C-3646	Sequence 3646, App
36	518	39.4	187	6	5196523-13	Patent No. 5196523
37	518	39.4	187	6	5196523-13	Patent No. 5196523
38	517	39.3	663	4	US-09-438-185A-505	Sequence 505, App
39	509.5	38.8	649	3	US-09-066-047-5	Sequence 5, Appli
40	500	38.1	636	4	US-09-540-236-2873	Sequence 2873, Ap
41	497	37.8	679	1	US-08-214-583-2	Sequence 2, Appli
42	489.5	37.3	516	4	US-09-248-796A-17736	Sequence 17736, A
43	488.5	37.2	199	4	US-09-581-001B-7	Sequence 7, Appli
44	488	37.1	208	4	US-09-248-796A-17615	Sequence 17615, A
45	488	37.1	660	4	US-09-328-352-4932	Sequence 4932, Ap
46	486	37.0	92	4	US-09-440-967-3	Sequence 3, Appli
47	484	36.8	562	4	US-09-207-388-14	Sequence 14, Appl
48	484	36.8	642	4	US-09-207-388-15	Sequence 15, Appl
49	484	36.8	662	4	US-09-207-388-16	Sequence 16, Appl
50	482.5	36.7	641	1	US-08-441-139-4	Sequence 4, Appli
51	480.5	36.6	657	4	US-09-352-991A-27358	Sequence 27358, A
52	480	36.5	569	4	US-09-302-540-12527	Sequence 12527, A
53	480	36.5	642	4	US-09-207-388-13	Sequence 13, Appl
54	472	35.9	607	2	US-08-472-534-5	Sequence 5, Appli
55	472	35.9	607	4	US-09-583-110-4651	Sequence 4651, Ap
56	472	35.9	612	4	US-09-107-433-3621	Sequence 3621, Ap
57	471	35.8	307	3	US-08-858-207A-481	Sequence 481, App
58	469	35.7	638	4	US-09-489-039A-8996	Sequence 8996, Ap
59	468.5	35.7	641	4	US-09-543-681A-6258	Sequence 6258, Ap
60	463	35.2	196	4	US-09-581-001B-9	Sequence 9, Appli
61	462.5	35.2	187	4	US-09-248-796A-17616	Sequence 17616, A
62	460.5	35.0	536	4	US-09-107-532A-6930	Sequence 6930, Ap
63	453.5	34.5	281	4	US-09-134-000C-3432	Sequence 3432, Ap
64	448.5	34.1	549	4	US-09-248-796A-19897	Sequence 19897, A
65	448.5	34.1	600	6	5240706-1	Patent No. 5240706
66	448.5	34.1	600	6	5240706-1	Patent No. 5240706
67	445	33.9	168	1	US-08-441-139-10	Sequence 10, Appl
68	443	33.7	539	4	US-09-198-452A-543	Sequence 543, App
69	406	30.9	122	4	US-09-270-767-42542	Sequence 42542, A
70	400	30.4	654	4	US-09-248-796A-17735	Sequence 17735, A
71	393	29.9	298	4	US-09-302-540-15923	Sequence 15923, A
72	379	28.8	96	4	US-09-248-796A-17616	Sequence 17616, A
73	376	28.6	192	4	US-09-581-001B-10	Sequence 10, Appl
74	354.5	27.0	623	4	US-09-252-991A-22906	Sequence 22906, A
75	334	25.4	622	4	US-08-540-236-3242	Sequence 3242, Ap
76	333	25.3	621	4	US-09-489-039A-11583	Sequence 11583, A
77	328	25.0	623	4	US-09-543-681A-7673	Sequence 7673, Ap
78	319.5	24.3	620	4	US-09-328-352-7730	Sequence 7730, Ap
79	285	21.7	415	4	US-09-207-388-12	Sequence 12, Appl
80	254	19.3	183	4	US-09-556-877-301	Sequence 301, App
81	254	19.3	183	4	US-08-620-412C-301	Sequence 301, App
82	254	19.3	183	4	US-09-598-419-301	Sequence 301, App
83	248.5	18.9	136	3	US-09-183-861-49	Sequence 49, Appl
84	248.5	18.9	136	3	US-09-022-765-49	Sequence 49, Appl
85	248.5	18.9	136	4	US-09-551-974A-49	Sequence 49, Appl
86	248.5	18.9	136	4	US-09-565-501A-49	Sequence 49, Appl
87	248.5	18.9	136	4	US-09-639-206A-49	Sequence 49, Appl
88	248.5	18.9	136	4	US-09-874-523-49	Sequence 49, Appl
89	234.5	17.8	535	4	US-09-302-540-15138	Sequence 15138, A
90	226.5	17.2	506	4	US-09-302-540-14235	Sequence 14235, A
91	223	17.0	69	4	US-09-581-001B-6	Sequence 6, Appli
92	217	16.5	690	4	US-09-302-540-10349	Sequence 10349, A
93	216	16.4	1027	4	US-09-302-540-11750	Sequence 11750, A
94	201	15.3	714	2	US-08-472-534-3	Sequence 3, Appli
95	193.5	14.7	222	4	US-09-581-001B-11	Sequence 11, Appl
96	190.5	14.5	608	4	US-09-302-540-14034	Sequence 14034, A
97	184	14.0	56	6	5196523-12	Patent No. 5196523
98	184	14.0	56	6	5196523-12	Patent No. 5196523
99	165	12.6	337	4	US-09-710-279-1876	Sequence 1876, Ap
100	119	9.1	941	4	US-09-513-783A-172	Sequence 172, App

ALIGNMENTS

```
RESULT 1
US-09-919-039-146
; Sequence 146, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaber, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 146
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 1678695CD1
US-09-919-039-146

Query Match      100.0%; Score 1314; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 6.1e-113;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KSENVODLLLDVAPLSGLGTAGGVTALIKENSTIPTKTQTFITYSDNQPGVLIQVY 60
DB      384 KSENVODLLLDVAPLSGLGTAGGVTALIKENSTIPTKTQTFITYSDNQPGVLIQVY 443

QY      61 EGERAMTKONLLGRFELSGLIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB      444 EGERAMTKONLLGRFELSGLIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 503

QY      121 TNDKGRLSKEIEIRMWQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDSLGKGIS 180
DB      504 TNDKGRLSKEIEIRMWQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDSLGKGIS 563

QY      181 EADKKVLDKQEVISWLDANTLAEKDPEFHKRKELEQVCNPIISGLYQAGGPGGFG 240
DB      564 EADKKVLDKQEVISWLDANTLAEKDPEFHKRKELEQVCNPIISGLYQAGGPGGFG 623

QY      241 AQGPKGSGSGPTIEVD 258
DB      624 AQGPKGSGSGPTIEVD 641

RESULT 2
US-09-440-967-2
; Sequence 2, Application US/09440967
; Patent No. 6730302
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: INTRACELLULAR TARGETED DELIVERY OF COMPOUNDS BY 70 KD HEAT SHOCK
; FILE REFERENCE: DB8
; CURRENT APPLICATION NUMBER: US/09/440,967
; CURRENT FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/109,872
; PRIOR FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-440-967-2
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Query Match      95.1%; Score 1249; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.6e-107;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 PLSLGLGTAGGVTALIKENSTIPTKTQTFITYSDNQPGVLIQVYEGERAMTKONLLG 74
DB      1 PLSLGLGTAGGVTALIKENSTIPTKTQTFITYSDNQPGVLIQVYEGERAMTKONLLG 60

QY      75 RFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITITNDKGRLSKEIEIR 134
DB      61 RFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITITNDKGRLSKEIEIR 120

QY      135 MVQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDSLGKGISADKKVLDKQEV 194
DB      121 MVQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDSLGKGISADKKVLDKQEV 180

QY      195 ISWLDANTLAEKDPEFHKRKELEQVCNPIISGLYQAGGPGGFGAOGPKGSGSGPTI 254
DB      181 ISWLDANTLAEKDPEFHKRKELEQVCNPIISGLYQAGGPGGFGAOGPKGSGSGPTI 240

QY      255 EEVD 258
DB      241 EEVD 244
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RESULT 3
US-09-919-039-11
; Sequence 11, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaber, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 11
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 1545176CD1
US-09-919-039-11
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Query Match      83.5%; Score 1097.5; DB 4; Length 646;
Best Local Similarity 81.4%; Pred. No. 6.5e-93;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

QY      1 KSENVODLLLDVAPLSGLGTAGGVTALIKENSTIPTKTQTFITYSDNQPGVLIQVY 60
DB      384 KSENVODLLLDVAPLSGLGTAGGVTALIKENSTIPTKTQTFITYSDNQPGVLIQVY 443

QY      61 EGERAMTKONLLGRFELSGLIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB      444 EGERAMTKONLLGRFELSGLIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 503

QY      121 TNDKGRLSKEIEIRMWQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDSLGKGIS 180
DB      504 TNDKGRLSKEIEIRMWQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDSLGKGIS 563

QY      181 EADKKVLDKQEVISWLDANTLAEKDPEFHKRKELEQVCNPIISGLYQAGGPG- PG 237
DB      564 DEDKQKILDKCNEIINWLDKNQTAKEEFHQKLEKVCNPIITKLYQSAGGPGMPG 623

QY      238 GF--GAQGPKGSGSGPTIEVD 258
DB      624 GPPGGAGPPSGGASSGPTIEVD 646
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RESULT 4

US-09-513-783A-174
 ; Sequence 174, Application US/09513783A
 ; Patent No. 6416959
 ; GENERAL INFORMATION:
 ; APPLICANT: Giuliano, Kenneth A.
 ; APPLICANT: Kapur, Ravi
 ; TITLE OF INVENTION: A System for Cell Based Screening
 ; FILE REFERENCE: 97-022-L1
 ; CURRENT APPLICATION NUMBER: US/09/513,783A
 ; CURRENT FILING DATE: 2000-02-25
 ; NUMBER OF SEQ ID NOS: 180
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 174
 ; LENGTH: 890
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: GFP-HSC70
 US-09-513-783A-174

Query Match 83.5%; Score 1097.5; DB 4; Length 890;
 Best Local Similarity 81.4%; Pred. No. 1e-92;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVQDLLLLDVAPLSLGLTAGVMTALIKRNTSTPTKQTQFTTYSNQPGLVLIQVY 60
 DB 628 KSENVQDLLLLDVAPLSLGLTAGVMTALIKRNTSTPTKQTQFTTYSNQPGLVLIQVY 687
 QY 61 EGERAMTKONLLGRFELSGIPAPRGVQIETVFDIDANGILNVATDKSTGKANKITI 120
 DB 688 EGERAMTKONLLGRFELSGIPAPRGVQIETVFDIDANGILNVATDKSTGKANKITI 747
 QY 121 TNDKGRLSKEIEIRWQAEKKAEDVQERVSANNALESYAFNMKSAVEDGLKGGKIS 180
 DB 748 TNDKGRLSKEIEIRWQAEKKAEDVQERVSANNALESYAFNMKSAVEDGLKGGKIS 807
 QY 181 EADKKVKLDKQEVISWLDANTLAEDFEHKEKELEQVNCNPIISGLYQAGG-PG--PG 237
 DB 808 DEDKQKILDKCNEIINWLDKNQTAKEEPEHQQEKELEKVCNPIITKLYQSAGGMPGMPG 867
 QY 238 GF--GAQGPKGSGSGPTIEVD 258
 DB 868 GFPGGGAPPSSGGSGPTIEVD 890

RESULT 5

US-09-949-016-10605
 ; Sequence 10605, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CU001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10605
 ; LENGTH: 894
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-949-016-10605
 Query Match 83.5%; Score 1097.5; DB 4; Length 894;
 Best Local Similarity 81.4%; Pred. No. 1e-92;

Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVQDLLLLDVAPLSLGLTAGVMTALIKRNTSTPTKQTQFTTYSNQPGLVLIQVY 60
 DB 632 KSENVQDLLLLDVAPLSLGLTAGVMTALIKRNTSTPTKQTQFTTYSNQPGLVLIQVY 691
 QY 61 EGERAMTKONLLGRFELSGIPAPRGVQIETVFDIDANGILNVATDKSTGKANKITI 120
 DB 692 EGERAMTKONLLGRFELSGIPAPRGVQIETVFDIDANGILNVATDKSTGKANKITI 751
 QY 121 TNDKGRLSKEIEIRWQAEKKAEDVQERVSANNALESYAFNMKSAVEDGLKGGKIS 180
 DB 752 TNDKGRLSKEIEIRWQAEKKAEDVQERVSANNALESYAFNMKSAVEDGLKGGKIS 811
 QY 181 EADKKVKLDKQEVISWLDANTLAEDFEHKEKELEQVNCNPIISGLYQAGG-PG--PG 237
 DB 812 DEDKQKILDKCNEIINWLDKNQTAKEEPEHQQEKELEKVCNPIITKLYQSAGGMPGMPG 871
 QY 238 GF--GAQGPKGSGSGPTIEVD 258
 DB 872 GFPGGGAPPSSGGSGPTIEVD 894
 RESULT 6
 US-08-441-139-14
 ; Sequence 14, Application US/08441139
 ; Patent No. 5773245
 ; GENERAL INFORMATION:
 ; APPLICANT: Witttrup, Dr. Karl D.
 ; APPLICANT: Robinson, Anne S.
 ; TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF RECOMBINANTLY EXPRESSED PROTEINS
 ; TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/441,139
 ; FILING DATE: 15-MAY-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/089,997
 ; FILING DATE: 06-JUL-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Digiglio, Frank S.
 ; REGISTRATION NUMBER: 31,346
 ; REFERENCE/DOCKET NUMBER: 8646
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 516-742-4343
 ; TELEFAX: 516-742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 646 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-441-139-14
 Query Match 83.3%; Score 1094.5; DB 1; Length 646;
 Best Local Similarity 81.4%; Pred. No. 1.2e-92;
 Matches 214; Conservative 23; Mismatches 21; Indels 5; Gaps 3;

QY 1 KSENVQDLLLLDVAPLSLGLTAGVMTALIKRNTSTPTKQTQFTTYSNQPGLVLIQVY 60

Db 384 KSENVQDLLLLDVTPSLGLETAGVMTALIKRNTTPTKQTQTLYSDNQPGVLIQVY 443
QY 61 EGERAMTKDNLLGRFELSGTIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTKDNLLGKFLGTIPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMWQAEAKYKAEDVQERVSNAKNALESYAFNMKSASVEDGLGKGIS 180
Db 504 TNDKGRLSKEDIERMWQAEAKYKAEDQKRDQVSSKNSLESYAFNMKATVEDEKJQKIN 563
QY 181 EADKKVLDKCOEVIISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGG-PG--PG 237
Db 564 EADKKVLDKCOEVIISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGG-PG--PG 237
QY 238 GP--GAQPKGGSGGPTIEVD 258
Db 624 GPGGGGAPPSSGSSGPTIEVD 646

RESULT 7
US-09-919-039-73
; Sequence 73, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 73
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6727066 701484CD1
US-09-919-039-73

Query Match 83.2%; Score 1093; DB 4; Length 641;
Best Local Similarity 81.5%; Pred. No. 1.7e-92;
Matches 216; Conservative 16; Mismatches 17; Indels 16; Gaps 2;
QY 1 KSENVQDLLLLDVAPLSGLGTAGVMTALIKRNTTPTKQTQTLYSDNQPGVLIQVY 60
Db 386 KSENVQDLLLLDVAPLSGLGTAGVMTALIKRNTTPTKQTQTLYSDNQPGVLIQVY 445
QY 61 EGERAMTKDNLLGRFELSGTIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 446 EGERAMTKDNLLGRFDTGTIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 505
QY 121 TNDKGRLSKEEIERMWQAEAKYKAEDVQERVSNAKNALESYAFNMKSASVEDGLGKGIS 180
Db 506 TNDKGRLSKEEIERMWQAEAKYKAEDVQERVSNAKNALESYAFNMKSASVEDGLGKGIS 565
QY 181 EADKKVLDKCOEVIISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGGPG 240
Db 566 ESDKNKILDKCOEVIISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGGPG 240
QY 241 AQGPKGGSG-----SGPTIEVD 258
Db 617 CTGPACGTGYVPRPATGPTIEVD 641

RESULT 8
US-09-949-016-7028
; Sequence 7028, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7028
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7028

Query Match 80.6%; Score 1059.5; DB 4; Length 639;
Best Local Similarity 79.1%; Pred. No. 2.1e-89;
Matches 204; Conservative 24; Mismatches 25; Indels 5; Gaps 1;
QY 1 KSENVQDLLLLDVAPLSGLGTAGVMTALIKRNTTPTKQTQTLYSDNQPGVLIQVY 60
Db 387 KSENVQDLLLLDVTPSLGLETAGVMTPLIKRNTTPTKQTQTLYSDNQSSVLVQVY 446
QY 61 EGERAMTKDNLLGRFELSGTIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 447 EGERAMTKDNLLGKFLGTIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 506
QY 121 TNDKGRLSKEEIERMWQAEAKYKAEDVQERVSNAKNALESYAFNMKSASVEDGLGKGIS 180
Db 507 TNDKGRLSKDDIDMWQAEARYKSEDEANRVAACNALESYTYNIKQTVEDEKLRGKIS 566
QY 181 EADKKVLDKCOEVIISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGGPG 240
Db 567 EQDNKILDKCOEVIISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGGPG 626
QY 241 AQGPKGGSGGPTIEVD 258
Db 627 S-----GASGPTIEVD 639

RESULT 9
US-09-949-016-8177
; Sequence 8177, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8177
; LENGTH: 664
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8177

Query Match 80.6%; Score 1059.5; DB 4; Length 664;
Best Local Similarity 79.1%; Pred. No. 2.2e-89;
Matches 204; Conservative 24; Mismatches 25; Indels 5; Gaps 1;

QY 1 KSENVODLLLDVAPLSGLGLETAGGVTALIKRNSTIPTKTQTFITYSDNQPGVLIQVY 60
DB 412 KSENVODLLLDVAPLSGLGLETAGGVTALIKRNSTIPTKTQTFITYSDNQPGVLIQVY 471
QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 472 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 531
QY 121 TNDKGRLSKEEIERMWQEAERYKAEDVQERVSAAKNALESYAFNMKSAVEDGLGKIS 180
DB 532 TNDKGRLSKDDIDRMVQEAERYKSEDEANDRVAANKNALESYTYNIKQTVDEDEKLKIS 591
QY 181 EADKKVLDKQCVISWLDANTLAEDKDFEHRKKELEQVNCNPIISGLYQAGGPGPGGFG 240
DB 592 EODKNKILDKQCVINWLDNRQMAEKDEYEHQKELERVNCNPIISGLYQAGGPGGSGGG 651
QY 241 AQGPKGSGSGPTIEVD 258
DB 652 S-----GASGPTIEVD 664

RESULT 10

US-09-919-039-204
; Sequence 204, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 204
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 1440032CD1
US-09-919-039-204

Query Match 77.0%; Score 1012; DB 4; Length 643;
Best Local Similarity 74.4%; Pred. No. 5.2e-85;
Matches 192; Conservative 33; Mismatches 33; Indels 0; Gaps 0;

QY 1 KSENVODLLLDVAPLSGLGLETAGGVTALIKRNSTIPTKTQTFITYSDNQPGVLIQVY 60
DB 386 KCEKVDLLLDVAPLSGLGLETAGGVTALIQRNATIPKTQTFITYSDNQPGVLIQVY 445
QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 446 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 505
QY 121 TNDKGRLSKEEIERMWQEAERYKAEDVQERVSAAKNALESYAFNMKSAVEDGLGKIS 180
DB 506 TNDKGRLSKEEVERMWHEAEOYKAEDQAQDRVAANKNSLEAHVHVHKGSLQESLKDIP 565
QY 181 EADKKVLDKQCVISWLDANTLAEDKDFEHRKKELEQVNCNPIISGLYQAGGPGPGGFG 240
DB 566 EEDRRKWKQDKCVLAWLHNLAEKDEYEHQKRELEQICRPIFSRLYGGPGVPGGSSCG 625
QY 241 AQGPKGSGSGPTIEVD 258
DB 626 TQARQGDPTSGPTIEVD 643

RESULT 11

US-08-797-358B-3
; Sequence 3, Application US/08797358B

; Patent No. 6268478
; GENERAL INFORMATION:
; APPLICANT: Adams, John
; TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/797,358B
; FILING DATE: 11-Feb-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,491
; FILING DATE: 12-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-CE 3165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 643 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-797-358B-3

Query Match 76.8%; Score 1009; DB 3; Length 643;
Best Local Similarity 74.4%; Pred. No. 9.8e-85;
Matches 192; Conservative 34; Mismatches 32; Indels 0; Gaps 0;

QY 1 KSENVODLLLDVAPLSGLGLETAGGVTALIKRNSTIPTKTQTFITYSDNQPGVLIQVY 60
DB 386 KCEKVDLLLDVAPLSGLGLETAGGVTALIQRNATIPKTQTFITYSDNQPGVLIQVY 445
QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 446 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 505
QY 121 TNDKGRLSKEEIERMWQEAERYKAEDVQERVSAAKNALESYAFNMKSAVEDGLGKIS 180
DB 506 TNDKGRLSKEEVERMWHEAEOYKAEDQAQDRVAANKNSLETHVHVHKGSLQESLKDIP 565
QY 181 EADKKVLDKQCVISWLDANTLAEDKDFEHRKKELEQVNCNPIISGLYQAGGPGPGGFG 240
DB 566 KEDRHVQDKQCVLAWLHNLAEKDEYEHQKRELEQICRPIFSRLYGGPGVPGGSSCG 625
QY 241 AQGPKGSGSGPTIEVD 258
DB 626 AQARQGDRTSGPTIEVD 643

RESULT 12

US-08-257-073-7
; Sequence 7, Application US/08257073
; Patent No. 5766597
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: de Taisne, Charles

APPLICANT: Time, John A.
TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue, 25th Floor
CITY: New York
STATE: New York
COUNTRY: UNITED STATES OF AMERICA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,073
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,783
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/852,305
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/672,183
FILING DATE: 20-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2570
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-257-073-7

Query Match 65.8%; Score 864.5; DB 1; Length 315;
Best Local Similarity 60.7%; Pred. No. 8.3e-72;
Matches 173; Conservative 37; Mismatches 48; Indels 27; Gaps 3;
Qy 1 KSENVQDLLLDVAPLSGLGTAGGVMTALIKRNSTIPTKQIQTFTYSDNQPGVLIQVY 60
Db 31 QSNVQDLLLDVCSLSGLGTAGGVMTALIKRNSTIPTAKSKQIFTYADNQPGVLIQVY 90
Qy 61 EGERAMTKDNLLGRFELSGIPAPRGVQIETVTDIDANGILNVATDKSTGKANKITI 120
Db 91 EGERALTKDNLLGKFLHDGIPAPRGVQIETVTDIDANGILNVATDKSTGKANKITI 150
Qy 121 TNDKGRLSKEEIERMVOEAKYKAEDVORERVSAKNALESYAFNMKSAVEDGLKKGKIS 180
Db 151 TNDKGRLSQSDIRVNDVAEAKYKAEDENRKRRIEARNLENICYGVKSSLEDQIKKQJQ 210
Qy 181 EADKKVKLDKQCEVISWLDANTLAEKDFEHRKLEQVNCNPIISGLYQAGG----- 233
Db 211 PAELETCKMTTITLWLEKNQLAGDEYEAQKEAESVCAPINSKIYQDAAGAAGMPG 270
Qy 234 -----PG-----PGGGAQGPKG--SGSGPTIEVD 258
Db 271 GMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPG 315

RESULT 13
US-09-270-767-32060

Sequence 32060, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 32060
LENGTH: 312
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-32060
Query Match 62.7%; Score 824; DB 4; Length 312;
Best Local Similarity 59.5%; Pred. No. 4.5e-68;
Matches 156; Conservative 49; Mismatches 45; Indels 12; Gaps 3;
Qy 1 KSENVQDLLLDVAPLSGLGTAGGVMTALIKRNSTIPTKQIQTFTYSDNQPGVLIQVY 60
Db 59 KSSEIKDVLVDVAPLSGLGTAGGVMTALIKRNSRIPCKQSKTFTTYADNQPAVTIOVF 118
Qy 61 EGERAMTKDNLLGRFELSGIPAPRGVQIETVTDIDANGILNVATDKSTGKANKITI 120
Db 119 EGERALTKDNVLTGTFDLTGVPAPRGVQIETVTDIDANGILNVATDKSTGKANKITI 178
Qy 121 TNDKGRLSKEEIERMVOEAKYKAEDVORERVSAKNALESYAFNMKSAVEDGLKKGKIS 180
Db 179 KNDKGRLSQADIDRLMSEAKYKAEDERHRIARNQLETYLFVKEAENG--DRIS 236
Qy 181 EADKKVKLDKQCEVISWLDANTLAEKDFEHRKLEQVNCNPIISGLYQAGGPGPGFG 240
Db 237 ADKSSIVERCSAMKWLDSNTAEKEEYKLEQFCSPIMTMKHG-----GGDG 290
Qy 241 AQGP-----KGGSGSGPTIEVD 258
Db 291 QQAPNFGQDGGYKGTVEVD 312

RESULT 14

US-09-270-767-47277
Sequence 47277, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 47277
LENGTH: 312
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-47277
Query Match 62.7%; Score 824; DB 4; Length 312;
Best Local Similarity 59.5%; Pred. No. 4.5e-68;
Matches 156; Conservative 49; Mismatches 45; Indels 12; Gaps 3;
Qy 1 KSENVQDLLLDVAPLSGLGTAGGVMTALIKRNSTIPTKQIQTFTYSDNQPGVLIQVY 60
Db 59 KSSEIKDVLVDVAPLSGLGTAGGVMTALIKRNSRIPCKQSKTFTTYADNQPAVTIOVF 118
Qy 61 EGERAMTKDNLLGRFELSGIPAPRGVQIETVTDIDANGILNVATDKSTGKANKITI 120
Db 119 EGERALTKDNVLTGTFDLTGVPAPRGVQIETVTDIDANGILNVATDKSTGKANKITI 178
Qy 121 TNDKGRLSKEEIERMVOEAKYKAEDVORERVSAKNALESYAFNMKSAVEDGLKKGKIS 180

Db 469 ERPLTKDNHLLGTFDLTGTPAPRGVQIEVTFEIDVNGILRVTAEDKGTGNKNIITTN 528

Qy 123 DKGRLSKEIERVMVQAEKYKAEDVQRRVSAKNALSVAFNMKSAVED-EGLGKGI SE 181

Db 529 DQNRLLTPEEIERVMVDAEKFADKKLERIDTRNELESAYSILKNQIGDKELGGKLS 588

Qy 182 ADKKKVLDDKQOEIVSWLDANTLAEKDFEHRKKELEQVCNPIISGLYQAGGPGPG 238

Db 589 EDKETWEKAVEEKIEWLESHODADIEDFAKKKELEIEVQPIISKLY-GSAGPPPTG 644

RESULT 19

US-09-919-039-260

Sequence 260, Application US/09919039

Patent No. 6727066

GENERAL INFORMATION:

APPLICANT: Kaber, Matthew R.

TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES

FILE REFERENCE: PA-0035 US

CURRENT APPLICATION NUMBER: US/09/919,039

CURRENT FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: 60/222,113

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 401

SOFTWARE: PERL Program

SEQ ID NO 260

LENGTH: 654

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No. 6727066 2993696CD1

US-09-919-039-260

Query Match 54.6%; Score 717; DB 4; Length 654;

Best Local Similarity 59.1%; Pred. No. 1e-57;

Matches 140; Conservative 44; Mismatches 51; Indels 2; Gaps 2;

Qy 3 ENVQDLLLDVAPLSIGLETAGGVMYALIKRNSTIPTKQTOIFTTYSNQNQGVLIQVYEG 62

Db 409 QDGTGDLVLLDVCPILGTIETVGGVMTKLI PRNTVVPVTKSQIFSTASDNQPTVTIKVYEG 468

Qy 63 ERAMTKDNHLLGRFELSGIIPAPRGVQIEVTFDIDANGILNVATADKSTGKANKIITTN 122

Db 469 ERPLTKDNHLLGTFDLTGTPAPRGVQIEVTFEIDVNGILRVTAEDKGTGNKNIITTN 528

Qy 123 DKGRLSKEIERVMVQAEKYKAEDVQRRVSAKNALSVAFNMKSAVED-EGLGKGI SE 181

Db 529 DQNRLLTPEEIERVMVDAEKFADKKLERIDTRNELESAYSILKNQIGDKELGGKLS 588

Qy 182 ADKKKVLDDKQOEIVSWLDANTLAEKDFEHRKKELEQVCNPIISGLYQAGGPGPG 238

Db 589 EDKETWEKAVEEKIEWLESHODADIEDFAKKKELEIEVQPIISKLY-GSAGPPPTG 644

RESULT 20

US-09-248-796A-19789

Sequence 19789, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstein

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDID

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 19789

LENGTH: 692

```
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19789

Query Match      54.5%; Score 716; DB 4; Length 692;
Best Local Similarity 57.9%; Pred. No. 1.3e-57;
Matches 140; Conservative 44; Mismatches 54; Indels 4; Gaps 2;

Qy 3 ENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTIPTKTQIIFTTYSNQPGLVLIQYEG 62
Db 433 EGVDDVLLDWNPLTIGTSGVMTLTKRNTAIPTKKSQIFSTAADNQPVTVLQYEG 492

Qy 63 ERAMTKNNLLGRPELSGIPPPAPRGVQIEVTPDIDANGILNVATDKSTGKANKITITN 122
Db 493 ERTMAKNNRLGKPELTGIPPPAPRGVQIEVTPFSLDANGILKVEAADKGTGKSESITITN 552

Qy 123 DKGRLSKEETERMVOEAEKYKAEDVQRRVRSKNALESYAFNMKSAVED---EGLKGKI 179
Db 553 EKGRLSKDEIDRMVEAEKYAQDQELKEIKRNLENVAHVLRGQSDTSETGLGSKL 612

Qy 180 SEADKKKVLDKCOEVIISWLDAN-TLAEKDBEFHKKRKELEQVNCNPIISGLYQGAGGPGPG 238
Db 613 DDDDKETLDDAIKETLEFIEDNPTATAEFEEQKQLIDVANPITAKLYGGAGGAGG 672

Qy 239 FG 240
Db 673 AG 674

RESULT 21
US-08-441-139-2
; Sequence 2, Application US/08441139
; Patent No. 5773245
; GENERAL INFORMATION:
; APPLICANT: Wittrup, Dr. Karl D.
; APPLICANT: Robinson, Anne S.
; TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
; TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,139
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,997
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8646
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 682 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-441-139-2

Query Match      54.5%; Score 703; DB 4; Length 253;
Best Local Similarity 58.2%; Pred. No. 5.2e-57;
Matches 138; Conservative 43; Mismatches 54; Indels 2; Gaps 2;

Qy 3 ENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTIPTKTQIIFTTYSNQPGLVLIQYEG 62
Db 8 QDTGDLVLLHVCPLTIGTSGVMTLTPSNVTVTKNSQIFSTASDNQPTVTIKYEG 67

Qy 63 ERAMTKNNLLGRPELSGIPPPAPRGVQIEVTPDIDANGILNVATDKSTGKANKITITN 122
Db 68 ERPLTKDNHLLGTDLTGIPPPAPRGVQIEVTPDIDANGILRVTAEDKGTGNKNKITITN 127

Qy 123 DKGRLSKEETERMVOEAEKYKAEDVQRRVRSKNALESYAFNMKSAVED-EGLKGKISE 181
Db 128 DQNRLLTPEETIERMVDNAEKFAEDKKLKERIDTRNLESYAYSLKQIGDKELGGKLS 187

Qy 182 ADKKKVLDKCOEVIISWLDANTLAEKDBEFHKKRKELEQVNCNPIISGLYQGAGGPGPG 238
Db 188 EDKETWEKAVEEKIEWLESHQDADIEDPKAKKKELEIVQPIISKLY-GSAGPPPTG 243

RESULT 23
US-08-441-139-7
; Sequence 7, Application US/08441139
; Patent No. 5773245
; GENERAL INFORMATION:
; APPLICANT: Wittrup, Dr. Karl D.
```

```

APPLICANT: Robinson, Anne S.
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF,
TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: NY
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,139
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8646
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 663 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-441-139-7

Query Match 51.6%; Score 678; DB 1; Length 6
Best Local Similarity 57.7%; Pred. No. 4.1e-54; Indels
Matches 135; Conservative 46; Mismatches 49;

QY 3 ENVQDLLLLDVAPLSGLSETAGGVWTLIKRNSTPTPKQIQIPTTVS
DB 413 EGSNDVLLDVLPITLGIETTGGVWTKLIGNTPIPTPKSQIFSTAV
QY 63 ERAMTKDNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVTADT
DB 473 ERTLTKNNLLGKFDLGRIPAPRGVQIEVTFEVDANGVLTVSADV
QY 122 NDKGRLSKEEIERMWQEAETKABEDVQORVRSKNALESYAFNMKSLG
DB 533 NDKGRLSSEEDIERMWKEAEFEAEEDKILKERIEARNTLENYAVSLGK
QY 181 EADKKVLDKQOEVLISWLDAN-TLAKDDEFFHKKELEQV/CNPLISG
DB 593 PEDKQAVLDAVEDVAEWLEIHGEDASKEEFEDQKLDVAVHPIPTK
RESULT 24
US-08-441-139-5
Sequence 5, Application US/08441139
Patent No. 5773245
GENERAL INFORMATION:
APPLICANT: Wittrup, Dr. Karl D.
APPLICANT: Robinson, Anne S.
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza

```

```

; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25.05
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,139
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,997
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8646
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 679 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-441-139-5

Query Match 48.2%; Score 634; DB 1;
Best Local Similarity 55.0%; Pred. No. 5e-50;
Matches 131; Conservative 37; Mismatches 68;

QY 3 ENVQDLLLDVAPLSLGLETAGGVMTALIKRNTIPTKQK
| | | | | | | | | | | | | | | | | | | | |
Db 430 EGVEDIVLDVNALTLGIETGGVMTPLIKRNTAIPTKK
| | | | | | | | | | | | | | | | | | | | |

QY 63 ERAMTKNNLLGPELSGIPPAFGVQPIEVTFDIDANG
| | | | | | | | | | | | | | | | | | | | |
Db 490 ERAMTKNNLLGNFELSDIRAAFGVQPIEVTFALDANG
| | | | | | | | | | | | | | | | | | | | |

QY 123 DKGRLSKEEIERMVQEAKEYKAEDVEQGRVSVAKNALES
| | | | | | | | | | | | | | | | | | | | |
Db 550 DKGRLSQDDIRVMVEAEKYAAEDAKPKAKSEARNTPEN
| | | | | | | | | | | | | | | | | | | | |

QY 183 DKKKVLQKQEVISWLDANT-LAEKDPEFKRKELEQVC
| | | | | | | | | | | | | | | | | | | | |
Db 609 DKETVLDNVNESLEWLEDNSDVAEADFEBKMASFKESIV
| | | | | | | | | | | | | | | | | | | | |

RESULT 25
US-09-902-540-13248
; Sequence 13248, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequ
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13248
; LENGTH: 430
; TYPE: PR

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; ORGANISM: Myxococcus xanthus
US-09-902-540-13248

Query Match          40.8%; Score 536.5; DB 4; Length 430;
Best Local Similarity 46.1%; Pred. No. 2.7e-41;
Matches 119; Conservative 43; Mismatches 89; Indels 7; Gaps 4;

Qy 2 5ENVODLLLDVAPLSGLGTAGGVM TALIKRNSTIPTKQTQI FTTSYDNQPGVLIQVYEG 61
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 170 SGEVKDILLDDVTPSLGVTGLGVM TKLIERNTTIPTRKSETFSTAADGQTQVEIHVLQ 229
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 62 GERAMTKNNLLGRFELSGIP PAPRGVPOIEVTFDIDANGILNVATDTKSTGKANKITIT 121
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 230 GEREMAGNRLGRFHLTGMP PAPRGVPOIEVTFDIDANGILNVASAKDKATGKEQKVTIT 289
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 122 NDKRLSKEETIERMVQAEKYKAEDVQ RVSNAKNALESYAFNMKSAVEDGLKGIKISE 181
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 290 HSSG-LAKDEVKVVADARSNEADKGR ELVEMKNQAESQSYAAEKLLKEN--KDKLSA 346
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 182 ADKKVKLDKCOEVI SWLDANTLAEKDBEFHKKRKELEQV CNPIISGLYQAGG-PGPGGFG 240
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 347 DTAKALEDVAELNKRVDGQ---DKDA IKTALDALQAASYKAAEBEMVRATGCGAPGAGAP 403
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 241 AQGPKGGSGSGPTIEEVD 258
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 404 GAGPSAAPGSOASAKDOD 421
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 26
US-09-501-097A-9
; Sequence 9, Application US/09501097A
; Patent No. 6734173
; GENERAL INFORMATION:
; APPLICANT: Tzyy-Chou Wu
; APPLICANT: Chien-Fu Hung
; TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
; FILE REFERENCE: 2240-169349
; CURRENT APPLICATION NUMBER: US/09/501.097A
; CURRENT FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 625
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis

US-09-501-097A-9

Query Match          40.4%; Score 531.5; DB 4; Length 625;
Best Local Similarity 47.7%; Pred. No. 1.3e-40;
Matches 125; Conservative 32; Mismatches 90; Indels 15; Gaps 6;

Qy 5  VODLLLDVAPLSGLGTAGGVM TALIKRNSTIPTKQTQI FTTSYDNQPGVLIQVYEG 64
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 360 VKDVLDDVTPSLGVTGLGVM TKLIERNTTIPTRKSETFTTADDNQPSVQIQVYQGER 419
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 65  AMTKNNLLGRFELSGIP PAPRGVPOIEVTFDIDANGILNVATDTKSTGKANKITITNDK 124
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 420 EIAAHNKLGSFELTGIP PAPRGIPQIEVTFDIDANGIVHVTA KDKGTGKENTIRIQEGS 479
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 125  GRLSKEETIERMVQAEKYKAEDVQ RVSNAKNALESYAFN----MKS AVEDEGLKGIKIS 180
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 480 G-LSKEDIDRMKDAEAAHAEEDRKR REEADV RNQAE TLVQTEKFVKEQREAEQ-GSKVP 537
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 181  EADKKVKLDKCOEVI SWLDANTL--AEKDEPEHKKRKE---LEQV CNPIISGLYQAGGPGP 236
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 538 EDTLNKVDAAVAEAKAALGGSDISA IKSAMEKLQESQALGQAIYEAQAASQATGAHP 597
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 237  GGFGAOGPKGGSGSGPTIEEVD 258
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 598 G-----GEPGGAHFGSADDDVD 614
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 27
```

```

US-09-501-097A-20
; Sequence 20, Application US/09501097A
; Patent No. 6734173
; GENERAL INFORMATION:
; APPLICANT: Tzyy-Chou Wu
; APPLICANT: Chien-Fu Hung
; TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
; FILE REFERENCE: 2240-169349
; CURRENT APPLICATION NUMBER: US/09/501.097A
; CURRENT FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 723
; TYPE: PRT
; ORGANISM: human papillomavirus/Mycobacterium tuberculosis

US-09-501-097A-20

Query Match          40.4%; Score 531.5; DB 4; Length 723;
Best Local Similarity 47.7%; Pred. No. 1.6e-40;
Matches 125; Conservative 32; Mismatches 90; Indels 15; Gaps 6;

Qy 5  VODLLLDVAPLSGLGTAGGVM TALIKRNSTIPTKQTQI FTTSYDNQPGVLIQVYEG 64
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 458 VKDVLDDVTPSLGVTGLGVM TKLIERNTTIPTRKSETFTTADDNQPSVQIQVYQGER 517
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 65  AMTKNNLLGRFELSGIP PAPRGVPOIEVTFDIDANGILNVATDTKSTGKANKITITNDK 124
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 518 EIAAHNKLGSFELTGIP PAPRGIPQIEVTFDIDANGIVHVTA KDKGTGKENTIRIQEGS 577
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 125  GRLSKEETIERMVQAEKYKAEDVQ RVSNAKNALESYAFN----MKS AVEDEGLKGIKIS 180
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 578 G-LSKEDIDRMKDAEAAHAEEDRKR REEADV RNQAE TLVQTEKFVKEQREAEQ-GSKVP 635
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 181  EADKKVKLDKCOEVI SWLDANTL--AEKDEPEHKKRKE---LEQV CNPIISGLYQAGGPGP 236
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 636 EDTLNKVDAAVAEAKAALGGSDISA IKSAMEKLQESQALGQAIYEAQAASQATGAHP 695
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 237  GGFGAOGPKGGSGSGPTIEEVD 258
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 696 G-----GEPGGAHFGSADDDVD 712
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 28
US-09-613-303-45
; Sequence 45, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence

US-09-613-303-45

Query Match          40.4%; Score 531.5; DB 4; Length 724;
Best Local Similarity 47.7%; Pred. No. 1.6e-40;
Matches 125; Conservative 32; Mismatches 90; Indels 15; Gaps 6;

Qy 5  VODLLLDVAPLSGLGTAGGVM TALIKRNSTIPTKQTQI FTTSYDNQPGVLIQVYEG 64
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
```

Db 459 VKDVLDDVTPLSLGIETKGGVMTLRIERTTPTKRSEFTTTADDNQPSVQIQVYQGER 518
QY 65 AMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITITNDK 124
Db 519 EIAAHNKLKLSFELTGIPAPRGIPQIEVTFDIDANGIVHVTAKDGTGKENTIRIQEGS 578
QY 125 GRLSKEIEIEMVQAEKYKAEDVQERVSAAKNALESYAFN----MKSAVEDGLKGKIS 180
Db 579 G-LSKEDIDRMIDKAEAAHEDKRREADVNRQAETLVYQTEKFVKEQREAG- GSKVP 636
QY 181 EADKKVKLDKQCVISWLDANTL-AEKDEFEHKKRKE---LEQVCNPIISGLYQAGGPGP 236
Db 637 EDTLNKVDAAVAEAKAALGSDISAISAMEKLQESQALGOAIYEAQAASQATGAHP 696
QY 237 GGFGAOGPKGSGSGPTIEVD 258
Db 697 G-----GEPGGAHPGSADDDVD 713
RESULT 29
US-10-267-311-45
; Sequence 45, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-45
Query Match 40.4%; Score 531.5; DB 4; Length 724;
Best Local Similarity 47.7%; Pred. No. 1.6e-40;
Matches 125; Conservative 32; Mismatches 90; Indels 15; Gaps 6;
QY 5 VQDLLLDVAPLSLGLTAGVMTALIKRSTIPTKTQIIFTYSNQPGVLIQVYQGER 64
Db 459 VKDVLDDVTPLSLGIETKGGVMTLRIERTTPTKRSEFTTTADDNQPSVQIQVYQGER 518
QY 65 AMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITITNDK 124
Db 519 EIAAHNKLKLSFELTGIPAPRGIPQIEVTFDIDANGIVHVTAKDGTGKENTIRIQEGS 578
QY 125 GRLSKEIEIEMVQAEKYKAEDVQERVSAAKNALESYAFN----MKSAVEDGLKGKIS 180
Db 579 G-LSKEDIDRMIDKAEAAHEDKRREADVNRQAETLVYQTEKFVKEQREAG- GSKVP 636
QY 181 EADKKVKLDKQCVISWLDANTL-AEKDEFEHKKRKE---LEQVCNPIISGLYQAGGPGP 236
Db 637 EDTLNKVDAAVAEAKAALGSDISAISAMEKLQESQALGOAIYEAQAASQATGAHP 696
QY 237 GGFGAOGPKGSGSGPTIEVD 258
Db 697 G-----GEPGGAHPGSADDDVD 713

RESULT 30
US-09-603-208A-32
; Sequence 32, Application US/09603208A

; Patent No. 6822084
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; APPLICANT: Lee, Heung-Shick
; APPLICANT: Kim, Hyung-Joon
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
; FILE REFERENCE: BGI-124CP
; CURRENT APPLICATION NUMBER: US/09/603,208A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142692
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: 60/151214
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930429.7
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931413.6
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931457.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931541.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932914.1
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19940764.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19941382.7
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 306
; SEQ ID NO 32
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-603-208A-32
Query Match 40.3%; Score 530; DB 4; Length 618;
Best Local Similarity 48.6%; Pred. No. 1.8e-40;
Matches 119; Conservative 35; Mismatches 75; Indels 16; Gaps 5;
QY 5 VQDLLLDVAPLSLGLTAGVMTALIKRSTIPTKTQIIFTYSNQPGVLIQVYQGER 64
Db 360 VKDVLDDVTPLSLGIETKGGVMTLRIERTTPTKRSEFTTTADDNQPSVQIQVYQGER 419
QY 65 AMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITITNDK 124
Db 420 EIAAHNKLKLSFELTGIPAPRGIPQIEVTFDIDANGIVHVTAKDGTGKENTIRIQEGS 479
QY 125 GRLSKEIEIEMVQAEKYKAEDVQERVSAAKNALESYAFNMSAYED-----EGLKGK 178
Db 480 G-LSQDEIDRMIDKAEAAHEDKRREADVNRQAETLVYQTEKFVKEQREAG- GSKVP 538
QY 179 ISEADKKVKLDKQCVISWLDANTLAEKDEFEHKKRKELEQVCNPIISGLYQAGGPGP 238
Db 539 VEEAAK-----GVEEALKGEDLEAI--KAAVEKLNTSEQEMGKAIYEA--DAAAGATQAD 589
QY 239 FGAQG 243
Db 590 AGAEG 594
RESULT 31
US-09-603-208A-34
; Sequence 34, Application US/09603208A

```

; Patent No. 6822084
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; APPLICANT: Lee, Heung-Shick
; APPLICANT: Kim, Hyung-Joon
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
; TITLE OF INVENTION: RESISTANCE AND TOLERANCE PROTEINS
; FILE REFERENCE: BGI-124CP
; CURRENT APPLICATION NUMBER: US/09/603,208A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142692
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: 60/151214
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930429.7
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931413.6
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931457.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931541.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932914.1
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19940764.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19941382.7
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 306
; SEQ ID NO 34
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; OTHER INFORMATION: All occurrences of xaa indicate any amino acid
US-09-603-208A-34

Query Match          40.1%; Score 526.5; DB 4; Length 618;
Best Local Similarity 58.1%; Pred. No. 3.8e-40;
Matches 108; Conservative 28; Mismatches 43; Indels 7; Gaps 2;

QY      5 VQDLLLDVAPLSLGLETAGVMTALIKRNSITPTKTQIFTTYSNQPQVLIQVYEGER 64
Db      360 VKDVLDDVTPLSLGIEIKGKGMKLIERNITPTKRSETFTTADNQPVSQIQVQGER 419

QY      65 AMTKNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITITNDK 124
Db      420 EIATANKLLGSFELGGIAPAPRGVPQIEVTFDIDANGIVHVTAKDKGTGKENTITIDGS 479

QY      125 GRLSKEEIERMVOAEKYKAEDVQRVRSKVALESYAFN-----EGLKKG 178
Db      480 G-LSQDEIDRMKDAEAHADEKRRREQEVRNNAESLVYQTRKFVEENSEKVSDELKAK 538

QY      179 ISEADK 184
Db      539 VEEAAK 544

RESULT 32
US-09-613-303-41
; Sequence 41, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:

```

```

; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-41

Query Match          40.0%; Score 525.5; DB 4; Length 711;
Best Local Similarity 48.2%; Pred. No. 5.7e-40;
Matches 123; Conservative 31; Mismatches 86; Indels 15; Gaps 6;

QY      5 VQDLLLDVAPLSLGLETAGVMTALIKRNSITPTKTQIFTTYSNQPQVLIQVYEGER 64
Db      459 VKDVLDDVTPLSLGIEIKGKGMKLIERNITPTKRSETFTTADNQPVSQIQVQGER 518

QY      65 AMTKNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITITNDK 124
Db      519 EIAHNKLLGSFELTGIIPAPRGVPQIEVTFDIDANGIVHVTAKDKGTGKENTIRQEGS 578

QY      125 GRLSKEEIERMVOAEKYKAEDVQRVRSKVALESYAFN-----MKSADVEGLKGIS 180
Db      579 G-LSKEDIDRMKDAEAHADEKRRREQEVRNNAESTLVYQTEKFVKEQREASG-GSKVP 636

QY      181 EADKKVLDKQCEVISWLDANTL-AEKDEFHKRKE---LEQVCNFIISGLYQAGGPGP 236
Db      637 EDTLNKVDAAVAEAKAALGGSDISATKSAMEKLGQESQALGQAIYBAQAASQATGAHP 696

QY      237 GGFAGQPKPGSGSG 251
Db      697 G-----GEFGAHPG 706

RESULT 33
US-10-267-311-41
; Sequence 41, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-41

Query Match          40.0%; Score 525.5; DB 4; Length 711;
Best Local Similarity 48.2%; Pred. No. 5.7e-40;
Matches 123; Conservative 31; Mismatches 86; Indels 15; Gaps 6;

```


Db 61 NDQNLTPBIEIERNVNDAEKFAEDKKLKERIDTRNELESYAYSLKNQIGDKELGKLS 120
Qy 181 EADKKVLDKQEVISWLDANTLAEDKDEFEHKKRKELEQVNCNPIISGLYQAGGPGG 238
Db 121 SEDKETMEKAVEKIEWLESHQDADIEDFKAKKKELEIIVQPIISKLY-GSAGPPPTG 177
RESULT 37
5196523-13
; Patent No. 5196523
; APPLICANT: LEE, AMY S.
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION BY GLUCOSE,
; CALCIUM AND TEMPERATURE
; NUMBER OF SEQUENCES: 28
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/354,988
; FILING DATE: 19-MAY-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 282,880
; FILING DATE: 05-DEC-1988
; APPLICATION NUMBER: 690,951
; FILING DATE: 01-JAN-1985
; SEQ ID NO:13:
; LENGTH: 187
5196523-13
Query Match 39.4%; Score 518; DB 6; Length 187;
Best Local Similarity 57.3%; Pred. No. 4.4e-40;
Matches 102; Conservative 33; Mismatches 41; Indels 2; Gaps 2;
Qy 62 GERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 1 GERPLTKDNHLLGTFDLTGIPPPAPRGVPOIEVTFEIDVNGILRVTAEDKGTGNKNKITIT 60
Qy 122 NDKGRLSKEIERMVOEAEKYKAEDEVORERSAKNALESYAFNMKSAVED-EGLKGGIS 180
Db 61 NDQNLTPBIEIERNVNDAEKFAEDKKLKERIDTRNELESYAYSLKNQIGDKELGKLS 120
Qy 181 EADKKVLDKQEVISWLDANTLAEDKDEFEHKKRKELEQVNCNPIISGLYQAGGPGG 238
Db 121 SEDKETMEKAVEKIEWLESHQDADIEDFKAKKKELEIIVQPIISKLY-GSAGPPPTG 177

RESULT 38
US-09-438-185A-505
; Sequence 505, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 505
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPn0503
US-09-438-185A-505

Query Match 39.3%; Score 517; DB 4; Length 663;
Best Local Similarity 44.6%; Pred. No. 3.2e-39;

Matches 121; Conservative 42; Mismatches 88; Indels 20; Gaps 5;
Qy 5 VODLLLDVAPLSGLTAGGVNTALIKRNSTIPTKQTQIFTTYSNQGVLIQVYEGER 64
Db 387 VKDVLDDVPLSLGIELTGGVWTLVVERNTTPTQKKQIFSTADNQPAVTIVLQGER 446
Qy 65 AMTKONNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITITNDK 124
Db 447 PMAKDNKEIGRFDLTIDPPAPRGHPQIEVSFDIDANGIFHVSADKVASGKEQKIRIEASS 506
Qy 125 GLSKEEIERMVOEAEKYKAEDEVORERSAKNALESYAFNMKSAVEDGLKGIKISEADK 184
Db 507 G-LQDEIQRMVDAEINKEDKKRREASDANKREASDMIFRAEKAIND--YKQIPETLV 563
Qy 185 KKVLDKQEVISWLDANTLAEK-----DEFEHKKRKELE-----QVCNPIISGLYQAGGPG 234
Db 564 KEIEERIEENVNALKDADAIEKIKEVTEDLSKHMQKIGESMQSQSASASAAANAKGGP 623
Qy 235 G-----PGFGAQGPKGSGSGGPTIEVD 258
Db 624 NINTEDLKKHSFSTKPPSNNGSSSEDHIEAD 654
RESULT 39
US-09-066-047-5
; Sequence 5, Application US/09066047A
; Patent No. 6306394
; GENERAL INFORMATION:
; APPLICANT: MURPHY, Cheryl
; STOREY, James
; BELTZ, Gerald A.
; COUGHLIN, Richard T.
; TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND METHODS OF
; USE OF GRANULOCYTIC ERHLICHA
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: United States
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/066,047A
; FILING DATE: 24-Apr-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/044,869
; FILING DATE: 25-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Superko, Colleen
; REGISTRATION NUMBER: 39,850
; REFERENCE/DOCKET NUMBER: 106.941.156
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 649 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-066-047-5

Query Match 38.8%; Score 509.5; DB 3; Length 649;
Best Local Similarity 44.7%; Pred. No. 1.5e-38;

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Matches 115; Conservative 44; Mismatches 91; Indels 7; Gaps 5;
Qy 4 NVQDILLDVAPLSLGLETAGGVTALIKRSTIPTKQIIFTTYSNDQPGVLIQVYGE 63
Db 383 DVRDVLDDVAPLSGLTETLGGVFTPLIERNTTPTKSGQVFSTAEDEGQTAVTIKYQGE 442
Qy 64 RAMTKDNNLLGRFELSGLPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITITND 123
Db 443 RKMAIDNKLQSLGSLGIPAPRGVQIEVTFDIDANGIVHVSADKASGKEQTIKI-OS 501
Qy 124 KGLSKKEEIERMVQAEKKADEQVORVSAKNALESYAFNMKSAVEDEGLKGISEAD 183
Db 502 SGLSDEEIKKWKADQAEADDEKRRKHKVELKNSSEGLIHSVEKSLKDYG--DKVAGAD 559
Qy 184 KKVLDKQCVISWL--DANTLAEKDEPEHKKLEQVNCNPIISGLYQAGGPGPGFGAQ 242
Db 560 KSNIESAIKDLRECLDSDN--CSTDTLQKYDALMNLMSKLGAEAYAAANKNDGAGSADQS 617
Qy 243 G-PKGGSGSGPTIEVD 258
Db 618 GSSSGSDGNGPERVVD 634

RESULT 40
US-09-540-236-2873
; Sequence 2873, Application US/09540236
; Patent No. 6671910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709-2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2873
; LENGTH: 636
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2873

Query Match 38.1%; Score 500; DB 4; Length 636;
Best Local Similarity 46.0%; Pred. No. 1.1e-37;
Matches 109; Conservative 48; Mismatches 68; Indels 12; Gaps 5;
Qy 2 SENVDILLDVAPLSLGLETAGGVTALIKRSTIPTKQIIFTTYSNDQPGVLIQVY 61
Db 383 SGDKKVDLLDVTPLTGLIETMGVMTPIETKNTMTPTKSGQVFSTAEDEGQTAVTIKYQ 442
Qy 62 GERAMTKDNNLLGRFELSGLPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITIT 121
Db 443 GERKIANONKLLGNFDTLIPPAAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITIT 502
Qy 122 NDKGLSKKEEIERMVQAEKKADEQVORVSAKNALESYAFNMKSAVEDEGLKGISE 181
Db 503 ADSG-LSESEITEEMIRTAENAADEDEKFAANLANEADGRHIAVQKALKEAG--DKVTT 559
Qy 182 ADKKVLDKQCVISWL--DANTLAEKDEPEHKKLEQVNCN--PIISGLYQAGGPG 235
Db 560 EETAV-----ESAISTLEA--AAKEDDADDIKKLEALDNLAFIPISQKIYADAGAQ 610

RESULT 41
US-08-214-583-2
; Sequence 2, Application US/08214583
; Patent No. 5627039
; GENERAL INFORMATION:
; APPLICANT: Pereira-Smith, Olivia
; APPLICANT: Wadhwa, Renu
; TITLE OF INVENTION: MORTALIN AND METHODS FOR DETERMINING
; TITLE OF INVENTION: COMPLEMENTATION GROUP ASSIGNMENT OF CANCER CELLS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSER: Howrey & Simon
; STREET: 1299 Pennsylvania Ave, NW
; CITY: Washington
; STATE: DC
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/214,583
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Auerbach, Jeffrey I.
; REGISTRATION NUMBER: 32,680
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-383-7451
; TELEFAX: 202-383-6610
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 679 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Murine
; IMMEDIATE SOURCE:
; CLONE: mortalin
US-08-214-583-2

Query Match 37.8%; Score 497; DB 1; Length 679;
Best Local Similarity 45.9%; Pred. No. 2.3e-37;
Matches 111; Conservative 41; Mismatches 78; Indels 12; Gaps 4;
Qy 4 NVQDILLDVAPLSLGLETAGGVTALIKRSTIPTKQIIFTTYSNDQPGVLIQVYGE 63
Db 431 DVTVDLLDVTPLSLGIETLGGVFTKLINRNTTPTKSGQVFSTAEDEGQTAVTIKYQGE 490
Qy 64 RAMTKDNNLLGRFELSGLPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITITND 123
Db 491 REMAGDNKLLGQFTLIGIPAPRGVQIEVTFDIDANGIVHVSADKGTGREQQIIV-OS 549
Qy 124 KGLSKKEEIERMVQAEKKADEQVORVSAKNALESYAFNMKSAVEDEGLKGISEAD 183
Db 550 SGLSKDDIENVMVKNKAEEDRRKKEVEAVNMAEGIIHDTETWEEFKDQLPADECN 609
Qy 184 K-KKVLDKQCVISWL--DANTLAEKDEPEHKKLEQVNCNPIISGLY-----QGAGGPG 235
Db 610 KLKKEEISKVALLARKDSET---GENIRQAASSLQASLKLPFEMAYKKMASREGSGSSG 666
Qy 236 PG 237
Db 667 TG 668

RESULT 42
US-09-248-7968-17736
; Sequence 17736, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13

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Db 516 ANSG-LSDAIEAMIXDAEANAEDRKFELAKARNEADALISSNKAVIDLG--DKVTE 572

Qy 182 ADKKVLDKQEVISWLDANTLAEDK-PEHKEKELEQVCNPIISGLYQ-----CAGGP 234

Db 573 DEKTAV-----NTAVSELEAKENDNEVVIKAKTEALQNILMPITQRAYEQAQAGGAE 628

Qy 235 GPGGFGAQQGPKG 247

Db 629 DPNAF--QGGDAG 639

RESULT 46

US-09-440-967-3

; Sequence 3, Application US/09440967

; Patent No. 6730302

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: INTRACELLULAR TARGETED DELIVERY OF COMPOUNDS BY 70 KD HEAT SHOCK

; FILE REFERENCE: DB8

; CURRENT APPLICATION NUMBER: US/09/440,967

; PRIOR FILING DATE: 1999-11-16

; PRIOR FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3

; LENGTH: 92

; TYPE: PRT

; ORGANISM: Homo Sapien

US-09-440-967-3

Query Match 37.0%; Score 486; DB 4; Length 92;

Best Local Similarity 100.0%; Pred. No. 1.5e-37;

Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 KSAVEDGLKGIKSEADKKVLDKQEVISWLDANTLAEDKPEHKEKELEQVCNPIISG 226

Db 1 KSAVEDGLKGIKSEADKKVLDKQEVISWLDANTLAEDKPEHKEKELEQVCNPIISG 60

Qy 227 LYQAGGPGGFGAQQGPKGSGGPTIEVD 258

Db 61 LYQAGGPGGFGAQQGPKGSGGPTIEVD 92

RESULT 47

US-09-207-388-14

; Sequence 14, Application US/09207388

; Patent No. 6497880

; GENERAL INFORMATION:

; APPLICANT: Wisniewski, Jan

; TITLE OF INVENTION: HEAT SHOCK GENES AND PROTEINS FROM

; TITLE OF INVENTION: NEISSERIA MENINGITIDIS, CANDIDA GLABRATA AND ASPERGILLUS

; FILE REFERENCE: 870109.411

; CURRENT APPLICATION NUMBER: US/09/207,388

; CURRENT FILING DATE: 1998-12-08

; NUMBER OF SEQ ID NOS: 102

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 14

; LENGTH: 562

; TYPE: PRT

; ORGANISM: Neisseria meningitidis

US-09-207-388-14

Query Match 36.8%; Score 484; DB 4; Length 562;

Best Local Similarity 51.2%; Pred. No. 2.8e-36;

Matches 105; Conservative 33; Mismatches 61; Indels 6; Gaps 3;

Qy 7 DLIILDVAPLSLGETAGVMTALIKRNSTIPTKQIETYSQVFNQPGVLIQVYGERAM 66

Db 309 DVLLLDVTPSLGIETMGVMTKLIQKNTIPTKASQVFSTADNQSAVTHVLQGERER 368

Qy 67 TKONLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITITNDKGR 126

Db 369 ASANKSLQGFNLGDIAPAPRGMPQIEVTFDIDANGILHVSADKGTGKAANITIQSSG- 427

Qy 127 LSKEETIEMVQAEKYKAEDQVQERVSANAKNALESYAFNMKSAVEDGLKGIKSEADKKK 186

Db 428 LSEETIEMVQAEANAEDKKLTVELVASRNOAEALIHVSVKSLADYG--DKLDAAEKEK 485

Qy 187 V---LDKQCEVISWLDANTLAEDK 208

Db 486 IEAALKEAEAEVKGDDKAAIDAKTE 510

RESULT 48

US-09-207-388-15

; Sequence 15, Application US/09207388

; Patent No. 6497880

; GENERAL INFORMATION:

; APPLICANT: Wisniewski, Jan

; TITLE OF INVENTION: HEAT SHOCK GENES AND PROTEINS FROM

; TITLE OF INVENTION: NEISSERIA MENINGITIDIS, CANDIDA GLABRATA AND ASPERGILLUS

; FILE REFERENCE: 870109.411

; CURRENT APPLICATION NUMBER: US/09/207,388

; CURRENT FILING DATE: 1998-12-08

; NUMBER OF SEQ ID NOS: 102

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 15

; LENGTH: 642

; TYPE: PRT

; ORGANISM: Neisseria meningitidis

US-09-207-388-15

Query Match 36.8%; Score 484; DB 4; Length 642;

Best Local Similarity 51.2%; Pred. No. 3.4e-36;

Matches 105; Conservative 33; Mismatches 61; Indels 6; Gaps 3;

Qy 7 DLIILDVAPLSLGETAGVMTALIKRNSTIPTKQIETYSQVFNQPGVLIQVYGERAM 66

Db 389 DVLLLDVTPSLGIETMGVMTKLIQKNTIPTKASQVFSTADNQSAVTHVLQGERER 448

Qy 67 TKONLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITITNDKGR 126

Db 449 ASANKSLQGFNLGDIAPAPRGMPQIEVTFDIDANGILHVSADKGTGKAANITIQSSG- 507

Qy 127 LSKEETIEMVQAEKYKAEDQVQERVSANAKNALESYAFNMKSAVEDGLKGIKSEADKKK 186

Db 508 LSEETIEMVQAEANAEDKKLTVELVASRNOAEALIHVSVKSLADYG--DKLDAAEKEK 565

Qy 187 V---LDKQCEVISWLDANTLAEDK 208

Db 566 IEAALKEAEAEVKGDDKAAIDAKTE 590

RESULT 49

US-09-207-388-16

; Sequence 16, Application US/09207388

; Patent No. 6497880

; GENERAL INFORMATION:

; APPLICANT: Wisniewski, Jan

; TITLE OF INVENTION: HEAT SHOCK GENES AND PROTEINS FROM

; TITLE OF INVENTION: NEISSERIA MENINGITIDIS, CANDIDA GLABRATA AND ASPERGILLUS

; FILE REFERENCE: 870109.411

; CURRENT APPLICATION NUMBER: US/09/207,388

; CURRENT FILING DATE: 1998-12-08

; NUMBER OF SEQ ID NOS: 102

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 16

; LENGTH: 662

; TYPE: PRT

; ORGANISM: Neisseria meningitidis

US-09-207-388-16

US-08-472-534-5
; Sequence 5, Application US/08472534
; Patent No. 5919620
; GENERAL INFORMATION:
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; TITLE OF INVENTION: HEAT SHOCK PROTEIN HSP72 FROM
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/472,534
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr. James F
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Biovac-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 607 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-472-534-5
Query Match 35.9%; Score 472; DB 2; Length 607;
Best Local Similarity 41.6%; Pred. No. 4.1e-35;
Matches 106; Conservative 46; Mismatches 89; Indels 14; Gaps 4;
Qy 4 NVQDILLVAPLSGLGTAGVMTALIKRNSTPTKQTQIFTYSNQPGLVLIQVEGER 63
Db 355 DVKDVLLDVTPLSGLGTAGVMTALIKRNSTPTKQTQIFTYSNQPGLVLIQVEGER 414
Qy 64 RAMTKDNLGRFELSGIPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITIND 123
Db 415 RPAADNKTILGRFQLTDIPAAPRGIPQIEVTFDIDANGILNVTATDKSTGKANKITIND 474
Qy 124 KGRLSKEIERMVQAEKYKAEDVQREVSNAKNALESYAFNMKSAVEDGLKGIKSEAD 183
Db 475 SG-LTDEEDIDRMKDAEANAESDKKKEVDLRNEVDQAFATEKTIKTEGKGFPAERD 533
Qy 184 KKVV---LDKQEVISWLDANTLAEKDFEHRKELEQVCNPIISGLYQGAGPGPGGF 239
Db 534 AAQAALDLKKAQE-----DNNL---DDMKAKLEALNEKAQGLAVKLVEQAAAAQAAQ 584
Qy 240 GAQPKGGSGSGPTI 254
Db 585 GAEGAQATGNAGDDV 599
RESULT 55
US-09-583-110-4651
; Sequence 4651, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.

US-09-646-835-1
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 12527
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-12527
Query Match 36.5%; Score 480; DB 4; Length 569;
Best Local Similarity 43.1%; Pred. No. 6.8e-36;
Matches 97; Conservative 55; Mismatches 65; Indels 8; Gaps 4;
Qy 5 VQDILLDVAPLSGLGTAGVMTALIKRNSTPTKQTQIFTYSNQPGLVLIQVEGER 64
Db 347 VKDVLDDVTPLSGLGTAGVMTALIKRNSTPTKQTQIFTYSNQPGLVLIQVEGER 406
Qy 65 AMTKDNLGRFELSGIPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITINDK 124
Db 407 EMAADNKTILARFELVGLPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITINDK 466
Qy 125 GRLSKEIERMVQAEKYKAEDVQREVSNAKNALESYAFNMKSAVEDGLKGIKSEADK 184
Db 467 G-LSEAEIQAMISDAQSHSDKKKELAEELRNADGLIYVTEKSLSE--YASILLSEKDR 523
Qy 185 KKVV---LDKQEVISWLDANTLAEKDFEHRKELEQVCNPIISG 226
Db 524 EEIKADLERLKEVLNLTSDAVAL--KESFORLEGSAYRIADIYTG 566
RESULT 53
US-09-207-388-13
; Sequence 13, Application US/09207388
; Patent No. 6497880
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Jan
; TITLE OF INVENTION: HEAT SHOCK GENES AND PROTEINS FROM
; TITLE OF INVENTION: NEISSERIA MENINGITIDIS, CANDIDA GLABRATA AND ASPERGILLUS
; TITLE OF INVENTION: FUMIGATUS
; FILE REFERENCE: 870109.411
; CURRENT APPLICATION NUMBER: US/09/207,388
; CURRENT FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 642
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-207-388-13
Query Match 36.5%; Score 480; DB 4; Length 642;
Best Local Similarity 50.7%; Pred. No. 8e-36;
Matches 104; Conservative 33; Mismatches 62; Indels 6; Gaps 3;
Qy 7 DLLLDVAPLSGLGTAGVMTALIKRNSTPTKQTQIFTYSNQPGLVLIQVEGERAM 66
Db 389 DVLLLDVTPLSGLGTAGVMTALIKRNSTPTKQTQIFTYSNQPGLVLIQVEGERAM 448
Qy 67 TKDNLGRFELSGIPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITINDKGR 126
Db 449 ASANKSLGQNLGDIAPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITINDKGR 507
Qy 127 LSKEIERMVQAEKYKAEDVQREVSNAKNALESYAFNMKSAVEDGLKGIKSEADKKK 186
Db 508 LGEEIEIERMVQAEKYKAEDVQREVSNAKNALESYAFNMKSAVEDGLKGIKSEADKKK 565
Qy 187 V---LDKQEVISWLDANTLAEKDE 208
Db 566 IEAALKEAEAVKGDKAIDAkte 590
RESULT 54

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneka
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3621:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 612 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...612
; SEQUENCE DESCRIPTION: SEQ ID NO: 3621:
; US-09-107-433-3621

Query Match          35.9%; Score 472; DB 4; Length 612;
Best Local Similarity 41.6%; Pred.No. 4.le-35;
Matches 106; Conservative 46; Mismatches 89; Indels 14; Gaps 4;

QY      4 NVDDLDDVAPLSLGLETAGGVMTALIKRNSTPTKQTQIFTTYSNDOPGVLIQVVEGE 63
       :|::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db      360 DVKDVLDDVTPLSLGIETMGVFTKLIDRNTTPTPSKSQVFSTAADNQPAVDIHLVGE 419
       :|::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:

QY      64 RAMTKDNNILGRPELGGIPAPRGVPQIVTFPIDANGILNVTATDKSGTGKANKITIND 123
       :|::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db      420 RPAADNKTLGRFLQFDTPAAPRGIPQIEVTFDIDKNGIVSVAKDLGTQKEQTIIVTSN 479
       :|::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:

QY      124 KGLSEKEELRMVOEAEKYKADEVORERSAQALESYAFNMKSAVEDGLGKISEAD 183
       :|::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db      480 SG-LITDEIDRMMDAAENAESDKKKKEVDLRNEVDQAIFATEKTIKETEGKGFOAERD 538
       :|::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:

QY      184 KKRV-----LDKCEVISWLDANTLAEKDBFEHRRKELEQVCNPPIISGLYGAGGPGPGGF 239
       :|::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db      539 AAQAALLDLKKAQE-----DNLL---DDMKALEALNEKAQLAVKLYEQAAAAQAQAE 589
       :|::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:

QY      240 GAQGPKGSGSGSPTI 254
       ||::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db      590 GAEGAQATGNAGDDV 604
       ||::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:

RESULT 57
US-08-858-207A-481
; Sequence 481, Application US/08858207A
; Patent No. 6348328
; GENERAL INFORMATION:
; APPLICANT: Black, Michael
; APPLICANT: Hodgson, John
; APPLICANT: Knowles, David
; APPLICANT: Nicholas, Richard
; APPLICANT: Stodola, Robert
; TITLE OF INVENTION: No. 6348328el Compounds
; NUMBER OF SEQUENCES: 552
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/858,207A

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385 DVKDVLDDVTPLSLGIETMGVMTALISKNTTPTKHSQVFSTARDNQSAVTIHLVQGE 444
QY 64 RAMTKDNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITITND 123
Db 445 RKRASDNKSLGQFNLDGINPAPRGMPQIEVTFDIDADGILHVSADKKNKSGKEQITIKAS 504
QY 124 KGRUSKKEIERMVQEAQKYKAEDVQRRRVSAAKNALESYAFNMKSAVDEGLKGKISEAD 183
Db 505 SG-LNEEBEIQWVREASAEASDRKFEELVQTRNQGDHLLHSTRKQAEAGYK---LPAD 560
QY 184 KKKVLDKQCEVISMLDANTLAE-KDEPHEKKELEQVNCNPIISGLYQAGGPGPGFGAQ 242
Db 561 DKTAL---ESALTLESLSKGEDKADTEAKWQALAAQASOKLMETAQQOHAQQOQAGSADAQ 617

RESULT 59
US-09-543-681A-6258
; Sequence 6258, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEIN
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543.681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6258
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6258

Query Match 35.7%; Score 468.5; DB 4; Length 641;
Best Local Similarity 41.4%; Pred. No. 9.3e-35;
Matches 106; Conservative 47; Mismatches 80; Indels 23; Gaps 5

QY 4 NVQDLLLLDVAPLSIGLETAGGVMTALKRNSTPTKOTQIFTVTSNDQPGVLIOVYGE 63
Db 385 DVKDVLDDVTPLSLGIETMGVMTSLAKNTTPTKHSQVFSTARDNQSAVTIHLVQGE 444
QY 64 RAMTKDNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITITND 123
Db 445 RKRASDNKSLGQFNLDGINPAPRGMPQIEVTFDIDADGILHVSADKKNKSGREQNITIKAS 504
QY 124 KGRUSKKEIERMVQEAQKYKAEDVQRRRVSAAKNALESYAFNMKSAVDEGLKGKISEAD 183
Db 505 SG-LNEEBEIQWVREASAEADRKFEELVQTRNQADQLVHGTRKQIEBAG--DKLAAND 561
QY 184 KKKVLDKQCEVISMLD-ANTLAEKDEPHEKKELEQVNCNPIISGLYQAGGPGPGFGAQ 242
Db 562 KEAT-----EKALSELETASKGEDKAAATEAKLQALVSEASKPLLETAQQQA----- 606
QY 243 GPKGGSGSGPTIEVD 258
Db 607 ---QAGAGNTADATD 618

RESULT 60
US-09-581-001B-9
; Sequence 9, Application US/09581001B
; Patent No. 6472142
; GENERAL INFORMATION:
; APPLICANT: No. 6472142eborn, Mathieu
; APPLICANT: Danan-Van Oorschot, Astrid
; TITLE OF INVENTION: METHODS AND MEANS FOR INDUCING APOPTOSIS BY INTERFERING
; TITLE OF INVENTION: BIP-LIKE PROTEINS
; FILE REFERENCE: 2906-4940US
; CURRENT APPLICATION NUMBER: US/09/581.001B
; CURRENT FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: PCT/NL98/00698

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; PRIOR FILING DATE: 1998-12-03
 ; PRIOR APPLICATION NUMBER: EP 97203783.2
 ; PRIOR FILING DATE: 1997-12-03
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 9
 ; LENGTH: 196
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (124)..(124)
 ; OTHER INFORMATION: The "Xaa" at position 124 may be any amino acid residue.
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (143)..(144)
 ; OTHER INFORMATION: The "Xaa" at positions 143-144 may be any amino acid residue.
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; LOCATION: (192)..(193)
 ; OTHER INFORMATION: The "Xaa" at positions 192-193 may be any amino acid residue.
 ; US-09-581-001B-9

Query Match 35.2%; Score 463; DB 4; Length 196;
 Best Local Similarity 49.0%; Pred. No. 5.7e-35;
 Matches 100; Conservative 32; Mismatches 46; Indels 26; Gaps 4;
 QY 32 KRSTPTKQTQFTTYSNDQPGVLIQVYGERAMTKNNLLGRFELSGIPAPRGVPOI 91
 DB 6 RRTVPTKKSQIFSTASNDQPTVIKVGEPRLTKNNLLGTFDTGIPAPRGVPOI 65
 QY 92 EVTFDIDANGILNVATDTSKANKITITNDKRLSKKEIERMVQAEKYKADEVORE 151
 DB 66 EVTFEIDVNGILRVTAEDKGTGNKKITITNDQNRLTPEIERMVNDAEKFAEDKXLX 125
 QY 152 RVSAKNALESYAFNMKSAVEDEG----LKGKISEADKKVL---DKQEVISWLDANTLA 204
 DB 126 RIDTKGKL--CLFSKESDWWXXKAGRTFLRGDHGKSCRRKMDAGKPPCHRL----- 173
 QY 205 EKDFEHRKLEQVNCNPIISGLY 228
 DB 174 -----QEELREIVQPIISKLY 190

RESULT 61
 US-09-248-796A-19329
 ; Sequence 19329, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Weinstock et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 ; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.132
 ; CURRENT APPLICATION NUMBER: US/09/248,796A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,725
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/096,409
 ; PRIOR FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 28208
 ; SEQ ID NO 19329
 ; LENGTH: 187
 ; TYPE: PRT
 ; ORGANISM: Candida albicans
 ; US-09-248-796A-19329

Query Match 35.2%; Score 462.5; DB 4; Length 187;
 Best Local Similarity 59.7%; Pred. No. 5.9e-35;
 Matches 95; Conservative 17; Mismatches 46; Indels 1; Gaps 1;
 QY 93 VTFDIDANGILNVATDTSKANKITITNDKRLSKKEIERMVQAEKYKADEVORE 152
 DB 17 VSPFIDANGILNVSALEKGTQKITITNDKRLSKKEIERMDKMSAEKFKEDKEAAR 76

QY 153 VSAKNALESYAFNMKSAVEDEGLKGKISEADKKVLDKQEVISWLDANTLAERKDFEHR 212
 DB 77 VQAKNQLESYAYPLKNTINDGEMKDKIGADDKEKLTAKAIDETISWLDASQAASTEVEDK 136
 QY 213 RKELEQVNCNPIISGLYQVAGGPGGFGAGGPKGSGSG 251
 DB 137 RKELESVANPIISGAY-GAAGGAPGGAGGFPFRAGGPPGG 174
 RESULT 62
 US-09-107-532A-6930
 ; Sequence 6930, Application US/09107532A
 ; Patent No. 6583275
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn A Doucette-Stamm and David Bush
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; CORRESPONDENCE ADDRESS: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
 ; ADDRESS: 100 Beaver Street
 ; CITY: Waltham
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02354
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: CD-ROM ISO9660
 ; OPERATING SYSTEM: <Unknown>
 ; SOFTWARE: ASCII
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/107,532A
 ; FILING DATE: 30-Jun-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/085,598
 ; FILING DATE: 14 May 1998
 ; APPLICATION NUMBER: 60/051571
 ; FILING DATE: July 2, 1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ariniello, Pamela Deneke
 ; REGISTRATION NUMBER: 40,489
 ; REFERENCE/DOCKET NUMBER: GTC-012
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (781)893-5007
 ; TELEFAX: (781)893-8277
 ; INFORMATION FOR SEQ ID NO: 6930:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 536 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: YES
 ; ORIGINAL SOURCE:
 ; ORGANISM: Enterococcus faecium
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (B) LOCATION 1...536
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 6930:
 US-09-107-532A-6930

Query Match 35.0%; Score 460.5; DB 4; Length 536;
 Best Local Similarity 53.8%; Pred. No. 4e-34;
 Matches 91; Conservative 33; Mismatches 44; Indels 1; Gaps 1;
 QY 4 NVODLLLDVAPLSGLGTAGGVMALIKRNSTIPTKQTFITYSDNPGVLIQVVEGE 63
 DB 368 DVKDVLLDVTPLSLGIETMGVFTKLIDRNTTPTSKSQVFSTAADNPVDIHLQGE 427
 QY 64 RMTKDNLLGRPELSGIPAPRGVPOIEVTFDIDANGILNVATDTSKANKITITND 123
 DB 428 RPAADNKTGRFQLTDIPAPRGVPOIEVTFDIDKNGIVNVSADKLGQKQIKTSS 487

Qy	2	SENVDLLILDVAPLSLGLETAGVMTALIKRNSTIPTKQTQIIFTTYSNQPGLVLIQVYE	61
Db	325	NDTDFDILLDVLPLSLGVAMQGNVFPVPRNTTVPITKRTFTTVAADHQTTFVQFPVYQ	384
Qy	62	GERAMTKDNNLLGRFELSGIPPPARGVPQIERTVDIDANGILNVTATDKSTGKANKITIT	121
Db	385	GERVNCENTILGFDLKNIPPMQAGPVLKAEIPEVDANGILKVTAVEKSTGRSANITIS	444
Qy	122	NDGRLSKEBRIERMVQAEKYKADEVQREVRVSAKNALESYAFNMKSAVEDEGLKGKISE	181
Db	445	NSIGRLSTEBIEKXIMISDAEKFSSDDAFAKRHEQKQLEAYVASVESTVTDPLVLSAKLKK	504
Qy	182	ADKKKVLDKCOEVISWLDANTLAEKDFEHRKKEEL	216
Db	505	SAKDKEAALSDALQTLTLE---IEBSSADDYKKAEL	536
RESULT 65			
5240706-1			
; Patent No. 5240706			
; APPLICANT: FAULTS, DARYL			
; TITLE OF INVENTION: INTRANASSAL ADMINISTRATION OF MYCOPLASMA			
; HYOPNEUMONIAE ANTIGEN			
; NUMBER OF SEQUENCES: 22			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/07/334,586			
; FILING DATE: 07-APR-1989			
; SEQ ID NO:1:			
; LENGTH: 600			
5240706-1			
Query Match 34.1%; Score 448.5; DB 6; Length 600;			
Best Local Similarity 44.0%; Pred. No. 6e-33;			
Matches 95; Conservative 45; Mismatches 65; Indels 11; Gaps 4			
Qy	5	VQDLLLLDVAPLSLGLETAGVMTALIKRNSTIPTKQTQIIFTTYSNQPGLVLIQVYGER	64
Db	358	ISDVLILLDVTPLTIGIETLGIATPLIPRNTTIPVTKSQIESTAEADNQTETVTSVVOGER	417
Qy	65	AMTKDNNLLGRFELSGIPPPARGVPQIERTVDIDANGILNVTATDKSTGKANKITITNDK	124
Db	418	QLAADNKLGRFNLGSEAPRGLPQIEVPSIDVNGITTVSAKDKTKTKEQTITIKN-T	476
Qy	125	GRLSKEBRIERMVQAEKYKADEVQREVRVSAKNALESYAFNMKSAVEDEGLKGKISEADK	184
Db	477	STLSEEBINKWIOBAEENREADALKDKIETTVAEGLINQLEKSITDQGEK---IDPKQ	533
Qy	185	KYVLDK-COEVISWLDANTLAEKDFEHRKKELEV	219
Db	534	KELLEKIQIEL-----KDLKEDKTDELKULKDOI	563
RESULT 66			
5240706-1			
; Patent No. 5240706			
; APPLICANT: FAULTS, DARYL			
; TITLE OF INVENTION: INTRANASSAL ADMINISTRATION OF MYCOPLASMA			
; HYOPNEUMONIAE ANTIGEN			
; NUMBER OF SEQUENCES: 22			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/07/334,586			
; FILING DATE: 07-APR-1989			
; SEQ ID NO:1:			
; LENGTH: 600			
5240706-1			
Query Match 34.1%; Score 448.5; DB 6; Length 600;			
Best Local Similarity 44.0%; Pred. No. 6e-33;			
Matches 95; Conservative 45; Mismatches 65; Indels 11; Gaps 4			
Qy	5	VQDLLLLDVAPLSLGLETAGVMTALIKRNSTIPTKQTQIIFTTYSNQPGLVLIQVYGER	64
Db	358	ISDVLILLDVTPLTIGIETLGIATPLIPRNTTIPVTKSQIESTAEADNQTETVTSVVOGER	417


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RESULT 71
US-09-902-540-15923
; Sequence 15923, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15949)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15923
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-15923

Query Match          29.9%;      Score 393;      DB 4;      Length 298;
Best Local Similarity 37.6%;
Pred. No. 3e-28;

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; SEQ ID NO 11583
; LENGTH: 621
; TYPE: PRF
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11583

Query Match      25.3%; Score 333; DB 4; Length 621;
Best Local Similarity 38.1%; Pred. No. 3e-22;
Matches 85; Conservative

QY 7 DIALLDVAPLSGLETAGGVTALIKRNSPTKQIPTTYSNQPQVLIQVVEGERAM 66
Db 390 ELLLDVPLSLGLETGGVLEKVPINPTTIPVARAQKFTFKDQGTAMSIHVMOGEREL 449
QY 67 TKDNNLLGRFELSGIPAPRGVPIEVTFDIDANGILNVTATDKSTGKANKITITNDKGR 126
Db 450 VQCRSLARFALGIPALPAGGAHIRTFFQVDADGLLSVTAMEKSTGVEASIQVKPSYG- 508
QY 127 LSKEETERMVQAEKYKAEDVQ-----RERVSAKNALESYAFNMK-----SAVEDGL 175
Db 509 LTDGEIATMIKDSMSY-AEQDIQARMLAEQKVEARVLESLSALAAADALLSAAERQAI 567
QY 176 KG---KISEADKKVLDKQCEVISWLDANTLAEKDFEHHKKE 215
Db 568 DAAAEQVRAAAGDDADAIKEATKIDTQT-----QEFPAARRMD 606

RESULT 77
US-09-543-681A-7673
; Sequence 7673, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7673
; LENGTH: 623
; TYPE: PRF
; ORGANISM: Proteus mirabilis
US-09-543-681A-7673

Query Match      25.0%; Score 328; DB 4; Length 623;
Best Local Similarity 36.5%; Pred. No. 8.7e-22;
Matches 81; Conservative 39; Mismatches 76; Indels 26; Gaps 6;

QY 7 DIALLDVAPLSGLETAGGVTALIKRNSPTKQIPTTYSNQPQVLIQVVEGERAM 66
Db 392 EMLLDVPLSLGLETGGVLEKVPINPTTIPVARAQKFTFKDQGTAMSVHVVOGEREM 451
QY 67 TKDNNLLGRFELSGIPAPRGVPIEVTFDIDANGILNVTATDKSTGKANKITITNDKGR 126
Db 452 VSDCRSLARTFLGIPPPAGGAHIRTFFQVDADGLLSVSAMEKSTGVEASVQVKPSYG- 510
QY 127 LSKEETERMVQAEKYKAED-----FVQERVSAKNALESYAFNMKSAVEDGLKGISEA 182
Db 511 LSDTEIANITQSSMENAKEDQARRLAEQKVEARVLES-----LTAALQED---AHLLTE 563
QY 183 DKKKVLDKQCEVISWLDANTLAEKDE-----FEHHKKELEQ 218
Db 564 DEXTAIDNV-----VDTLIESVEGTDPAIENAIKQLDK 597

RESULT 78
US-09-328-352-7730
; Sequence 7730, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; SEQ ID NO 7730
; LENGTH: 620
; TYPE: PRF
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7730

Query Match      24.3%; Score 319.5; DB 4; Length 620;
Best Local Similarity 37.7%; Pred. No. 5.3e-21;
Matches 81; Conservative 37; Mismatches 78; Indels 19; Gaps 4;

QY 4 NVQD-LLLLDVAPLSGLETAGGVTALIKRNSPTKQIPTTYSNQPQVLIQVVEG 62
Db 381 NSQDGLLLDVTPLSLGLETGGVLEKVPINPTTIPVARAQKFTFKDQGTAMLIHVVOG 440
QY 63 ERAMTKDNNLLGRFELSGIPAPRGVPIEVTFDIDANGILNVTATDKSTGKANKITITN 122
Db 441 ERDLVEHCRSLGRFVLHGIPPTAGQARIEVTFQVDADGLLTVSAREATSGVQAHDIKP 500
QY 123 DKGRLSKEETERMVQAEKYKAED-----VQERVSAKNALESYAFNMKSAVE----- 171
Db 501 SYG-LSEADTERLLISGFQHAEDKNLRLHETKVEARELEALEQALKVDADLLDEKQL 559
QY 172 -----DEGLKGKISADKKVLDKQCEVISWLD 200
Db 560 EALNSAKESLKAQLEGSDIQAIEQAVQOLKVHSDA 594

RESULT 79
US-09-207-388-12
; Sequence 12, Application US/09207388
; Patent No. 6497880
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Jan
; TITLE OF INVENTION: HEAT SHOCK GENES AND PROTEINS FROM
; TITLE OF INVENTION: NEISSERIA MENINGITIDIS, CANDIDA GLABRATA AND ASPERGILLUS
; FILE REFERENCE: 870109.411
; CURRENT APPLICATION NUMBER: US/09/207,388
; CURRENT FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 415
; TYPE: PRF
; ORGANISM: Neisseria meningitidis
US-09-207-388-12

Query Match      21.7%; Score 285; DB 4; Length 415;
Best Local Similarity 62.9%; Pred. No. 4.7e-18;
Matches 56; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 7 DIALLDVAPLSGLETAGGVTALIKRNSPTKQIPTTYSNQPQVLIQVVEGERAM 66
Db 327 DVLLLDVPLSLGLETGGVMTKLIQKNTTIPTKASQVFSTABDNQSAVTIHLQGERER 386
QY 67 TKDNNLLGRFELSGIPAPRGVPIEVTF 95
Db 387 ASANKSLGQFNLDIAPAPRGMPQIEVTF 415

RESULT 80
US-09-556-877-301
; Sequence 301, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
```

```
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 301
; LENGTH: 183
; TYPE: PR1
; ORGANISM: Chlamydia
US-09-556-877-301

Query Match      19.3%; Score 254; DB 4; Length 183;
Best Local Similarity 36.6%; Pred. No. 1.1e-15;
Matches 68; Conservative 32; Mismatches 64; Indels 22; Gaps 7;

QY      81  IPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITITNDKGRLSKEEIERMVQAE 140
Db      1  IPPAPRGHPQIEVTFDIDANGILHVSADKASGREGKIRIEASSG-LKEDEIQOMIRDAE 59

QY      141 KYKAEDVQRRVSNAKNALESYAFNMKSASVEDGLKGKISEADKKV---LDKQCEVISM 197
Db      60  LHKEEDQKREASDVKNEDGMIFRAEKAVKD--YHDKIPAEVLKIEEIEHKVQRAIK- 116

QY      198 LDANTLAEK---DEFEHKREL-----EQVCNPIISGLYQAGGPG-----PGGFGAQ 242
Db      117 EDASTTAIKAASDELSTRMOKIGEAMQASASAAASANAQGGPNINSEDLKXHSFSTR 176

QY      243 GPKGGS 248
Db      177 PPAGGS 182

RESULT 81
US-09-620-412C-301
; Sequence 301, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 301
; LENGTH: 183
; TYPE: PR1
; ORGANISM: Chlamydia
US-09-620-412C-301

Query Match      19.3%; Score 254; DB 4; Length 183;
Best Local Similarity 36.6%; Pred. No. 1.1e-15;
Matches 68; Conservative 32; Mismatches 64; Indels 22; Gaps 7;

QY      81  IPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITITNDKGRLSKEEIERMVQAE 140
Db      1  IPPAPRGHPQIEVTFDIDANGILHVSADKASGREGKIRIEASSG-LKEDEIQOMIRDAE 59

QY      141 KYKAEDVQRRVSNAKNALESYAFNMKSASVEDGLKGKISEADKKV---LDKQCEVISM 197
Db      60  LHKEEDQKREASDVKNEDGMIFRAEKAVKD--YHDKIPAEVLKIEEIEHKVQRAIK- 116

QY      198 LDANTLAEK---DEFEHKREL-----EQVCNPIISGLYQAGGPG-----PGGFGAQ 242
Db      117 EDASTTAIKAASDELSTRMOKIGEAMQASASAAASANAQGGPNINSEDLKXHSFSTR 176
```

```
QY      243 GPKGGS 248
Db      177 PPAGGS 182

RESULT 82
US-09-598-419-301
; Sequence 301, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 301
; LENGTH: 183
; TYPE: PR1
; ORGANISM: Chlamydia
US-09-598-419-301

Query Match      19.3%; Score 254; DB 4; Length 183;
Best Local Similarity 36.6%; Pred. No. 1.1e-15;
Matches 68; Conservative 32; Mismatches 64; Indels 22; Gaps 7;

QY      81  IPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITITNDKGRLSKEEIERMVQAE 140
Db      1  IPPAPRGHPQIEVTFDIDANGILHVSADKASGREGKIRIEASSG-LKEDEIQOMIRDAE 59

QY      141 KYKAEDVQRRVSNAKNALESYAFNMKSASVEDGLKGKISEADKKV---LDKQCEVISM 197
Db      60  LHKEEDQKREASDVKNEDGMIFRAEKAVKD--YHDKIPAEVLKIEEIEHKVQRAIK- 116

QY      198 LDANTLAEK---DEFEHKREL-----EQVCNPIISGLYQAGGPG-----PGGFGAQ 242
Db      117 EDASTTAIKAASDELSTRMOKIGEAMQASASAAASANAQGGPNINSEDLKXHSFSTR 176

QY      243 GPKGGS 248
Db      177 PPAGGS 182

RESULT 83
US-09-183-861-49
; Sequence 49, Application US/09183861
; Patent No. 6365165
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/183,861
; FILING DATE:
```

```
/
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/022,765
/ FILING DATE: 12-FEB-1998
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Maki, David J.
/ REGISTRATION NUMBER: 31,392
/ REFERENCE/DOCKET NUMBER: 210121.420C3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 49:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 136 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ ORIGINAL SOURCE:
/ ORGANISM: Leishmania chagasi
/
/ US-09-183-861-49
/
/ Query Match 18.9%; Score 248.5; DB 3; Length 136;
/ Best Local Similarity 44.6%; Pred. No. 2.3e-15;
/ Matches 50; Conservative 28; Mismatches 33; Indels 1; Gaps 1;
/
/ QY 125 GRLSKEEIERMVQAEKYKAEDVQERVSAKNALESYAFNMKSASVEDEGLKG-KISEAD 183
/ Db 1 GRLSKEEIERMVQAEKYKAEDVQERVSAKNALESYAFNMKSASVEDEGLKG-KISEAD 60
/
/ QY 184 KKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVCNPIISGLYQAGGPG 235
/ Db 61 KKAIEBAVKDALDFVHENPNADREEFEAARTKLSQVTNPPIQKVYQGAAGSG 112
/
/ RESULT 84
/ US-09-022-765-49
/ Sequence 49, Application US/09022765
/ Patent No. 6375955
/ GENERAL INFORMATION:
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Campos-Neto, Antonio
/ APPLICANT: Webb, John R.
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Skeiky, Yasir A.W.
/ TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND
/ NUMBER OF SEQUENCES: 87
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SEED and BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ FILING DATE: 12-FEB-1998
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Maki, David J.
/ REGISTRATION NUMBER: 31,392
/ REFERENCE/DOCKET NUMBER: 210121.420C3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 49:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 136 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ ORIGINAL SOURCE:
/ ORGANISM: Leishmania chagasi
/
/ US-09-183-861-49
/
/ Query Match 18.9%; Score 248.5; DB 3; Length 136;
/ Best Local Similarity 44.6%; Pred. No. 2.3e-15;
/ Matches 50; Conservative 28; Mismatches 33; Indels 1; Gaps 1;
/
/ QY 125 GRLSKEEIERMVQAEKYKAEDVQERVSAKNALESYAFNMKSASVEDEGLKG-KISEAD 183
/ Db 1 GRLSKEEIERMVQAEKYKAEDVQERVSAKNALESYAFNMKSASVEDEGLKG-KISEAD 60
/
/ QY 184 KKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVCNPIISGLYQAGGPG 235
/ Db 61 KKAIEBAVKDALDFVHENPNADREEFEAARTKLSQVTNPPIQKVYQGAAGSG 112
/
/ RESULT 85
/ US-09-551-974A-49
/ Sequence 49, Application US/09551974A
/ Patent No. 6500437
/ GENERAL INFORMATION:
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Campos-Neto, Antonio
/ APPLICANT: Webb, John R.
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Skeiky, Yasir A.W.
/ TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND DIAGNOSIS OF LEISHMANIASIS
/ FILE REFERENCE: 210121.420C5
/ CURRENT APPLICATION NUMBER: US/09/551,974A
/ CURRENT FILING DATE: 2000-04-14
/ NUMBER OF SEQ ID NOS: 101
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 49
/ LENGTH: 136
/ TYPE: PRT
/ ORGANISM: Leishmania chagasi
/
/ US-09-551-974A-49
/
/ Query Match 18.9%; Score 248.5; DB 4; Length 136;
/ Best Local Similarity 44.6%; Pred. No. 2.3e-15;
/ Matches 50; Conservative 28; Mismatches 33; Indels 1; Gaps 1;
/
/ QY 125 GRLSKEEIERMVQAEKYKAEDVQERVSAKNALESYAFNMKSASVEDEGLKG-KISEAD 183
/ Db 1 GRLSKEEIERMVQAEKYKAEDVQERVSAKNALESYAFNMKSASVEDEGLKG-KISEAD 60
/
/ QY 184 KKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVCNPIISGLYQAGGPG 235
/ Db 61 KKAIEBAVKDALDFVHENPNADREEFEAARTKLSQVTNPPIQKVYQGAAGSG 112
/
/ RESULT 86
/ US-09-565-501A-49
/ Sequence 49, Application US/09565501A
/ Patent No. 6607731
/ GENERAL INFORMATION:
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Campos-Neto, Antonio
/ APPLICANT: Webb, John R.
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Bhatia, Ajay
/ APPLICANT: Coler, Rhea
/ APPLICANT: Peter, Probst
/ TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND DIAGNOSIS OF LEISHMANIASIS
/ FILE REFERENCE: 210121.420C6
```

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/
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ ORIGINAL SOURCE:
/ ORGANISM: Leishmania chagasi
/
/ US-09-022-765-49
/
/ Query Match 18.9%; Score 248.5; DB 3; Length 136;
/ Best Local Similarity 44.6%; Pred. No. 2.3e-15;
/ Matches 50; Conservative 28; Mismatches 33; Indels 1; Gaps 1;
/
/ QY 125 GRLSKEEIERMVQAEKYKAEDVQERVSAKNALESYAFNMKSASVEDEGLKG-KISEAD 183
/ Db 1 GRLSKEEIERMVQAEKYKAEDVQERVSAKNALESYAFNMKSASVEDEGLKG-KISEAD 60
/
/ QY 184 KKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVCNPIISGLYQAGGPG 235
/ Db 61 KKAIEBAVKDALDFVHENPNADREEFEAARTKLSQVTNPPIQKVYQGAAGSG 112
/
/ RESULT 85
/ US-09-551-974A-49
/ Sequence 49, Application US/09551974A
/ Patent No. 6500437
/ GENERAL INFORMATION:
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Campos-Neto, Antonio
/ APPLICANT: Webb, John R.
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Skeiky, Yasir A.W.
/ TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND DIAGNOSIS OF LEISHMANIASIS
/ FILE REFERENCE: 210121.420C5
/ CURRENT APPLICATION NUMBER: US/09/551,974A
/ CURRENT FILING DATE: 2000-04-14
/ NUMBER OF SEQ ID NOS: 101
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 49
/ LENGTH: 136
/ TYPE: PRT
/ ORGANISM: Leishmania chagasi
/
/ US-09-551-974A-49
/
/ Query Match 18.9%; Score 248.5; DB 4; Length 136;
/ Best Local Similarity 44.6%; Pred. No. 2.3e-15;
/ Matches 50; Conservative 28; Mismatches 33; Indels 1; Gaps 1;
/
/ QY 125 GRLSKEEIERMVQAEKYKAEDVQERVSAKNALESYAFNMKSASVEDEGLKG-KISEAD 183
/ Db 1 GRLSKEEIERMVQAEKYKAEDVQERVSAKNALESYAFNMKSASVEDEGLKG-KISEAD 60
/
/ QY 184 KKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVCNPIISGLYQAGGPG 235
/ Db 61 KKAIEBAVKDALDFVHENPNADREEFEAARTKLSQVTNPPIQKVYQGAAGSG 112
/
/ RESULT 86
/ US-09-565-501A-49
/ Sequence 49, Application US/09565501A
/ Patent No. 6607731
/ GENERAL INFORMATION:
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Campos-Neto, Antonio
/ APPLICANT: Webb, John R.
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Bhatia, Ajay
/ APPLICANT: Coler, Rhea
/ APPLICANT: Peter, Probst
/ TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND DIAGNOSIS OF LEISHMANIASIS
/ FILE REFERENCE: 210121.420C6
```

```

; APPLICANT: Coler, Rhea
; APPLICANT: Probat, Peter
; APPLICANT: Brannon, Mark
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121.420C8
; CURRENT APPLICATION NUMBER: US/09/874,923
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Leishmania chagasi
US-09-874-923--49

Query Match      18.9%; Score 248.5; DB 4; Length 136;
Best Local Similarity 44.8%; Pred.No. 2.3e-15;
Matches 50; Conservative 28; Mismatches 33; Indels 1; Gaps 1;

Qy      125  GRLSKEEIERMWQAEABKYKAEDVQRRVRSAKNALESYAFNMKSASVEDEGLKG-KISEAD 183
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1  GRLSEIEIERMWREAAEFEDDRKVRERVKAKNLSLEIAYSLRNQINDKDKGLKLAADD 60

Qy      184  KKKVLKQCEVTSWLDANTLAEKDFEHKKELEQVCNPIISGLYQAGGPG 235
          ||: : : : : : : : : : : : : : : : : : : : : : : : : :
Db      61  KKAIEBAVKDALDFVHENPNADREEFEAARTKLQSVTNPIIQVYQGAAGSG 112

RESULT 89
US-09-902-540-15138
; Sequence 15138, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15138
; LENGTH: 535
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-15138

Query Match      17.8%; Score 234.5; DB 4; Length 535;
Best Local Similarity 38.3%; Pred.No. 3.1e-13;
Matches 49; Conservative 31; Mismatches 47; Indels 1; Gaps 1;

Qy      10  LLDVAPLSLGLTAGGVMTALIKRNSTIPTKQTQFIETTSYSDNPQGVLIQVYGERAMTKD 69
          :||:|||||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db      389  LVDVTPLSLRIGTVGGYTEKIDKNTPVPIDRSKTTTTSRDGQEKVKIRYQGESNRADE 448

Qy      70  NNLLGRFELSGIPPPARGVPQIEVTPDIDANGILNATATDKSTGKANKKTIITNDKGRLSK 129
          :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db      449  CEMLGFEFAGFRIGYRGEVKIEVTEINDGLVHVHSACDTAQKTSITLSSG-MSE 507

Qy      130  EIERMVQ 137
          :||: :||:
Db      508  ADIQQSIQ 515

RESULT 90
US-09-902-540-14235
; Sequence 14235, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:

```



```
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14235
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-14235

Query Match      17.2%; Score 226.5; DB 4; Length 506;
Best Local Similarity 35.5%; Pred. No. 1.6e-12;
Matches 44; Conservative 29; Mismatches 46; Indels 5; Gaps 1;

QY 2 SENVQD-----LLLDVAPLSGLGTAGGVMTALIKRNSTIPTKOTQIFTTYSNQPGLV 56
Db 378 AHSIQDNTNRIQLLDVIPAIGLEKAGAFHVFPRNASIPNAKQLATISMDNQTELA 437

QY 57 IQYVEGERAMTKNNLLGRFELSGIPPPAPRGVPGQIEVTFDIDANGILNVTATDKSTGKAN 116
Db 438 VRIFQGNELVARNDMLGETTFSGIQPRAGPALVEITFDANVEGILTWEARDPVSGREM 497

QY 117 KITI 120
Db 498 KTTV 501

RESULT 91
US-09-581-001B-6
; Sequence 6, Application US/09581001B
; Patent No. 6472142
; GENERAL INFORMATION:
; APPLICANT: Danan-Van Oorschot, Astrid
; APPLICANT: Danan-Van Oorschot, Astrid
; TITLE OF INVENTION: METHODS AND MEANS FOR INDUCING APOPTOSIS BY INTERFERING WITH
; FILE REFERENCE: 2906-4940US
; CURRENT APPLICATION NUMBER: US/09/581.001B
; CURRENT FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: PCT/NL98/00688
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: EP 97203783.2
; PRIOR FILING DATE: 1997-12-03
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-581-001B-6

Query Match      17.0%; Score 223; DB 4; Length 69;
Best Local Similarity 78.2%; Pred. No. 2e-13;
Matches 43; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 49 SDNPQGLVIOYVEGERAMTKNNLLGRFELSGIPPPAPRGVPGQIEVTFDIDANGIL 103
Db 12 SDNQPTVIKVEGERPLTKDNLHLLGTFTVGTGIPPPAPRGVPGQIEVTFIDVNGIL 66

RESULT 92
US-09-902-540-10349
; Sequence 10349, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
```

```
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10349
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-10349

Query Match      16.5%; Score 217; DB 4; Length 690;
Best Local Similarity 31.9%; Pred. No. 1.8e-11;
Matches 43; Conservative 35; Mismatches 51; Indels 6; Gaps 1;

QY 5 VQDLLLDVAPLSGLGTAGGVMTALIKRNSTIPTKOTQIFTTYSNQPGLVIOYVEGER 64
Db 474 LEGVLLIDVLPMAIGVGLPGREFKAVMERTSLPSTKSYTLATHRDGQTELELTVPQDS 533

QY 65 AMTKNNLLGRFELSGIPPPAPRGVPGQIEVTFDIDANGILNVTATDKSTGKANKITIND- 123
Db 534 DKAADNEYLTKLEGLPKLPRGAVQVNVTFEVSNESSLKLVTAAREASSGREVTSTFTTRD 593

QY 124 -----KGRLSKEIE 133
Db 594 TPEAVKARLAQLESE 608

RESULT 93
US-09-902-540-11750
; Sequence 11750, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11750
; LENGTH: 1027
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11750

Query Match      16.4%; Score 216; DB 4; Length 1027;
Best Local Similarity 30.8%; Pred. No. 4e-11;
Matches 45; Conservative 37; Mismatches 60; Indels 4; Gaps 2;

QY 3 ENVQDLLLDVAPLSGLGTAGGVMTALIKRNSTIPTKOTQIFTTYSNQPGLVIOYVEG 62
Db 861 DKVSSVLLIDVLPMTGVAMPGGAFKRVIERNSPLPAQRSAFNTTKDNEVFLSIFQG 920

QY 63 ERAMTKNNLLGRFELSGIPPPAPRGVPGQIEVTFDIDANGILNVTATDKSTGKANKITIN 122
Db 921 EDHSISANEYLGTVRIEGLPKGPGSVRVAVTLKIDSECVLHVAREYSTKKEVKATLAT 980

QY 123 DKGRLSKEIERMVQ-EAEKYKADE 147
Db 981 ---RYSPEELQKQLQVSKESVKAEE 1003

RESULT 94
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US-08-472-534-3
; Sequence 3, Application US/08472534
; Patent No. 5919620
; GENERAL INFORMATION:
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; TITLE OF INVENTION: HEAT SHOCK PROTEIN HSP72 FROM
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,534
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr. James P
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Biovac-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 714 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-472-534-3

Query Match 15.3%; Score 201; DB 2; Length 714;
Best Local Similarity 31.6%; Pred. No. 5.8e-10;
Matches 54; Conservative 33; Mismatches 71; Indels 14; Gaps 4;

QY 88 VPOIEVTFDIDANGILNVATDKSTGKANKITITNDKGRLSKEEIERMVOEAEKYAEDE 147
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
546 IPQIEVTFDIDKRGIVSVKADLGTQKEQTIVIQNSG-LTDEEIDRMKDAEANAESDK 604

QY 148 VQREYSVAKNALESYAFNMKSAVEDEGLKGKISEADKKKV---LDKCRQVISWLDANTL 203
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
605 KRKEVDLRNEVDQAIPTATKTIKETEGKGFDAERDAQAALDDLKKAQE-----DNNL- 658

QY 204 AEKDEFEHKEKLEQVCNPIISGLYQAGGPGFGFGAQQGPKGSGSGPTI 254
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
659 ---DDMKAKLEALNEKAQGLAVKLYEQAAAAQAQGAEGGAQATGNAGDDV 706

RESULT 95
US-09-581-001B-11
; Sequence 11, Application US/09581001B
; Patent No. 6472142
; GENERAL INFORMATION:
; APPLICANT: No. 6472142eborn, Mathieu
; APPLICANT: Danan-Van Orschot, Astrid
; TITLE OF INVENTION: METHODS AND MEANS FOR INDUCING APOPTOSIS BY INTERFERING WITH
; TITLE OF INVENTION: BIP-LIKE PROTEINS
; FILE REFERENCE: 2506-4940US
; CURRENT APPLICATION NUMBER: US/09/581,001B
; CURRENT FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: PCT/NL98/00688
; PRIOR FILING DATE: 1998-12-03
;
; PRIOR APPLICATION NUMBER: EP 97203783.2
; PRIOR FILING DATE: 1997-12-03
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (21)..(21)
; OTHER INFORMATION: The "Xaa" at position 21 may be any amino acid residue.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (36)..(36)
; OTHER INFORMATION: The "Xaa" at position 36 may be any amino acid residue.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (46)..(46)
; OTHER INFORMATION: The "Xaa" at position 46 may be any amino acid residue.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (59)..(61)
; OTHER INFORMATION: The "Xaa" at positions 59-61 may be any amino acid residue.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (67)..(67)
; OTHER INFORMATION: The "Xaa" at position 67 may be any amino acid residue.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (72)..(73)
; OTHER INFORMATION: The "Xaa" at positions 72-73 may be any amino acid residue.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (77)..(77)
; OTHER INFORMATION: The "Xaa" at position 77 may be any amino acid residue.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (79)..(80)
; OTHER INFORMATION: The "Xaa" at positions 79-80 may be any amino acid residue.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (82)..(82)
; OTHER INFORMATION: The "Xaa" at position 82 may be any amino acid residue.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (84)..(84)
; OTHER INFORMATION: The "Xaa" at position 84 may be any amino acid residue.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (91)..(91)
; OTHER INFORMATION: The "Xaa" at position 91 may be any amino acid residue.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (97)..(98)
; OTHER INFORMATION: The "Xaa" at positions 97-98 may be any amino acid residue.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (110)..(110)
; OTHER INFORMATION: The "Xaa" at position 110 may be any amino acid residue.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (123)..(124)
; OTHER INFORMATION: The "Xaa" at positions 123-124 may be any amino acid residue.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (128)..(129)
; OTHER INFORMATION: The "Xaa" at positions 128-129 may be any amino acid residue.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (133)..(133)
; OTHER INFORMATION: The "Xaa" at position 133 may be any amino acid residue.
; FEATURE:
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Matches 62; Conservative 32; Mismatches 95; Indels 19; Gaps 4;
QY 9 LLLDVAPLSIGLETAGGVTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVYGERAMTK 68
Db 389 LLLDVAAQSLGVMGSRVKRLIPKNTGVPVARDIFYPGSSGQEARIPVYQGESEFQD 448
QY 69 DNNLLGRFELSGIPPPAPRGVPQIEVTFDDANGILNVTATDKSTGKANKITINDKGRLS 128
Db 449 ENYKLGSEVVLKRLHVAARGEVPLEVVPFELSSEALSVKATDLTSGNMEAVRLEARAG-LP 507
QY 129 KERIERMVOEAEYKAEDEQVRRERSAKNALESY-----AFNMKSAVEDSGLKG 177
Db 508 QGAEKLGAEQYARSGV-----VDAKRAELFRKLLERGEKARLLQKSAQENSPEA 563
QY 178 KISEADKKYKLDKQCEVISWLDANTLAE 205
Db 564 QATLGTVQRLLDGGR---SALDSGNAQ 588

RESULT 97
5196523-12
; Patent No. 5196523
; APPLICANT: LEE, AMY S.
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION BY GLUCOSE,
; CALCIUM AND TEMPERATURE
; NUMBER OF SEQUENCES: 28
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/354,988
; FILING DATE: 19-MAY-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 282,880
; FILING DATE: 05-DEC-1988
; APPLICATION NUMBER: 690,951
; FILING DATE: 01-JAN-1985
; SEQ ID NO:12:
; LENGTH: 56
5196523-12

Query Match 14.0%; Score 184; DB 6; Length 56;
Best Local Similarity 65.5%; Pred. No. 6.1e-10;
Matches 36; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
QY 7 DLLLDVAPLSIGLETAGGVTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVYE 61
Db 2 DLVLLHVCPLTLGIETVGGVMTKLIPSNVTVPVTKNSQIFSTASDNOPTVTIKVYE 56

RESULT 98
5196523-12
; Patent No. 5196523
; APPLICANT: LEE, AMY S.
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION BY GLUCOSE,
; CALCIUM AND TEMPERATURE
; NUMBER OF SEQUENCES: 28
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/354,988
; FILING DATE: 19-MAY-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 282,880
; FILING DATE: 05-DEC-1988
; APPLICATION NUMBER: 690,951
; FILING DATE: 01-JAN-1985
; SEQ ID NO:12:
; LENGTH: 56
5196523-12

Query Match 14.0%; Score 184; DB 6; Length 56;
Best Local Similarity 65.5%; Pred. No. 6.1e-10;
Matches 36; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
QY 7 DLLLDVAPLSIGLETAGGVTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVYE 61
Db 2 DLVLLHVCPLTLGIETVGGVMTKLIPSNVTVPVTKNSQIFSTASDNOPTVTIKVYE 56
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RESULT 99
US-09-710-279-1876
; Sequence 1876, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1876
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-1876
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Query Match 12.6%; Score 165; DB 4; Length 337;
Best Local Similarity 56.6%; Pred. No. 4.4e-07;
Matches 30; Conservative 14; Mismatches 9; Indels 0; Gaps 0;
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QY 4 NVQDLLLDVAPLSIGLETAGGVTALIKRNSTIPTKQTQIFTTYSNDQPGVL 56
Db 285 DVKDVLLDVTPLSLGIEIMGGRMNTLIERTTIPTSKSQVYSTAADNQPAVV 337
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RESULT 100
US-09-513-783A-172
; Sequence 172, Application US/09513783A
; Patent No. 6416959
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-L1
; CURRENT APPLICATION NUMBER: US/09/513,783A
; CURRENT FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 172
; LENGTH: 941
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GFP-HSP70
US-09-513-783A-172
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Query Match 9.1%; Score 119; DB 4; Length 941;
Best Local Similarity 16.9%; Pred. No. 0.033;
Matches 51; Conservative 54; Mismatches 110; Indels 86; Gaps 8;
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QY 5 VQDLLLDVAPLSIGLE-----TAGGVMTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQV 59
Db 630 VREFSITDVVPYPISLRWNSPAEGSSDCVFSKNHAAFPKSV---LTFYRKGPFTLEAY 686
QY 60 YEGERAMTKDNNLLGRFELSGIPPAERG-VPOLEVTFDIDANGILNVT----- 107
Db 687 YSSPQDLPPYDPAIAQFSQVKVTPQSDGSSSKVKVRVNVHGFVSSSASLVEVHKSEE 746
QY 108 -----TDKSTGKANKITINDKGR-----SKEIERM----- 135
Db 747 NEBPMETDQNAKEEKQVDEPHVEEQOQTPAENKAESSEMETSQAGSKDKMDQPP 806
QY 136 -----VQEAKEYKAEDVQPERVSAKNALBSYA 163
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Db 807 QCQEGKSEDQYCGPANRESAIWQIDREMLNLYIENEGKIMQDKLEKERNDAKNAVEEYV 866
Qy 164 FNMKSAVEDGLKGKISEADKKVLDKQCVISWL-DANTLAEKDBFEHKKRKELEQVCNP 222
Db 867 YEMDKLSGHEYK-FVSEDDRNSTFLKLEDYENWLYEDGEDQPKQVYVDKLAELKNLGQP 925
Qy 223 I 223
Db 926 I 926

Search completed: April 6, 2005, 17:25:45
Job time : 49 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 6, 2005, 17:24:24 ; Search time 146 Seconds
(without alignments)

586.680 Million cell updates/sec

Title: US-09-646-835-1_COPY_384_641

Perfect score: 1314

Sequence: 1 KSENVODLLLDVAPLSLGL.....FGAGPKGSGSGPTIEVD 258

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA:*
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2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep:*
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9: /cgn2_6/prodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/prodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/prodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/prodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1314	100.0	641	9	US-09-759-010-3
2	1314	100.0	641	10	US-09-935-642-1
3	1314	100.0	641	10	US-09-919-039-146
4	1314	100.0	641	15	US-10-380-408A-5
5	1314	100.0	641	17	US-10-792-571-14
6	1309	99.6	476	15	US-10-108-260A-3466
7	1298.5	98.8	640	16	US-10-408-765A-255
8	1258	95.7	641	14	US-10-316-253-28
9	1258	95.7	641	14	US-10-316-253-97
10	1228.5	93.5	642	9	US-09-761-534A-10
11	1228.5	93.5	642	17	US-10-885-523-10
12	1223	93.1	622	14	US-10-132-556A-2
13	1103	83.9	641	16	US-10-408-765A-1675
14	1100.5	83.8	14	14	US-10-205-331-106
15	1100.5	83.8	16	16	US-10-380-408A-7
16	1099	83.6	17	17	US-10-408-765A-1753
17	1097.5	83.5	18	18	US-09-759-010-4
18	1097.5	83.5	19	19	US-09-870-759-43
19	1097.5	83.5	20	20	US-09-935-642-16
20	1097.5	83.5	21	21	US-09-919-039-11
21	1097.5	83.5	22	22	US-09-751-708A-43
22	1097.5	83.5	23	23	US-10-126-103-147
23	1097.5	83.5	24	24	US-10-431-096-147
24	1097.5	83.5	25	25	US-10-408-765A-703
25	1097.5	83.5	26	26	US-10-737-350-1
26	1097.5	83.5	27	27	US-10-841-207-4
27	1097.5	83.5	28	28	US-10-100-957A-174
28	1097.5	83.5	29	29	US-10-108-260A-4141
29	1097	83.5	30	30	US-09-919-039-73
30	1093	83.2	31	31	US-10-380-408A-6
31	1091.5	83.1	32	32	US-10-108-260A-3524
32	1089.5	82.9	33	33	US-10-108-260A-4616
33	1059.5	80.6	34	34	US-10-408-765A-1693
34	1059.5	80.6	35	35	US-10-408-765A-1723
35	1059.5	80.6	36	36	US-10-369-493-6233
36	1034	78.7	37	37	US-10-108-605-75
37	1030	78.4	38	38	US-09-733-179A-11
38	1012	77.0	39	39	US-09-919-039-204
39	1012	77.0	40	40	US-10-755-889-396
40	1012	77.0	41	41	US-09-925-302-724
41	1012	77.0	42	42	US-10-424-599-156572
42	1012	77.0	43	43	US-10-424-599-156571
43	965	73.4	44	44	US-10-424-599-156568
44	963.5	73.3	45	45	US-10-424-599-156571
45	963	73.3	46	46	US-10-424-599-156571
46	957	72.8	47	47	US-10-424-599-156571
47	957	72.8	48	48	US-10-424-599-156571
48	956	72.7	49	49	US-10-424-599-156571
49	955	72.7	50	50	US-10-424-599-156571
50	954	72.6	51	51	US-10-424-599-156571
51	954	72.6	52	52	US-10-424-599-156571
52	954	72.6	53	53	US-10-424-599-156571
53	954	72.6	54	54	US-10-424-599-156571
54	954	72.6	55	55	US-10-424-599-156571
55	952.5	72.5	56	56	US-10-424-599-156571
56	952	72.5	57	57	US-10-424-599-156571
57	951	72.4	58	58	US-10-424-599-156571
58	949	72.2	59	59	US-10-424-599-156571
59	949	72.2	60	60	US-10-424-599-156571
60	946	72.0	61	61	US-10-424-599-156571
61	946	72.0	62	62	US-10-424-599-156571
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64	946	72.0	65	65	US-10-424-599-156571
65	944	71.8	66	66	US-10-424-599-156571
66	942	71.7	67	67	US-10-424-599-156571
67	942	71.7	68	68	US-10-424-599-156571
68	939.5	71.5	69	69	US-10-424-599-156571
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70	939	71.5	71	71	US-10-424-599-156571
71	939	71.5	72	72	US-10-424-599-156571
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73	939	71.5	74	74	US-10-424-599-156571
74	939	71.5	75	75	US-10-424-599-156571
75	939	71.5	76	76	US-10-424-599-156571
76	939	71.5	77	77	US-10-424-599-156571
77	939	71.5	78	78	US-10-424-599-156571
78	939	71.5	79	79	US-10-424-599-156571
79	939	71.5	80	80	US-10-424-599-156571
80	939	71.5	81	81	US-10-424-599-156571
81	939	71.5	82	82	US-10-424-599-156571
82	939	71.5	83	83	US-10-424-599-156571
83	939	71.5	84	84	US-10-424-599-156571
84	939	71.5	85	85	US-10-424-599-156571
85	939	71.5	86	86	US-10-424-599-156571

87 938 71.4 652 15 US-10-425-114-38995 Sequence 38995, A
88 938 71.4 652 15 US-10-425-114-55225 Sequence 55225, A
89 938 71.4 652 15 US-10-425-114-59328 Sequence 59328, A
90 938 71.4 652 15 US-10-425-114-61345 Sequence 61345, A
91 938 71.4 652 15 US-10-425-114-62560 Sequence 62560, A
92 938 71.4 652 15 US-10-425-114-63240 Sequence 63240, A
93 938 71.4 652 15 US-10-425-114-63457 Sequence 63457, A
94 938 71.4 652 15 US-10-425-114-63505 Sequence 63505, A
95 938 71.4 652 15 US-10-425-114-65274 Sequence 65274, A
96 928.5 70.7 649 16 US-10-437-963-193938 Sequence 193938, A
97 920.5 70.1 461 15 US-10-425-114-54413, A
98 918.5 69.9 658 15 US-10-425-114-57892, A
99 912.5 69.4 653 15 US-10-425-114-65502 Sequence 65502, A
100 911 69.3 656 16 US-10-451-467A-536 Sequence 536, App

ALIGNMENTS

RESULT 1

US-09-759-010-3
; Sequence 3, Application US/09759010
; Patent No. US2001003042A1
; GENERAL INFORMATION:
; APPLICANT: Strivastava, Pramod K.
; TITLE OF INVENTION: COMPLEXES OF PEPTIDE BINDING FRAGMENTS OF HEAT-SHOCK
; TITLE OF INVENTION: PROTEINS AND THEIR USE AS IMMUNOTHERAPEUTIC AGENTS
; FILE REFERENCE: 8449-135
; CURRENT APPLICATION NUMBER: US/09/759,010
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; TYPE: PRF
; LENGTH: 641
; ORGANISM: Homo sapiens
US-09-759-010-3

Query Match 100.0%; Score 1314; DB 9; Length 641;
Best Local Similarity 100.0%; Pred. No. 2.8e-95;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSENVQDLLLDVAPLSGLGLETAGGVTALIKRNSIPTKQTOIFTTYSNQPGLIQVY 60
DB 384 KSENVQDLLLDVAPLSGLGLETAGGVTALIKRNSIPTKQTOIFTTYSNQPGLIQVY 443
QY 61 EGERAMTKONLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKONLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVQEAKEYKAEDVQERVSAKNALESYAFNMKMSAVEDGLKKGKIS 180
DB 504 TNDKGRLSKEEIERMVQEAKEYKAEDVQERVSAKNALESYAFNMKMSAVEDGLKKGKIS 563
QY 181 EADKKVLDKQCVISWLDANTLAEDFEHKKKELEQVNCNPIISGLYQAGGPGGFG 240
DB 564 EADKKVLDKQCVISWLDANTLAEDFEHKKKELEQVNCNPIISGLYQAGGPGGFG 623
QY 241 AQGPKGSGSGPTIEVD 258
DB 624 AQGPKGSGSGPTIEVD 641

RESULT 2

US-09-935-642-1
; Sequence 1, Application US/09935642
; Publication No. US20030044795A1
; GENERAL INFORMATION:
; APPLICANT: BYRJALSEN, Inger
; APPLICANT: LARSEN, Peter
; APPLICANT: STEPHEN, John
; TITLE OF INVENTION: Biochemical Markers for the Human
; TITLE OF INVENTION: Endometrium

; FILE REFERENCE: 8969-014
; CURRENT APPLICATION NUMBER: US/09/935,642
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: PCT/GB97/02394
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: PCT/GB9707132.8
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: PCT/GB9618600.2
; PRIOR FILING DATE: 1996-09-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 641
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-935-642-1

Query Match 100.0%; Score 1314; DB 10; Length 641;
Best Local Similarity 100.0%; Pred. No. 2.8e-95;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSENVQDLLLDVAPLSGLGLETAGGVTALIKRNSIPTKQTOIFTTYSNQPGLIQVY 60
DB 384 KSENVQDLLLDVAPLSGLGLETAGGVTALIKRNSIPTKQTOIFTTYSNQPGLIQVY 443
QY 61 EGERAMTKONLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKONLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVQEAKEYKAEDVQERVSAKNALESYAFNMKMSAVEDGLKKGKIS 180
DB 504 TNDKGRLSKEEIERMVQEAKEYKAEDVQERVSAKNALESYAFNMKMSAVEDGLKKGKIS 563
QY 181 EADKKVLDKQCVISWLDANTLAEDFEHKKKELEQVNCNPIISGLYQAGGPGGFG 240
DB 564 EADKKVLDKQCVISWLDANTLAEDFEHKKKELEQVNCNPIISGLYQAGGPGGFG 623
QY 241 AQGPKGSGSGPTIEVD 258
DB 624 AQGPKGSGSGPTIEVD 641

RESULT 3

US-09-919-039-146
; Sequence 146, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 146
; LENGTH: 641
; TYPE: PRF
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 1678695CD1
US-09-919-039-146

Query Match 100.0%; Score 1314; DB 10; Length 641;
Best Local Similarity 100.0%; Pred. No. 2.8e-95;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSENVQDLLLDVAPLSGLGLETAGGVTALIKRNSIPTKQTOIFTTYSNQPGLIQVY 60
DB 384 KSENVQDLLLDVAPLSGLGLETAGGVTALIKRNSIPTKQTOIFTTYSNQPGLIQVY 443

Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503
Qy 121 TNDKGRLSKEEIERMVOEAEKYAEDEVQERVSNAKNALESYAFNMKSAVEDEGLGKIS 180
Db 504 TNDKGRLSKEEIERMVOEAEKYAEDEVQERVSNAKNALESYAFNMKSAVEDEGLGKIS 563
Qy 181 EADKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVNCNPIISGLYQAGGPGPGFG 240
Db 564 EADKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVNCNPIISGLYQAGGPGPGFG 623
Qy 241 AQPCKGSGSGPTIEVD 258
Db 624 AQPCKGSGSGPTIEVD 641

RESULT 4

US-10-380-408A-5
; Sequence 5, Application US/10380408A
; Publication No. US20040063173A1
; GENERAL INFORMATION:
; APPLICANT: MUTHOFF, Gabriele
; TITLE OF INVENTION: An Hsp70 peptide stimulating Natural Killer (NK) cell activity
; FILE REFERENCE: E 2022 PCT
; CURRENT APPLICATION NUMBER: US/10/380,408A
; PRIOR FILING DATE: 2003-08-25
; PRIOR APPLICATION NUMBER: EP 00119933.0
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-380-408A-5

Query Match 100.0%; Score 1314; DB 15; Length 641;
Best Local Similarity 100.0%; Pred. No. 2.8e-95;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLLDVAPLSGLGTAGGVMTALIKRNSTIPTKTQIFTTYSNQPGVLIQVY 60
Db 384 KSENVQDLLLLDVAPLSGLGTAGGVMTALIKRNSTIPTKTQIFTTYSNQPGVLIQVY 443
Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503
Qy 121 TNDKGRLSKEEIERMVOEAEKYAEDEVQERVSNAKNALESYAFNMKSAVEDEGLGKIS 180
Db 504 TNDKGRLSKEEIERMVOEAEKYAEDEVQERVSNAKNALESYAFNMKSAVEDEGLGKIS 563
Qy 181 EADKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVNCNPIISGLYQAGGPGPGFG 240
Db 564 EADKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVNCNPIISGLYQAGGPGPGFG 623
Qy 241 AQPCKGSGSGPTIEVD 258
Db 624 AQPCKGSGSGPTIEVD 641

RESULT 5

US-10-792-571-14
; Sequence 14, Application US/10792571
; Publication No. US20050048608A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Sham-Yuen
; APPLICANT: Tang, Hsin-yi
; APPLICANT: Tao, Yiwen
; APPLICANT: Wu, Yongjian
; APPLICANT: Kelly, Ruth

; TITLE OF INVENTION: Use of Molecular Chaperones for the Enhanced Production of
; TITLE OF INVENTION: Secreted, Recombinant Proteins in Mammalian Cells
; FILE REFERENCE: 03-302-A
; CURRENT APPLICATION NUMBER: US/10/792,571
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/483,505
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-792-571-14

Query Match 100.0%; Score 1314; DB 17; Length 641;
Best Local Similarity 100.0%; Pred. No. 2.8e-95;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLLDVAPLSGLGTAGGVMTALIKRNSTIPTKTQIFTTYSNQPGVLIQVY 60
Db 384 KSENVQDLLLLDVAPLSGLGTAGGVMTALIKRNSTIPTKTQIFTTYSNQPGVLIQVY 443
Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503
Qy 121 TNDKGRLSKEEIERMVOEAEKYAEDEVQERVSNAKNALESYAFNMKSAVEDEGLGKIS 180
Db 504 TNDKGRLSKEEIERMVOEAEKYAEDEVQERVSNAKNALESYAFNMKSAVEDEGLGKIS 563
Qy 181 EADKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVNCNPIISGLYQAGGPGPGFG 240
Db 564 EADKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVNCNPIISGLYQAGGPGPGFG 623
Qy 241 AQPCKGSGSGPTIEVD 258
Db 624 AQPCKGSGSGPTIEVD 641

RESULT 6

US-10-108-260A-3466
; Sequence 3466, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3466
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-3466

Query Match 99.6%; Score 1309; DB 15; Length 476;
Best Local Similarity 99.6%; Pred. No. 4.7e-95;
Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLLDVAPLSGLGTAGGVMTALIKRNSTIPTKTQIFTTYSNQPGVLIQVY 60
Db 219 KSENVQDLLLLDVAPLSGLGTAGGVMTALIKRNSTIPTKTQIFTTYSNQPGVLIQVY 278
Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 279 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 338
Qy 121 TNDKGRLSKEEIERMVOEAEKYAEDEVQERVSNAKNALESYAFNMKSAVEDEGLGKIS 180
Db 339 TNDKGRLSKEEIERMVOEAEKYAEDEVQERVSNAKNALESYAFNMKSAVEDEGLGKIS 398

RESULT 8
US-10-316-253-28
; Sequence 28, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316.253

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RESULT 9
US-10-316-253-97
; Sequence 97, Application US/10316253
; Publication NO. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Grels, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 97
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-97

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Query Match	95.7%	Score 1258;	DB 14;	Length 641;
Best Local Similarity	95.3%;	Pred. No. 7.5e-91;		
Matches 246;	Conservative 7;	Mismatches 5;	Indels 0;	Gaps 0;

QY	1	KSENVQDLLILLDVAPISLGLGTAGGVTWTAIIKENSTIPKQTQITFTTYSNQEGVLIQVY	60
Db	384	KSENVQDLLILLDVAPISLGLGTAGGVTWTAIIKENSTIPKQTQITFTTYSNQEGVLIQVY	443
QY	61	EGERAMTKNNLLGRFELSGIIPAPRGVPQIEVFTFIDANGILNVTATDKSTGKANKITI	120
Db	444	EGERAMTRDNNLLGRFELSGIIPAPRGVPQIEVFTFIDANGILNVTATDKSTGKANKITI	503
QY	121	TNDKGRLSKETIRMYOEAOKYKAEDVORERSAKNALESYAFNMKSAVEDEGLKGKIS	180

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Db 504 TNDKGRLSKEEIERMVOEAEYKAEDVQERVAAKNALESYAFNMKSAVEDGLGKIS 563
Qy 181 EADKKVLDKQCVISWLDANTLAEDKDFEHKKELEOVNPIISGLYQAGAGPGPGFG 240
Db 564 EADKKVLDKQCVISWLDANTLAEDKDFEHKKELEOVNPIISGLYQAGAGPGPGFG 623
Qy 241 AQPKGGSGSGPTIEVD 258
Db 624 AQPKGGSGSGPTIEVD 641

RESULT 10
US-09-761-534A-10
; Sequence 10, Application US/09761534A
; Patent No. US20020146426A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Qian
; APPLICANT: Richmond, Joan F.L.
; APPLICANT: Cho, Bryan K.
; APPLICANT: Palliser, Deborah
; APPLICANT: Chen, Jianzhu
; APPLICANT: Eisen, Herman N.
; APPLICANT: Young, Richard A.
; TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock
; TITLE OF INVENTION: Protein Fusion Proteins Maps To A Discrete Domain and is
; FILE REFERENCE: 0399.2006-003
; CURRENT APPLICATION NUMBER: US/09/761,534A
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/US00/32831
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/176,143
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 642
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Murine hsp70
US-09-761-534A-10

Query Match 93.5%; Score 1228.5; DB 9; Length 642;
Best Local Similarity 93.1%; Pred. No. 1.6e-88;
Matches 241; Conservative 11; Mismatches 6; Indels 1; Gaps 1;

Qy 1 KSENVQDLLLDVAPLSGLGTAGGVMTALIKRNSTIPTKTQTFITYSDNQPGVLIQVY 60
Db 384 KSENVQDLLLDVAPLSGLGTAGGVMTALIKRNSTIPTKTQTFITYSDNQPGVLIQVY 443
Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVQIETVTFDANGILNVATDSTGKANKITI 120
Db 444 EGERAMTRDNNLLGRFELSGIPAPRGVQIETVTFDANGILNVATDSTGKANKITI 503
Qy 121 TNDKGRLSKEEIERMVOEAEYKAEDVQERVAAKNALESYAFNMKSAVEDGLGKIS 180
Db 504 TNDKGRLSKEEIERMVOEAEYKAEDVQERVAAKNALESYAFNMKSAVEDGLGKIS 563
Qy 181 EADKKVLDKQCVISWLDANTLAEDKDFEHKKELEOVNPIISGLYQAGAGPGPGFG 240
Db 564 EADKKVLDKQCVISWLDANTLAEDKDFEHKKELEOVNPIISGLYQAGAGPGPGFG 623
Qy 241 AQPKGGSGSGPTIEVD 258
Db 624 AQPKGGSGSGPTIEVD 642

RESULT 11
US-10-885-523-10
; Sequence 10, Application US/10885523
; Publication No. US20050048079A1
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; GENERAL INFORMATION:
; APPLICANT: Huang, Qian
; APPLICANT: Richmond, Joan F.L.
; APPLICANT: Cho, Bryan K.
; APPLICANT: Palliser, Deborah
; APPLICANT: Chen, Jianzhu
; APPLICANT: Eisen, Herman N.
; APPLICANT: Young, Richard A.
; TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock
; TITLE OF INVENTION: Protein Fusion Proteins Maps To A Discrete Domain and is
; FILE REFERENCE: 0399.2006-003
; CURRENT APPLICATION NUMBER: US/10/885,523
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: US/09/761,534
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/US00/32831
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/176,143
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 642
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Murine hsp70
US-10-885-523-10

Query Match 93.5%; Score 1228.5; DB 17; Length 642;
Best Local Similarity 93.1%; Pred. No. 1.6e-88;
Matches 241; Conservative 11; Mismatches 6; Indels 1; Gaps 1;

Qy 1 KSENVQDLLLDVAPLSGLGTAGGVMTALIKRNSTIPTKTQTFITYSDNQPGVLIQVY 60
Db 384 KSENVQDLLLDVAPLSGLGTAGGVMTALIKRNSTIPTKTQTFITYSDNQPGVLIQVY 443
Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVQIETVTFDANGILNVATDSTGKANKITI 120
Db 444 EGERAMTRDNNLLGRFELSGIPAPRGVQIETVTFDANGILNVATDSTGKANKITI 503
Qy 121 TNDKGRLSKEEIERMVOEAEYKAEDVQERVAAKNALESYAFNMKSAVEDGLGKIS 180
Db 504 TNDKGRLSKEEIERMVOEAEYKAEDVQERVAAKNALESYAFNMKSAVEDGLGKIS 563
Qy 181 EADKKVLDKQCVISWLDANTLAEDKDFEHKKELEOVNPIISGLYQAGAGPGPGFG 240
Db 564 EADKKVLDKQCVISWLDANTLAEDKDFEHKKELEOVNPIISGLYQAGAGPGPGFG 623
Qy 241 AQPKGGSGSGPTIEVD 258
Db 624 AQPKGGSGSGPTIEVD 642

RESULT 12
US-10-132-556A-2
; Sequence 2, Application US/10132556A
; Publication No. US20030082629A1
; GENERAL INFORMATION:
; APPLICANT: Volloch, Vladimir
; APPLICANT: Sherman, Michael
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL
; TITLE OF INVENTION: IN THE REGULATION OF CELL PROLIFERATION
; FILE REFERENCE: A32367-PCT-USA-A 066290.0106
; CURRENT APPLICATION NUMBER: US/10/132,556A
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 09/936,879
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/07350
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,046
; PRIOR FILING DATE: 1999-03-18
```

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; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-556A-2

Query Match      93.1%; Score 1223; DB 14; Length 622;
Best Local Similarity 100.0%; Pred. No. 4.2e-88;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVMTALIKRNSIPTPTKQTQIFFTYSDNQPGVLIQVY 60
DB 382 KSENVQDLLLLDVAPLSGLGLETAGGVMTALIKRNSIPTPTKQTQIFFTYSDNQPGVLIQVY 441
QY 61 EGERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 442 EGERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 501
QY 121 TNDKGRLSKEIEIRMVQAEKYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 180
DB 502 TNDKGRLSKEIEIRMVQAEKYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 561
QY 181 EADKKKVLDRKQEVISWLDANTLAERKDEFEHKKRKELEQVNCNPIISGLYQAGGPGGFG 240
DB 562 EADKKKVLDRKQEVISWLDANTLAERKDEFEHKKRKELEQVNCNPIISGLYQAGGPGGFG 621
QY 241 A 241
DB 622 A 622

RESULT 13
US-10-408-765A-1675
; Sequence 1675, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 1675
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1675

Query Match      83.9%; Score 1103; DB 16; Length 641;
Best Local Similarity 82.3%; Pred. No. 1.4e-78;
Matches 218; Conservative 16; Mismatches 15; Indels 16; Gaps 2;

QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVMTALIKRNSIPTPTKQTQIFFTYSDNQPGVLIQVY 60
DB 386 KSENVQDLLLLDVAPLSGLGLETAGGVMTALIKRNSIPTPTKQTQIFFTYSDNQPGVLIQVY 445
QY 61 EGERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 446 EGERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 505
QY 121 TNDKGRLSKEIEIRMVQAEKYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 180
DB 506 TNDKGRLSKEIEIRMVQAEKYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 565
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QY 181 EADKKKVLDRKQEVISWLDANTLAERKDEFEHKKRKELEQVNCNPIISGLYQAGGPGGFG 240
DB 566 ESDKNKILLDKCNELLSWLEVNQLAERKDEFEHKKRKELEQVNCNPIISGLYQAGGPGGFG 616
QY 241 AOGPKGGSG-----SGPTIEVD 258
DB 617 CTGPACGTGYVPRPATGPTIEVD 641

RESULT 14
US-10-205-331-106
; Sequence 106, Application US/10205331
; Publication No. US20040058326A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Finnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018199
; CURRENT APPLICATION NUMBER: US/10/205,331
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Heat shock cognate protein 70
US-10-205-331-106
```

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Query Match      83.8%; Score 1100.5; DB 15; Length 646;
Best Local Similarity 81.7%; Pred. No. 2.2e-78;
Matches 215; Conservative 23; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVMTALIKRNSIPTPTKQTQIFFTYSDNQPGVLIQVY 60
DB 384 KSENVQDLLLLDVAPLSGLGLETAGGVMTALIKRNSIPTPTKQTQIFFTYSDNQPGVLIQVY 443
QY 61 EGERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 444 EGERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 503
QY 121 TNDKGRLSKEIEIRMVQAEKYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 180
DB 504 TNDKGRLSKEIEIRMVQAEKYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 563
QY 181 EADKKKVLDRKQEVISWLDANTLAERKDEFEHKKRKELEQVNCNPIISGLYQAGGPGGFG 237
DB 564 DEDKQKILLDKCNELLSWLEVNQLAERKDEFEHKKRKELEQVNCNPIISGLYQAGGPGGFG 623
QY 238 GF--GAQPGKGGSGGPTIEVD 258
DB 624 GFPGGGAPPGSGGSGPTIEVD 646

RESULT 15
US-10-841-207-2
; Sequence 2, Application US/10841207
; Publication No. US20050009772A1
; GENERAL INFORMATION:
; APPLICANT: Caprioli, Joseph
; TITLE OF INVENTION: Methods and Compositions for the Treatment of Glaucoma and Other
; TITLE OF INVENTION: Retinal Diseases
; FILE REFERENCE: A-72263/TAL/MWR (468290-00515)
; CURRENT APPLICATION NUMBER: US/10/841,207
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: US 60/468,554
```

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; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-841-207-2

Query Match      83.8%; Score 1100.5; DB 17; Length 646;
Best Local Similarity 81.7%; Pred. No. 2.2e-78;
Matches 215; Conservative 23; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVQDLLLDVAPLSGLGLETAGGVTALIKRNTSTPTKQTQIFTTYSNQPGVLIOVY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 384 KSENVQDLLLDVTPLSGLGLETAGGVTALIKRNTTPTKQTQIFTTYSNQPGVLIOVY 443

QY 61 EGERAMTKNNLGRFELSGIPAPRGVPOIETFDIDANGILNVATDKSTGKANKITI 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 444 EGERAMTKNNLGRFELSGIPAPRGVPOIETFDIDANGILNVATDKSTGKANKITI 503

QY 121 TNDKGRLSKEEIERMWQAEKYKAEDVQREVRSKNALESYAFNMKSASVEDGLGKIS 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 504 TNDKGRLSKEDIERMWQAEKYKAEDKQDKVSSKNSLESYAFNMKATVEDEKLQKIN 563

QY 181 EADKKVLDKQEVISWLDANTLAEKDEFHKKRKELEQVNCNPIISGLYQAGG-PG--PG 237
    :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 564 DEDKQKILDKCNEIISWLDKNQTAKEEFHKKRKELEKVCNPIITKLYQSAGGMPGMPG 623

QY 238 GF--GAQPKGSGSGPTIEVD 258
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 624 GPFPGGAPPSGGSGPTIEVD 646

RESULT 16
US-10-380-408A-7
; Sequence 7, Application US/10380408A
; Publication No. US20040063173A1
; GENERAL INFORMATION:
; APPLICANT: MULTHOPE, Gabriele
; TITLE OF INVENTION: An Hep70 peptide stimulating Natural Killer (NK) cell activity
; FILE REFERENCE: E 2022 PCT
; CURRENT APPLICATION NUMBER: US/10/380,408A
; PRIOR FILING DATE: 2003-08-25
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-380-408A-7

Query Match      83.6%; Score 1099; DB 15; Length 641;
Best Local Similarity 81.9%; Pred. No. 2.8e-78;
Matches 217; Conservative 16; Mismatches 16; Indels 16; Gaps 2;

QY 1 KSENVQDLLLDVAPLSGLGLETAGGVTALIKRNTSTPTKQTQIFTTYSNQPGVLIOVY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 386 KSENVQDLLLDVAPLSGLGLETAGGVTALIKRNTTTPPKQTQIFTTYSNQPGVLIOVY 445

QY 61 EGERAMTKNNLGRFELSGIPAPRGVPOIETFDIDANGILNVATDKSTGKANKITI 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 446 EGERAMTKNNLGRFELSGIPAPRGVPOIETFDIDANGILNVATDKSTGKANKITI 505

QY 121 TNDKGRLSKEEIERMWQAEKYKAEDVQREVRSKNALESYAFNMKSASVEDGLGKIS 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 506 TNDKGRLSKEEIERMWLDKAEKYKAEDVQREKIAAKNALESYAFNMKSVDSEGLGKIS 565

QY 181 EADKKVLDKQEVISWLDANTLAEKDEFHKKRKELEQVNCNPIISGLYQAGGPGPGFG 240
    :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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Db 566 ESDKNKILDKCNELLNWLAEVQLAEKDFDHRKKELEQMCNPIITKLYQG-----G 616
QY 241 AQGPKGSG-----SGPTIEVD 258
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 617 CTGPACGTGYVGRPATGPTIEVD 641

RESULT 17
US-10-408-765A-1753
; Sequence 1753, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1753
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1753

Query Match      83.5%; Score 1097.5; DB 16; Length 586;
Best Local Similarity 81.4%; Pred. No. 3.3e-78;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVQDLLLDVAPLSGLGLETAGGVTALIKRNTSTPTKQTQIFTTYSNQPGVLIOVY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 324 KSENVQDLLLDVTPLSGLGLETAGGVTALIKRNTTPTKQTQIFTTYSNQPGVLIOVY 383

QY 61 EGERAMTKNNLGRFELSGIPAPRGVPOIETFDIDANGILNVATDKSTGKANKITI 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 384 EGERAMTKNNLGRFELSGIPAPRGVPOIETFDIDANGILNVATDKSTGKANKITI 443

QY 121 TNDKGRLSKEEIERMWQAEKYKAEDVQREVRSKNALESYAFNMKSASVEDGLGKIS 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 444 TNDKGRLSKEDIERMWQAEKYKAEDKQDKVSSKNSLESYAFNMKATVEDEKLQKIN 503

QY 181 EADKKVLDKQEVISWLDANTLAEKDEFHKKRKELEQVNCNPIISGLYQAGG-PG--PG 237
    :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 504 DEDKQKILDKCNEIINWLDKNQTAKEEFHKKRKELEKVCNPIITKLYQSAGGMPGMPG 563

QY 238 GF--GAQPKGSGSGPTIEVD 258
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 564 GPFPGGAPPSGGSGPTIEVD 586

RESULT 18
US-09-759-010-4
; Sequence 4, Application US/09759010
; Patent No. US20010034042A1
; GENERAL INFORMATION:
; APPLICANT: Srivastava, Pramod K.
; TITLE OF INVENTION: COMPLEXES OF PEPTIDE BINDING FRAGMENTS OF HEAT-SHOCK
; FILE REFERENCE: 8449-135
; CURRENT APPLICATION NUMBER: US/09/759,010
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 646
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-759-010-4

Query Match      83.5%; Score 1097.5; DB 9; Length 646;
Best Local Similarity 81.4%; Pred. No. 3.7e-78;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

Qy 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNTIPTKTQITFTTYSNQPGLVLIQVY 60
Db 384 KSENVQDLLLLDVTPLSGIETAGGVTALIKRNTIPTKTQITFTTYSNQPGLVLIQVY 443

Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKDNNLLGKFLTGIPPPAPRGVPOIEVTFDIDANGILNVSADKSTGKANKITI 503

Qy 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAAKNALESYAFNMKSAYEDELKLGKIS 180
Db 504 TNDKGRLSKEDIERMVOEAEKYKAEDQKQKRDVSSKNLSLESYAFNMKATVEDEKLQKIN 563

Qy 181 EADKKVKLDKCOEIVSWLDANTLAEKDFEHEKKELEQVNCNPIISGLYQAGG-PG--PG 237
Db 564 DEDQKILDKCNEIINWLDKNQTAKEEHEHQKELEKVCNPIITKLYQSAGGMPGMPG 623

Qy 238 GF--GAQGPKGSGSGPTIEEVD 258
Db 624 GFPGGGAPPSGGASSGPTIEEVD 646

RESULT 19
US-09-870-759-43
; Sequence 43, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 43
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-870-759-43

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Query Match      83.5%; Score 1097.5; DB 9; Length 646;
Best Local Similarity 81.4%; Pred. No. 3.7e-78;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

Qy 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNTIPTKTQITFTTYSNQPGLVLIQVY 60
Db 384 KSENVQDLLLLDVTPLSGIETAGGVTALIKRNTIPTKTQITFTTYSNQPGLVLIQVY 443

Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKDNNLLGKFLTGIPPPAPRGVPOIEVTFDIDANGILNVSADKSTGKANKITI 503

Qy 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAAKNALESYAFNMKSAYEDELKLGKIS 180
Db 504 TNDKGRLSKEDIERMVOEAEKYKAEDQKQKRDVSSKNLSLESYAFNMKATVEDEKLQKIN 563

Qy 181 EADKKVKLDKCOEIVSWLDANTLAEKDFEHEKKELEQVNCNPIISGLYQAGG-PG--PG 237
Db 564 DEDQKILDKCNEIINWLDKNQTAKEEHEHQKELEKVCNPIITKLYQSAGGMPGMPG 623

Qy 238 GF--GAQGPKGSGSGPTIEEVD 258
Db 624 GFPGGGAPPSGGASSGPTIEEVD 646

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RESULT 20
US-09-935-642-16
; Sequence 16, Application US/09935642
; Publication No. US20030044795A1
; GENERAL INFORMATION:
; APPLICANT: BYRJALSEN, Inger
; APPLICANT: LARSEN, Peter
; TITLE OF INVENTION: Biochemical Markers for the Human
; TITLE OF INVENTION: Endometrium
; FILE REFERENCE: 8969-014
; CURRENT APPLICATION NUMBER: US/09/935,642
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: PCT/GB97/02394
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: PCT/GB9707132.8
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: PCT/GB9618600.2
; PRIOR FILING DATE: 1996-09-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-642-16

Query Match      83.5%; Score 1097.5; DB 10; Length 646;
Best Local Similarity 81.4%; Pred. No. 3.7e-78;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

Qy 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNTIPTKTQITFTTYSNQPGLVLIQVY 60
Db 384 KSENVQDLLLLDVTPLSGIETAGGVTALIKRNTIPTKTQITFTTYSNQPGLVLIQVY 443

Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKDNNLLGKFLTGIPPPAPRGVPOIEVTFDIDANGILNVSADKSTGKANKITI 503

Qy 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAAKNALESYAFNMKSAYEDELKLGKIS 180
Db 504 TNDKGRLSKEDIERMVOEAEKYKAEDQKQKRDVSSKNLSLESYAFNMKATVEDEKLQKIN 563

Qy 181 EADKKVKLDKCOEIVSWLDANTLAEKDFEHEKKELEQVNCNPIISGLYQAGG-PG--PG 237
Db 564 DEDQKILDKCNEIINWLDKNQTAKEEHEHQKELEKVCNPIITKLYQSAGGMPGMPG 623

Qy 238 GF--GAQGPKGSGSGPTIEEVD 258
Db 624 GFPGGGAPPSGGASSGPTIEEVD 646

RESULT 21
US-09-919-039-11
; Sequence 11, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 11
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 1545176CD1

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US-09-919-039-11

Query Match 83.5%; Score 1097.5; DB 10; Length 646;
 Best Local Similarity 81.4%; Pred. No. 3.7e-78;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNTSTPTKQTQITFTTYSNQPGLVLIQVY 60
 DB 384 KSENVQDLLLLDVTPLSGLGLETAGGVTALIKRNTTPTKQTQITFTTYSNQPGLVLIQVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
 DB 444 EGERAMTKNNLLGKFLTGIPPPAPRGVPOIEVTFDIDANGILNVSAVDSTGKANKITI 503
 QY 121 TNDKGRLSKEIERMVOEAKYKAEDVQRRVSNAKNALESYAFNMKSAVEDGLKGIS 180
 DB 504 TNDKGRLSKEDIEMVQEAKEYKAEDKQDRKVSNNLSYAFNMKATVEDEKLQKIN 563
 QY 181 EADKKVLDKQCVISWLDANTLAEDKDFEHKKELEFQVNCNPIITKLYQSAGGMPGMPG 237
 DB 564 DEDQKILDKCNEIINWLDKNTAEKEEFHQKELEKVCNPIITKLYQSAGGMPGMPG 623
 QY 238 GP-GAOPKGGSGSGPTIEVD 258
 DB 624 GPPGGAPPSSGSGPTIEVD 646
 RESULT 22
 US-09-751-708A-43
 ; Sequence 43, Application US/09751708A
 ; Publication No. US20030157113A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TERMAN, David S
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 ; FILE REFERENCE: 751708
 ; CURRENT APPLICATION NUMBER: US/09751.708A
 ; PRIOR FILING DATE: 2002-10-15
 ; PRIOR APPLICATION NUMBER: US 60/173,371
 ; NUMBER OF SEQ ID NOS: 166
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 43
 ; LENGTH: 646
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-751-708A-43

Query Match 83.5%; Score 1097.5; DB 10; Length 646;
 Best Local Similarity 81.4%; Pred. No. 3.7e-78;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNTSTPTKQTQITFTTYSNQPGLVLIQVY 60
 DB 384 KSENVQDLLLLDVTPLSGLGLETAGGVTALIKRNTTPTKQTQITFTTYSNQPGLVLIQVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
 DB 444 EGERAMTKNNLLGKFLTGIPPPAPRGVPOIEVTFDIDANGILNVSAVDSTGKANKITI 503
 QY 121 TNDKGRLSKEIERMVOEAKYKAEDVQRRVSNAKNALESYAFNMKSAVEDGLKGIS 180
 DB 504 TNDKGRLSKEDIEMVQEAKEYKAEDKQDRKVSNNLSYAFNMKATVEDEKLQKIN 563
 QY 181 EADKKVLDKQCVISWLDANTLAEDKDFEHKKELEFQVNCNPIITKLYQSAGGMPGMPG 237
 DB 564 DEDQKILDKCNEIINWLDKNTAEKEEFHQKELEKVCNPIITKLYQSAGGMPGMPG 623
 QY 238 GP-GAOPKGGSGSGPTIEVD 258
 DB 624 GPPGGAPPSSGSGPTIEVD 646

RESULT 23

US-10-126-103-147
 ; Sequence 147, Application US/10126103
 ; Publication No. US20030224486A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB PATHWAY
 ; FILE REFERENCE: D0108.np
 ; CURRENT APPLICATION NUMBER: US/10/126,103
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: US 60/284,962
 ; PRIOR FILING DATE: 2001-04-19
 ; PRIOR APPLICATION NUMBER: US 60/286,645
 ; PRIOR FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: US 60/346,986
 ; PRIOR FILING DATE: 2002-01-09
 ; NUMBER OF SEQ ID NOS: 284
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 147
 ; LENGTH: 646
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-126-103-147

Query Match 83.5%; Score 1097.5; DB 15; Length 646;
 Best Local Similarity 81.4%; Pred. No. 3.7e-78;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNTSTPTKQTQITFTTYSNQPGLVLIQVY 60
 DB 384 KSENVQDLLLLDVTPLSGLGLETAGGVTALIKRNTTPTKQTQITFTTYSNQPGLVLIQVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
 DB 444 EGERAMTKNNLLGKFLTGIPPPAPRGVPOIEVTFDIDANGILNVSAVDSTGKANKITI 503
 QY 121 TNDKGRLSKEIERMVOEAKYKAEDVQRRVSNAKNALESYAFNMKSAVEDGLKGIS 180
 DB 504 TNDKGRLSKEDIEMVQEAKEYKAEDKQDRKVSNNLSYAFNMKATVEDEKLQKIN 563
 QY 181 EADKKVLDKQCVISWLDANTLAEDKDFEHKKELEFQVNCNPIITKLYQSAGGMPGMPG 237
 DB 564 DEDQKILDKCNEIINWLDKNTAEKEEFHQKELEKVCNPIITKLYQSAGGMPGMPG 623
 QY 238 GP-GAOPKGGSGSGPTIEVD 258
 DB 624 GPPGGAPPSSGSGPTIEVD 646

RESULT 24
 US-10-431-096-147
 ; Sequence 147, Application US/10431096
 ; Publication No. US20040086896A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
 ; FILE REFERENCE: D0108A CIP
 ; CURRENT APPLICATION NUMBER: US/10/431,096
 ; CURRENT FILING DATE: 2003-05-07
 ; PRIOR APPLICATION NUMBER: US 60/284,962
 ; PRIOR FILING DATE: 2001-04-19
 ; PRIOR APPLICATION NUMBER: US 10/126,103
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: US 60/286,645
 ; PRIOR FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: US 60/346,986
 ; PRIOR FILING DATE: 2002-01-09
 ; NUMBER OF SEQ ID NOS: 307
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 147
 ; LENGTH: 646
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-10-431-096-147

Query Match 83.5%; Score 1097.5; DB 15; Length 646;
 Best Local Similarity 81.4%; Pred. No. 3.7e-78;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNTSTPTKQTOIFTTYSNQPGLVLIQVY 60
 DB 384 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNTSTPTKQTOIFTTYSNQPGLVLIQVY 443
 QY 61 EGERAMTKONNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 444 EGERAMTKONNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEEIERMWQAEKYKAEDVQERVSNAKNALESYAFNMKSASVEDGLKKGKIS 180
 DB 504 TNDKGRLSKEDIERMWQAEKYKAEDKQDKVSSKNSLESYAFNMKATVEDEKLQKIN 563
 QY 181 EADKKVLDKQEVISWLDANTLAEDKDEFEHKKRKELEQVNCNPIISGLYQAGG-PG--PG 237
 DB 564 DEDKQKILDKCNEIINWLDKNQTAKEEPEHQQKELEKVCNPIITTKLYQSAGGMPGMPG 623
 QY 238 GF--GAQGPKGSGSGPTIEVD 258
 DB 624 GFPGGAPPSSGSGPTIEVD 646

RESULT 25

US-10-408-765A-703
 ; Sequence 703, Application US/10408765A
 ; Publication No. US20040101874A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Fahy, Eoin D.
 ; APPLICANT: Zhang, Bing
 ; APPLICANT: Gibson, Bradford W.
 ; APPLICANT: Taylor, Steven W.
 ; APPLICANT: Warnock, Dale E.
 ; APPLICANT: Glenn, Gary M.
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
 ; FILE REFERENCE: 660088.465
 ; CURRENT FILING DATE: 2003-04-04
 ; PRIOR FILING DATE: 2003-04-04
 ; NUMBER OF SEQ ID NOS: 3077
 ; SOFTWARE: Fast-Seq for Windows Version 4.0
 ; SEQ ID NO 703
 ; LENGTH: 646
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-408-765A-703

Query Match 83.5%; Score 1097.5; DB 16; Length 646;
 Best Local Similarity 81.4%; Pred. No. 3.7e-78;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNTSTPTKQTOIFTTYSNQPGLVLIQVY 60
 DB 384 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNTSTPTKQTOIFTTYSNQPGLVLIQVY 443
 QY 61 EGERAMTKONNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 444 EGERAMTKONNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEEIERMWQAEKYKAEDVQERVSNAKNALESYAFNMKSASVEDGLKKGKIS 180
 DB 504 TNDKGRLSKEDIERMWQAEKYKAEDKQDKVSSKNSLESYAFNMKATVEDEKLQKIN 563
 QY 181 EADKKVLDKQEVISWLDANTLAEDKDEFEHKKRKELEQVNCNPIISGLYQAGG-PG--PG 237
 DB 564 DEDKQKILDKCNEIINWLDKNQTAKEEPEHQQKELEKVCNPIITTKLYQSAGGMPGMPG 623
 QY 238 GF--GAQGPKGSGSGPTIEVD 258

Db 624 GFPGGAPPSSGSGPTIEVD 646

RESULT 26

US-10-737-350-1
 ; Sequence 1, Application US/10737350
 ; Publication No. US20040185511A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GEORGES, ELIAS
 ; TITLE OF INVENTION: HSC70 DIRECTED DIAGNOSTICS AND THERAPEUTICS FOR
 ; FILE REFERENCE: 112418.149US (AUR-011US)
 ; CURRENT FILING DATE: 2003-12-15
 ; PRIOR FILING DATE: 2003-01-03
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patent In Ver. 3.2
 ; SEQ ID NO 1
 ; LENGTH: 646
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-737-350-1

Query Match 83.5%; Score 1097.5; DB 16; Length 646;
 Best Local Similarity 81.4%; Pred. No. 3.7e-78;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNTSTPTKQTOIFTTYSNQPGLVLIQVY 60
 DB 384 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNTSTPTKQTOIFTTYSNQPGLVLIQVY 443
 QY 61 EGERAMTKONNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 444 EGERAMTKONNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEEIERMWQAEKYKAEDVQERVSNAKNALESYAFNMKSASVEDGLKKGKIS 180
 DB 504 TNDKGRLSKEDIERMWQAEKYKAEDKQDKVSSKNSLESYAFNMKATVEDEKLQKIN 563
 QY 181 EADKKVLDKQEVISWLDANTLAEDKDEFEHKKRKELEQVNCNPIISGLYQAGG-PG--PG 237
 DB 564 DEDKQKILDKCNEIINWLDKNQTAKEEPEHQQKELEKVCNPIITTKLYQSAGGMPGMPG 623
 QY 238 GF--GAQGPKGSGSGPTIEVD 258
 DB 624 GFPGGAPPSSGSGPTIEVD 646

RESULT 27

US-10-841-207-4
 ; Sequence 4, Application US/10841207
 ; Publication No. US20050009772A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Caprioli, Joseph
 ; TITLE OF INVENTION: Methods and Compositions for the Treatment of Glaucoma and Other
 ; FILE REFERENCE: A-72263/TAL/MWR (468290-00515)
 ; CURRENT FILING DATE: 2004-05-06
 ; PRIOR FILING DATE: 2003-05-06
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: Patent In version 3.2
 ; SEQ ID NO 4
 ; LENGTH: 646
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-841-207-4
 Query Match 83.5%; Score 1097.5; DB 17; Length 646;
 Best Local Similarity 81.4%; Pred. No. 3.7e-78;

```
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
Qy 1 KSENVQDLLLLDVAPLSGLGSETAGVMTALIKRNSTIPTKTQTQITFTTYSNQPGLIQVY 60
Db 384 KSENVQDLLLLDVAPLSGLGSETAGVMTALIKRNSTIPTKTQTQITFTTYSNQPGLIQVY 443
Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
Db 444 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 503
Qy 121 TNDKGRLSKEIERMWQAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGGKIS 180
Db 504 TNDKGRLSKEIERMWQAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGGKIN 563
Qy 181 EADKKVLDKQCOVISWLDANTLAEDKDEFEHKKRKELEQVNCNPIISGLYQAGG--PG 237
Db 564 DEDKQKILDKCNEIINWLDKNQTAKEKEFEHKKRKELEQVNCNPIITKLYQSAGGMPGMPG 623
Qy 238 GF--GAQPGKGGSGGPTIEVD 258
Db 624 GFPGGAPPSSGGASSGPTIEVD 646

RESULT 28
US-10-100-957A-174
; Sequence 174, Application US/10100957A
; Publication No. US20030096322A1
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-LIA
; CURRENT APPLICATION NUMBER: US/10/100,957A
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 174
; LENGTH: 890
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GFP-HSC70
US-10-100-957A-174

Query Match 83.5%; Score 1097.5; DB 14; Length 890;
Best Local Similarity 81.4%; Pred. No. 5.7e-78;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
Qy 1 KSENVQDLLLLDVAPLSGLGSETAGVMTALIKRNSTIPTKTQTQITFTTYSNQPGLIQVY 60
Db 628 KSENVQDLLLLDVAPLSGLGSETAGVMTALIKRNSTIPTKTQTQITFTTYSNQPGLIQVY 687
Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
Db 688 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 747
Qy 121 TNDKGRLSKEIERMWQAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGGKIS 180
Db 748 TNDKGRLSKEIERMWQAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGGKIN 807
Qy 181 EADKKVLDKQCOVISWLDANTLAEDKDEFEHKKRKELEQVNCNPIISGLYQAGG--PG 237
Db 808 DEDKQKILDKCNEIINWLDKNQTAKEKEFEHKKRKELEQVNCNPIITKLYQSAGGMPGMPG 867
Qy 238 GF--GAQPGKGGSGGPTIEVD 258
Db 868 GFPGGAPPSSGGASSGPTIEVD 890

RESULT 29
US-10-108-260A-4141
; Sequence 4141, Application US/10108260A
; Publication No. US20040005560A1
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; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4141
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-4141

Query Match 83.5%; Score 1097; DB 15; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.2e-78;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 46 TTYSDNQPGLIQVYEGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNV 105
Db 38 TTYSDNQPGLIQVYEGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNV 97
Qy 106 TATDKSTGKANKITITNDKGRLSKEIERMWQAEKYKAEDVQERVSNAKNALESYAFN 165
Db 98 TATDKSTGKANKITITNDKGRLSKEIERMWQAEKYKAEDVQERVSNAKNALESYAFN 157
Qy 166 MKSAVEDGLKGGKISSEADKKVLDKQCOVISWLDANTLAEDKDEFEHKKRKELEQVNCNPIIS 225
Db 158 MKSAVEDGLKGGKISSEADKKVLDKQCOVISWLDANTLAEDKDEFEHKKRKELEQVNCNPIIS 217
Qy 226 GLYQAGGPGPGFGAQQPGKGGSGGPTIEVD 258
Db 218 GLYQAGGPGPGFGAQQPGKGGSGGPTIEVD 250

RESULT 30
US-09-919-039-73
; Sequence 73, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 73
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 701484CD1
US-09-919-039-73

Query Match 83.2%; Score 1093; DB 10; Length 641;
Best Local Similarity 81.5%; Pred. No. 8.4e-78;
Matches 216; Conservative 16; Mismatches 17; Indels 16; Gaps 2;
Qy 1 KSENVQDLLLLDVAPLSGLGSETAGVMTALIKRNSTIPTKTQTQITFTTYSNQPGLIQVY 60
Db 386 KSENVQDLLLLDVAPLSGLGSETAGVMTALIKRNSTIPTKTQTQITFTTYSNQPGLIQVY 445
Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
Db 446 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 505
Qy 121 TNDKGRLSKEIERMWQAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGGKIS 180
Db 506 TNDKGRLSKEIERMWQAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGGKIS 565
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Query Match	82.9%;	Score 1089.5;	DB 15;	Length 621;
Best Local Similarity	81.0%;	Pred. No. 1.5e-77;		
Matches	213;	Conservative	24;	Mismatches 21; Indels 5; Gaps 1;

Qy	1	KSENVQDLLLDDVAPLSLGLTETAGGVTALIKENSTIPTKQTQFTTYSNQPGVLQVY	60
Db	359	KSENVQDLLLDDVTPLSLGLTETAGGVTVLTKRNTTIPTKQTQFTTYSNQPGVLQVY	418
Qy	61	EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI	120
Db	419	EGERAMTKNNLLGKFLTGIPAPRGVPOIEVTFDIDANGILNVSADVSTGKANKITI	478
Qy	121	TNDKGRLSKEEIERMWQEAERYKAEDVQREYRSKNALESYAFNMKSAVEDSGLKGKIS	180
Db	479	TNDKGRLSKEDIERMWQEAERYKAEDKQDKVSSKNSLESYAFNMKATVEDEKLGKIN	538
Qy	181	EADKKKVLDKCQEVISWLDANTLAEKDEPFHKKELEQVNCPIISGLYQGAGG-PG--PG	237
Db	539	EDKQKILDKCNEILNWLDRNQTAKEEFHQKLEKVCNPIITKLYQSGAGGPGGMPG	598
Qy	238	GF--GAQPGKGGSGGPTIEVD	258
Db	599	GFGGAGPPGSGASSRPTIEVD	621


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RESULT 33
US-10-108-260A-4616
; Sequence 4616, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4616
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-4616

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Query Match	80.6%;	Score 1059.5;	DB 15;	Length 413;
Best Local Similarity	79.1%;	Pred. No. 2.1e-75;		
Matches	204;	Conservative	24;	Mismatches 25; Indels 5; Gaps 1;

Qy	1	KSENVQDLLLDDVAPLSLGLTETAGGVTALIKENSTIPTKQTQFTTYSNQPGVLQVY	60
Db	161	KSENVQDLLLDDVTPLSLGLTETAGGVTPLIKRNTTIPTKQTQFTTYSNQSSVLQVY	220
Qy	61	EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI	120
Db	221	EGERAMTKNNLLGKFLDTGIPAPRGVPOIEVTFDIDANGILNVTAAADKSTGKANKITI	280
Qy	121	TNDKGRLSKEEIERMWQEAERYKAEDVQREYRSKNALESYAFNMKSAVEDSGLKGKIS	180
Db	281	TNDKGRLSKDDIDRWQEAERYKSEDEANRDRVAANKALESYTYNTKQTVEDEKLGKIS	340
Qy	181	EADKKKVLDKCQEVISWLDANTLAEKDEPFHKKELEQVNCPIISGLYQGAGGPGGFG	240
Db	341	EQDKNKLDKCQEVINWLDRNQAEKDEYHKQELERVCNPIISKLYQGPGGGSGGG	400
Qy	241	AQGPKGSGSGGPTIEVD	258
Db	401	S-----GASGGPTIEVD	413


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RESULT 34
US-10-408-765A-1693
; Sequence 1693, Application US/10408765A
; Publication No. US20040101874A1

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; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1693
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1693

Query Match      80.6%; Score 1059.5; DB 16; Length 639;
Best Local Similarity 79.1%; Pred. No. 3.7e-75;
Matches 204; Conservative 24; Mismatches 25; Indels 5; Gaps 1;

QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNSTIPTKTQITFTTYSNQPGVLIQVY 60
Db 387 KSENVQDLLLLDVTPLSGLGLETAGGVTPLIKRNTTIPTKTQITFTTYSNQSSVLQVY 446
QY 61 EGERAMTKONNLGRFELSGIPAPRGVQPIETFDIDANGILNVATDKSTGKANKITI 120
Db 447 EGERAMTKONNLGKFDLTGIPAPRGVQPIETFDIDANGILNVTAADKSTGKANKITI 506
QY 121 TNDKGRLSKEEIERMWQAEKYKAEDVQREVRSYAKNALESYAFNMKSAVEDGLKKGKIS 180
Db 507 TNDKGRLSKDDIDRMVQEAERYKSEDEANRDRVAANKALESYTYNKTQVDESKLRGKIS 566
QY 181 EADKKVKLDKQEVISWLDANTLAEDFEHKEKELEQVNCNPIISGLYQAGGPGGFG 240
Db 567 EQDKNKILDKQEVINWLDNRNQMAEKDEYEHKQKELERVNCNPIISKLYQGPGGGSGGG 626
QY 241 AOGPKGGSGSGPTIEVD 258
Db 627 S-----GASGGPTIEVD 639

RESULT 35
US-10-408-765A-1723
; Sequence 1723, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1723
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1723

Query Match      80.6%; Score 1059.5; DB 16; Length 639;
Best Local Similarity 79.1%; Pred. No. 3.7e-75;
Matches 204; Conservative 24; Mismatches 25; Indels 5; Gaps 1;

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Matches 204; Conservative 24; Mismatches 25; Indels 5; Gaps 1;

QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNSTIPTKTQITFTTYSNQPGVLIQVY 60
Db 387 KSENVQDLLLLDVTPLSGLGLETAGGVTPLIKRNTTIPTKTQITFTTYSNQSSVLQVY 446
QY 61 EGERAMTKONNLGRFELSGIPAPRGVQPIETFDIDANGILNVATDKSTGKANKITI 120
Db 447 EGERAMTKONNLGKFDLTGIPAPRGVQPIETFDIDANGILNVTAADKSTGKANKITI 506
QY 121 TNDKGRLSKEEIERMWQAEKYKAEDVQREVRSYAKNALESYAFNMKSAVEDGLKKGKIS 180
Db 507 TNDKGRLSKDDIDRMVQEAERYKSEDEANRDRVAANKALESYTYNKTQVDESKLRGKIS 566
QY 181 EADKKVKLDKQEVISWLDANTLAEDFEHKEKELEQVNCNPIISGLYQAGGPGGFG 240
Db 567 EQDKNKILDKQEVINWLDNRNQMAEKDEYEHKQKELERVNCNPIISKLYQGPGGGSGGG 626
QY 241 AOGPKGGSGSGPTIEVD 258
Db 627 S-----GASGGPTIEVD 639

RESULT 36
US-10-369-493-6233
; Sequence 6233, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6233
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6233

Query Match      78.7%; Score 1034; DB 15; Length 640;
Best Local Similarity 77.9%; Pred. No. 3.9e-73;
Matches 201; Conservative 21; Mismatches 34; Indels 2; Gaps 1;

QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNSTIPTKTQITFTTYSNQPGVLIQVY 60
Db 385 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNTTIPTKTQITFTTYSNQPGVLIQVY 444
QY 61 EGERAMTKONNLGRFELSGIPAPRGVQPIETFDIDANGILNVATDKSTGKANKITI 120
Db 445 EGERAMTKONNLGKFDLTGIPAPRGVQPIETFDIDANGILNVSATDKSTGKANKITI 504
QY 121 TNDKGRLSKEEIERMWQAEKYKAEDVQREVRSYAKNALESYAFNMKSAVEDGLKKGKIS 180
Db 505 TNDKGRLSKDDIDRMVQEAERYKADDEAOKDRIGAKNGLESYAFNLKQTIETDESKLRGKIS 564
QY 181 EADKKVKLDKQEVISWLDANTLAEDFEHKEKELEQVNCNPIISGLYQAGGPGGFG 240
Db 565 PEDKKKIEDKDEILKWLDSNQTAEKEEPEHQOQLEGLANPIISKLYQSAGGAPPG--A 622
QY 241 AOGPKGGSGSGPTIEVD 258
Db 623 APGAAGGAGGPTIEVD 640

RESULT 37

```


RESULT 40
US-10-755-889-396
; Sequence 396, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; FILE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; PRIOR FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 396
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-396

Query Match 77.0%; Score 1012; DB 16; Length 643;
Best Local Similarity 74.4%; Pred. No. 2.1e-71;
Matches 192; Conservative 33; Mismatches 33; Indels 0; Gaps 0;
QY 1 KSENVQDLLLDVAPLSGLTAGGVTALIKENSTIPTKTQTQTFITYSDNQPGVLIQVY 60
DB 386 KCEKVDLLLDVAPLSGLTAGGVTALIKENSTIPTKTQTQTFITYSDNQPGVLIQVY 445
QY 61 EGERAMTKONNLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 446 EGERAMTKONNLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 505
QY 121 TNDKGRLSKEEIERMVOEAKYKAEDVQERVSAAKNALSYAFNMKSAVEDSLGKGKIS 180
DB 506 TNDKGRLSKEEIERMVOEAKYKAEDVQERVSAAKNALSYAFNMKSAVEDSLGKGKIS 565
QY 181 EADKKKVLKCOEIVSWLDANTILAEKDEPEHKKLEQVCNPIISGLYQAGGPGGFG 240
DB 566 EEDRRKMQDKREVLAHNLAEKEEYEHQKRELEQICRPIFSRLYGGPGVPGSSCG 625
QY 241 AQGPKGSGSGPTIEVD 258
DB 626 TQARQGDPSGTPIIEVD 643

RESULT 41
US-09-925-302-724
; Sequence 724, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 724
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (216)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (298)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-724

; NAME/KEY: SITE
; LOCATION: (298)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-724
Query Match 77.0%; Score 1012; DB 9; Length 665;
Best Local Similarity 74.4%; Pred. No. 2.2e-71;
Matches 192; Conservative 33; Mismatches 33; Indels 0; Gaps 0;
QY 1 KSENVQDLLLDVAPLSGLTAGGVTALIKENSTIPTKTQTQTFITYSDNQPGVLIQVY 60
DB 408 KCEKVDLLLDVAPLSGLTAGGVTALIKENSTIPTKTQTQTFITYSDNQPGVLIQVY 467
QY 61 EGERAMTKONNLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 468 EGERAMTKONNLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 527
QY 121 TNDKGRLSKEEIERMVOEAKYKAEDVQERVSAAKNALSYAFNMKSAVEDSLGKGKIS 180
DB 528 TNDKGRLSKEEIERMVOEAKYKAEDVQERVSAAKNALSYAFNMKSAVEDSLGKGKIS 587
QY 181 EADKKKVLKCOEIVSWLDANTILAEKDEPEHKKLEQVCNPIISGLYQAGGPGGFG 240
DB 588 EEDRRKMQDKREVLAHNLAEKEEYEHQKRELEQICRPIFSRLYGGPGVPGSSCG 647
QY 241 AQGPKGSGSGPTIEVD 258
DB 648 TQARQGDPSGTPIIEVD 665

RESULT 42
US-09-925-302-724
; Sequence 724, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 724
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (216)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (298)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-724

Query Match 77.0%; Score 1012; DB 10; Length 665;
Best Local Similarity 74.4%; Pred. No. 2.2e-71;
Matches 192; Conservative 33; Mismatches 33; Indels 0; Gaps 0;
QY 1 KSENVQDLLLDVAPLSGLTAGGVTALIKENSTIPTKTQTQTFITYSDNQPGVLIQVY 60
DB 408 KCEKVDLLLDVAPLSGLTAGGVTALIKENSTIPTKTQTQTFITYSDNQPGVLIQVY 467
QY 61 EGERAMTKONNLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 468 EGERAMTKONNLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 527
QY 121 TNDKGRLSKEEIERMVOEAKYKAEDVQERVSAAKNALSYAFNMKSAVEDSLGKGKIS 180

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Db 528 TNDKRLSKKEVERMVHAEQYKAEDBAQRDRVAAKNSLEAHVPHVKSLQEELRDKIP 587
Qy 181 EADKKVLDKQCVISWLDANTLAEKDBFEHKKRKELEQVNCNPIISGLYQAGGPGGCGFG 240
Db 588 EEDRRKQDKCREVLAWLHNQLEAKEEYEHQKRELEQICNPITFSRLYGGPGVPGSSCG 647
Qy 241 AQPKGKGGSGPTIEEVD 258
Db 648 TQARQGDPTGPIIEEVD 665

RESULT 43
US-10-424-599-234323
; Sequence 234323, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 234323
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_53620C.1.pap
US-10-424-599-234323

Query Match 73.4%; Score 965; DB 15; Length 655;
Best Local Similarity 70.2%; Pred. No. 1.1e-67;
Matches 186; Conservative 32; Mismatches 39; Indels 8; Gaps 1;

Qy 2 SENVDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQITFTTYSNDQPGVLIQVYE 61
Db 391 NEKVDLLLDVTPLSLGLTAGGVTALIPRNTIPTKKEQVFSTYSNDQPGVLIQVFE 450
Qy 62 GERAMTKDNLLGRFELSGIPPRGVPQIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 451 GERARTKDNLLGKFLSGIPPRGVPQITVCFDIDANGILNVSAEDKTTGQKNKITIT 510
Qy 122 NDKGRLSKEIERMVQAEKYKAEDVQERVSNAKNALESYAFNMKSAAVEDEGLKGKISE 181
Db 511 NDKGRLSKEDIKRWQAEKYKSEDEHKKKVEAKNALENYAYNMRNTVKDDKIGEKLDP 570
Qy 182 ADKKVKLDKQCVISWLDANTLAEKDBFEHKKRKELEQVNCNPIISGLYQAGGPGGFGA 241
Db 571 ADKKKIEDAEQALWLDNSQLAEADFEDEKMELESICNPIIAKMYQGGAGPDVGAGA 630
Qy 242 QG-----PKGSGSGPTIEEVD 258
Db 631 GAAEDDYAPPSPGSGGAGPKIEEVD 655

RESULT 44
US-10-437-963-186650
; Sequence 186650, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 203543
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_98717C.1.pap
US-10-437-963-186650

Query Match 73.3%; Score 963; DB 16; Length 646;
Best Local Similarity 72.0%; Pred. No. 1.6e-67;
Matches 185; Conservative 28; Mismatches 44; Indels 0; Gaps 0;

Qy 2 SENVDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQITFTTYSNDQPGVLIQVYE 61
Db 390 NEKVDLLLDVTPLSLGLTAGGVTALIPRNTIPTKKEQVFSTYSNDQPGVLIQVFE 449
```

```
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 186650
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_8342C.1.pap
US-10-437-963-186650

Query Match 73.3%; Score 963.5; DB 16; Length 653;
Best Local Similarity 71.9%; Pred. No. 1.5e-67;
Matches 189; Conservative 25; Mismatches 42; Indels 7; Gaps 2;

Qy 2 SENVDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQITFTTYSNDQPGVLIQVYE 61
Db 392 NORVDLLLDVTPLSLGLTAGGVTALIPRNTIPTKKEQVFSTYSNDQPGVLIQVFE 451
Qy 62 GERAMTKDNLLGRFELSGIPPRGVPQIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 452 GERTRTKDNLLGKFLSGIPPRGVPQINVTDFDIDANGILNVSAEDKTTGKKNKITIT 511
Qy 122 NDKGRLSKEIERMVQAEKYKAEDVQERVSNAKNALESYAFNMKSAAVEDEGLKGKISE 181
Db 512 NDKGRLSKEIERMVQAEKYKAEDVQERVHVKVARNALENYAYNMRNTVDEKIASLPA 571
Qy 182 ADKKVKLDKQCVISWLDANTLAEKDBFEHKKRKELEQVNCNPIISGLYQAGGPGGFG-- 239
Db 572 DDKKKIEDAIEDAIKWLDGNQLAEADFEDEKMELESICNPIISKMYQGGAG-GPAGMDE 630
Qy 240 ----GAQPKGSGSGPTIEEVD 258
Db 631 DAPNGSAGTGGSGGAGPKIEEVD 653

RESULT 45
US-10-437-963-203543
; Sequence 203543, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 203543
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_98717C.1.pap
US-10-437-963-203543

Query Match 73.3%; Score 963; DB 16; Length 646;
Best Local Similarity 72.0%; Pred. No. 1.6e-67;
Matches 185; Conservative 28; Mismatches 44; Indels 0; Gaps 0;

Qy 2 SENVDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQITFTTYSNDQPGVLIQVYE 61
Db 390 NEKVDLLLDVTPLSLGLTAGGVTALIPRNTIPTKKEQVFSTYSNDQPGVLIQVFE 449
```


Qy 62 GERAMTKONNLLGRFELSGIPPPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 450 GERARTKONNLLGKFLSGIPPPAPRGVQPIVNCFDIDANGILNVSAEDKTTGQKNKITIT 509
Qy 122 NDGRSLKSEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDGLKGKISE 181
Db 510 NDGRSLKSEIERMVQAEKYKAEDHEKKKVDKNALENYAYNMRNTIKDKIASKLSA 569
Qy 182 ADKKKVLDCQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGGPGPGFGA 241
Db 570 DDKKRIEADIGAIWLDTNQLAEADFEDKMKLEGINPIITAKMTYQGPADWAGGMD 629
Qy 242 QGPKGGSGSGPTIEVD 258
Db 630 DAPAGSGGAGPKIEVD 646

RESULT 46
US-10-425-114-43012
; Sequence 43012, Application US/10425114
; Publication No. US20040034889A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaka, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 43012
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700567610_FLI.pap
US-10-425-114-43012

Query Match 72.8%; Score 957; DB 15; Length 365;
Best Local Similarity 71.0%; Pred. No. 2.3e-67;
Matches 184; Conservative 29; Mismatches 44; Indels 2; Gaps 1;
Qy 2 SENVDLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTOIFTTYSNDQPGVLIQVYE 61
Db 107 NEKVQDLLLDVTPLSIGLETAGVMTVLPRTTIPTRKEQVFSTYSNDQPGVLIQVYE 166
Qy 62 GERAMTKONNLLGRFELSGIPPPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 167 GERTRDNNLLGKFLSGIPPPAPRGVQPIVNCFDIDANGILNVSAEDKTTGQKNKITIT 226
Qy 122 NDGRSLKSEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDGLKGKISE 181
Db 227 NDGRSLKSEIERMVQAEKYKAEDHEKKKVEAKNTLENYAYNMRNTIKDKIASKLSA 286
Qy 182 ADKKKVLDCQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGGPGPGFGA 241
Db 287 DDKKRIEADIGAIWLDGNQLAEADFEDKMKLESICNPIITAKMTYQAGGAGGAMDE 346
Qy 242 QGPKGGSGSGSGPTIEVD 258
Db 347 DGPAGSGSGAGPKIEVD 365

RESULT 47
US-10-424-599-156571
; Sequence 156571, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 156571
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_112404C.1.pap
US-10-424-599-156571

Query Match 72.8%; Score 957; DB 15; Length 648;
Best Local Similarity 71.0%; Pred. No. 4.8e-67;
Matches 184; Conservative 29; Mismatches 44; Indels 2; Gaps 1;
Qy 2 SENVDLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTOIFTTYSNDQPGVLIQVYE 61
Db 390 NEKVQDLLLDVTPLSIGLETAGVMTVLPRTTIPTRKEQVFSTYSNDQPGVLIQVYE 449
Qy 62 GERAMTKONNLLGRFELSGIPPPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 450 GERTRDNNLLGKFLSGIPPPAPRGVQPIVNCFDIDANGILNVSAEDKTTGQKNKITIT 509
Qy 122 NDGRSLKSEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDGLKGKISE 181
Db 510 NDGRSLKSEIERMVQAEKYKAEDHEKKKVEAKNTLENYAYNMRNTIKDKIASKLSA 569
Qy 182 ADKKKVLDCQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGGPGPGFGA 241
Db 570 DDKKRIEADIGAIWLDGNQLAEADFEDKMKLESICNPIITAKMTYQAGGAGGAMDE 629
Qy 242 QGPKGGSGSGSGPTIEVD 258
Db 630 DGPAGSGSGAGPKIEVD 648

RESULT 48
US-10-767-701-46962
; Sequence 46962, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 46962
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C49_296.pap
US-10-767-701-46962

Query Match 72.8%; Score 956; DB 16; Length 649;
Best Local Similarity 71.8%; Pred. No. 5.8e-67;
Matches 186; Conservative 31; Mismatches 40; Indels 2; Gaps 1;
Qy 2 SENVDLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTOIFTTYSNDQPGVLIQVYE 61
Db 391 NEKVQDLLLDVPSLSIGLETAGVMTVLPRTTIPTRKEQVFSTYSNDQPGVLIQVYE 450
Qy 62 GERAMTKONNLLGRFELSGIPPPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITIT 121

```

; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 43851
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700567825_FLI.pep
; US-10-425-114-43851

Query Match 72.6%; Score 954; DB 15; Length 282;
Best Local Similarity 70.7%; Pred. No. 2.8e-67;
Matches 183; Conservative 30; Mismatches 44; Indels 2; Gaps 1;

QY 2 SENVDLLLDVAPLSGLGTAGVMTALIKRSTIPTKTOTFTTYSNPGVLIQVYE 61
DB 24 NEKVQDLLLDVTPLSGLGTAGVMTVLPRTTTPKKEQVFTSYSDNPGVLIQVYE 83
QY 62 GERAMTKDNLGRFELSGIPPPAPRGVPOIETVTFDIDANGILNVATDKSTGKANKITIT 121
DB 84 GERTRDNNLLGKFLSGIPPPAPRGVPOITVCFDIDANGILNVSAEDKTTGQKNKITTIT 143
QY 122 NDKGRLSKEEIERMVQAEKYKAEDVQREVRSKNALESYAFNMKSAAVEDEGLKGKISE 181
DB 144 NDKGRLSKEEIERMVQAEKYKAEDVQREVRSKNALESYAFNMKSAAVEDEGLKGKISE 203
QY 182 ADKKKVLDDKQEVISWLDANTLAERKFEHKKRKELEQVNCPIISGLYQAGGPGPGFGA 241
DB 204 DDKKKIEDAIVQAIQWLDGNQLAEDFEDEKKELESICNPITAKMTQAGAGDAGGAMD 263
QY 242 QGPKGGSGS--GPTIEVD 258
DB 264 DGPAAGSGSGAGPKIEVD 282

RESULT 51
US-10-424-599-156568
; Sequence 156568, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 156568
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(323)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_112401C.1.pep
; US-10-424-599-156568

Query Match 72.6%; Score 954; DB 15; Length 323;
Best Local Similarity 70.7%; Pred. No. 3.3e-67;
Matches 183; Conservative 30; Mismatches 44; Indels 2; Gaps 1;

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; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 62894
; LENGTH: 651
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB143-053-G1_FLI.pep
; US-10-425-114-62894

Query Match 72.7%; Score 955; DB 15; Length 651;
Best Local Similarity 72.2%; Pred. No. 7e-67;
Matches 187; Conservative 28; Mismatches 42; Indels 2; Gaps 2;

QY 2 SENVDLLLDVAPLSGLGTAGVMTALIKRSTIPTKTOTFTTYSNPGVLIQVYE 61
DB 393 NEKVQDLLLDVTPLSGLGTAGVMTVLPRTTTPKKEQVFTSYSDNPGVLIQVYE 452
QY 62 GERAMTKDNLGRFELSGIPPPAPRGVPOIETVTFDIDANGILNVATDKSTGKANKITIT 121
DB 453 GERARTKDNLLGKFLSGIPPPAPRGVPOITVTFDIDANGILNVSAEDKTTGQKNKITTIT 512
QY 122 NDKGRLSKEEIERMVQAEKYKAEDVQREVRSKNALESYAFNMKSAAVEDEGLKGKISE 181
DB 513 NDKGRLSKEEIERMVQAEKYKAEDVQREVRSKNALESYAFNMKSAAVEDEGLKGKISE 572
QY 182 ADKKKVLDDKQEVISWLDANTLAERKFEHKKRKELEQVNCPIISGLYQAGGPGPGFGA 239
DB 573 DDKKKIEDAIVQAIQWLDGNQLAEDFEDEKKELESICNPITAKMTQAGAGDAGGAMD 632
QY 240 GAQGPKGSGSGPTIEVD 258
DB 633 DEDAPSGSGAGPKIEVD 651

RESULT 50
US-10-425-114-43851
; Sequence 43851, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua

```

[illegible]

```

RESULT 52
US-10-424-599-156572
; Sequence 156572, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovacic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 156572
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_112405C.1.pep
US-10-424-599-156572

```

```

? Publication No. US20040034888A1
?
? GENERAL INFORMATION:
?
? APPLICANT: Liu, Jingdong
? APPLICANT: Zhou, Yihua
? APPLICANT: Kovacic, David K.
? APPLICANT: Screen, Steven E
? APPLICANT: Tabaska, Jack E
? APPLICANT: Cao, Yongwei
?
? TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
?
? TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
?
? FILE REFERENCE: 38-21(53313)B
?
? CURRENT APPLICATION NUMBER: US/10/425,114
?
? CURRENT FILING DATE: 2003-04-28
?
? NUMBER OF SEQ ID NOS: 73128
?
? SEQ ID NO 43825
?
? LENGTH: 651
?
? TYPE: PRT
?
? ORGANISM: Glycine max
?
? FEATURE:
?
? OTHER INFORMATION: Clone ID: 700651328_FLI.pep
?
? US-10-425-114-43825

```

RESULT 53
US-10-425-114-43825
: Sequence 43825, Application US/10425114

[illegible]

```

RESULT 55
US-10-424-599-195814
; Sequence 195814, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement.
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 195814
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_18846C.1.pep
US-10-424-599-195814

```

Query Match	72.5%;	Score	952.5;	DB	15;	Length	444;
Best Local Similarity	70.5%;	Pred.	No. 6,7e-67;				
Matches	182;	Conservative	32;	Mismatches	43;	Indels	1;
Gaps	1;						

QY	2	SENVDLILLDDVAPLSLGLGTAGVMTALIKRNSTIPTKTQTPTTYSNDNQVGLIQVYE	61
DB	187	NEKRVQDLLLLDDVTPLSLGLGTAGVMTVLIPRNTIPTTKEQVFSYSDNQVGLIQVYE	246
QY	62	GERAMTKDNNLGRFELSGIIPAPRGVQPIEVTFDDANGILNVATDTSKGANKITIT	121
DB	247	GERTRTRDNNLKGKFLSGIIPAPRGVQPIETVCFDDANGILNVAEDKTTQGNKITIT	306
QY	122	NDKGRLSKEEIERMWQEAERYKAEDEVQREVSARKNALSYAFNMKSAVDEGLKGKISE	181
DB	307	NDKGRLSKEEIERKWQEAERYKSEDEEHKKCKVEAKNALENYSNMNTIKDEKIGKGLDP	366
QY	182	ADKKKVLDKCQEVISMLDANTLAEKDFEHRKLELQVCNPIISGLIYQAGGPGPGG-FG	240
DB	367	ADKKKLTDAETAEQIAOWLDSNQLGEAFEDFKMKELSCINPIITAKRYQGGAGPDVGAMD	426
QY	241	AQPGKGGSGGPTIEBD	258
DB	427	DDVPAAGSGAGPKIEVD	444

RESULT 56

```

US-10-424-599-197829
; Sequence 197829, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 197829
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_20665C.1.pgp
US-10-424-599-197829

```

Query Match	72.5%;	Score	952;	DB	15;	Length	649;
Best Local Similarity	71.4%;	Pred.	No. 1.2e-66;				
Matches	185;	Conservative	30;	Mismatches	42;	Indels	2;
Gaps	2;						
QY	2	SEN	VQD	L	L	L	L
		D	V	A	P	L	S
		L	G	L	E	T	A
		G	T	A	G	V	M
		T	A	L	I	K	R
		N	S	T	I	P	T
		K	T	Q	T	F	T
		S	D	N	Q	P	G
		V	L	I	O	V	E
		61					
DB	391	NEK	VQD	L	L	L	L
		D	V	A	P	L	S
		L	G	L	E	T	A
		G	T	A	G	V	M
		T	A	L	I	K	R
		N	S	T	I	P	T
		K	T	Q	T	F	T
		S	D	N	Q	P	G
		V	L	I	O	V	E
		450					
QY	62	GER	A	M	T	K	D
		N	N	L	L	G	R
		F	E	L	S	G	I
		P	P	A	P	R	G
		V	P	Q	T	E	V
		F	D	I	D	A	N
		G	I	L	I	N	V
		A	T	D	T	K	S
		T	G	K	A	N	K
		I	T	I	T		
		121					
DB	451	GER	A	R	T	R	N
		L	L	G	F	E	L
		S	G	I	P	P	A
		P	R	G	V	P	Q
		T	I	V	C	F	D
		I	D	A	N	G	I
		L	I	N	V	A	E
		D	K	T	T	G	O
		K	N	I	T		
		510					
QY	122	N	D	K	G	R	L
		S	K	E	E	I	R
		M	V	O	E	A	E
		K	A	E	D	E	V
		Q	R	E	R	V	S
		A	K	N	A	L	E
		S	A	F	N	M	K
		S	A	V	E	D	E
		G	L	K	G	K	I
		S	E	181			
DB	511	N	D	K	G	R	L
		S	K	E	E	I	R
		M	V	O	E	A	E
		K	A	E	D	E	V
		Q	R	E	R	V	S
		A	K	N	A	L	E
		S	A	F	N	M	R
		N	T	I	N	D	E
		K	T	A	S	K	L
		S	570				
QY	182	A	D	K	K	V	L
		D	K	C	O	E	V
		I	S	W	L	D	A
		N	T	A	L	E	K
		D	E	F	E	K	R
		E	L	E	V	C	N
		P	I	S	G	L	Y
		Q	O	G	A	P	G
		P	G	240			
DB	571	D	D	K	K	I	E
		A	E	S	A	I	Q
		L	D	G	N	Q	L
		A	R	A	E	F	E
		D	K	M	K	E	L
		S	I	C	N	P	I
		A	K	M	Y	Q	G
		A	P	D	M	A	G
		M	630				
QY	241	A	O	G	P	K	G
		S	-	G	S	G	T
		I	E	V	D	258	
DB	631	E	D	V	P	P	S
		G	S	G	A	G	P
		K	I	E	V	D	649
		I					

```

RESULT 57
US-10-437-963-102982
; Sequence 102982, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 102982
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(648)

```

```
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_100455C.1.pap
US-10-437-963-102982

Query Match      72.4%; Score 951; DB 16; Length 648;
Best Local Similarity 71.0%; Pred. No. 1.4e-66;
Matches 184; Conservative 29; Mismatches 44; Indels 2; Gaps 1;

QY 2 SENVDLLLDVAPLSGLGTAGVMTALIKRSTPTKOTQIFTTYSNDNQPGVLIQVYE 61
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 390 NEKVQDLLLDVTPLSGLGTAGVMTVLIPTNTTPTKKEQVFSTYSNDNQPGVLIQVYE 449
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 GERAMTKONNLLGRFELSGIPPRGVPQIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 450 GERAMTKONNLLGRFELSGIPPRGVPQITVCFDIDANGILNVSAEDKTTGQKNKITTIT 509
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 122 NDKGRLSKEIEIRMVQAEKYKAEDVQVRERVAKNALESYAFNMKSAVEDEGLKGKISE 181
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 510 NDKGRLSKEIEIRMVQAEKYKAEDVQVRERVAKNALESYAFNMKSAVEDEGLKGKISE 569
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 182 ADKKKVLDDKQEVISWLDANTLAEKDFEHRKKELEOVNPIISGLYQAGGPF--GPGGF 239
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 570 DDKKKTIEDAVDGAISWLDNQLAEEVEFEDEKMKLESGICNPITAKMYQEGAGMGAAGM 629
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 240 GAQPKGSGSGPTIEVD 258
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 630 DEDAPSGSGAGPKIEVD 648
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 58
US-10-425-114-62493
; Sequence 62493, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 62493
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB143-057-HI_FLI.pap
US-10-425-114-62884

Query Match      72.2%; Score 949; DB 15; Length 662;
Best Local Similarity 71.4%; Pred. No. 2.1e-66;
Matches 185; Conservative 29; Mismatches 43; Indels 2; Gaps 1;

QY 2 SENVDLLLDVAPLSGLGTAGVMTALIKRSTPTKOTQIFTTYSNDNQPGVLIQVYE 61
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 404 NEKVQDLLLDVTPLSGLGTAGVMTVLIPTNTTPTKKEQVFSTYSNDNQPGVLIQVYE 463
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 GERAMTKONNLLGRFELSGIPPRGVPQIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 464 GERAMTKONNLLGRFELSGIPPRGVPQITVTFDIDANGILNVSAEDKTTGQKNKITTIT 523
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 122 NDKGRLSKEIEIRMVQAEKYKAEDVQVRERVAKNALESYAFNMKSAVEDEGLKGKISE 181
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 524 NDKGRLSKEIEIRMVQAEKYKAEDVQVRERVAKNALESYAFNMKSAVEDEGLKGKISE 583
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 182 ADKKKVLDDKQEVISWLDANTLAEKDFEHRKKELEOVNPIISGLYQ--GAGGPGGPF 239
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 584 EDKKKTIEDAVDGAISWLDNQLAEEVEFEDEKMKLESGICNPITAKMYQEGAGMGAAGM 643
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 240 GAQPKGSGSGPTIEVD 258
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 644 DEDAPSGSGAGPKIEVD 662
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 60
US-10-259-165-98
; Sequence 98, Application US/10259165
; Publication No. US20030135888A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Wang, Xun
; APPLICANT: Chang, Hur-song
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
```

; APPLICANT: Ricke, Darrell
 ; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
 ; FILE REFERENCE: 70030-NP
 ; CURRENT APPLICATION NUMBER: US/10/259,165
 ; CURRENT FILING DATE: 2002-09-26
 ; PRIOR APPLICATION NUMBER: US 60/370,620
 ; PRIOR FILING DATE: 2002-04-04
 ; PRIOR APPLICATION NUMBER: US 60/368,327
 ; PRIOR FILING DATE: 2002-03-27
 ; PRIOR APPLICATION NUMBER: US 60/325,277
 ; PRIOR FILING DATE: 2001-09-26
 ; NUMBER OF SEQ ID NOS: 782
 ; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
 ; SEQ ID NO 98
 ; LENGTH: 337
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 US-10-259-165-98

Query Match 72.0%; Score 946; DB 14; Length 337;
 Best Local Similarity 70.3%; Pred. No. 1.5e-66;
 Matches 182; Conservative 31; Mismatches 44; Indels 2; Gaps 1;
 QY 2 SENVDLLLDVAPLSGLGTAGGVTALIKRSTIPTKTQTFYTSNQPGLVQVYE 61
 DB 79 NEKVDLLLDVTPLSGLGTAGGVTALIPRNTTIPTKKEQVFSTYSNQPGLVQVYE 138
 QY 62 GERAMTKNNLLGRFELSGIPPPAPRGVPOIETVDFIDANGILNVATDKSTGKANKITIT 121
 DB 139 GERTRDNNLLGKFLSGIPPPAPRGVPOITVCFDIDANGILNVSAEDKTTGKKNKITT 198
 QY 122 NDKGRLSKEEIERMVQAEKYKADEVRERVSANAKNALESYAFNMKSASVEDEGLKGIKISE 181
 DB 199 NDKGRLSKEEIERMVQAEKYKSEDEHKKVKESKNALENYAVNMRTIKDEKIASKLPA 258
 QY 182 ADKKKVLDCQEVISWLDANTLAERKDEFEHKKLEQVNCNPIISGLYQAGGPGGFGA 241
 DB 259 ADKKKIEDAIDQAIQWLDGNQLAABEFDKMKLEGCINPIIAKMYQAGADMGMD 318
 QY 242 QG--PKGSGSGPTIEVD 258
 DB 319 DDAPPAGSGAGPKIEVD 337

RESULT 61
 US-10-259-165-426
 ; Sequence 426, Application US/10259165
 ; Publication No. US20030135888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhu, Tong
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Chang, Hur-song
 ; APPLICANT: Briggs, Steven P.
 ; APPLICANT: Cooper, Bret
 ; APPLICANT: Glazebrook, Jane
 ; APPLICANT: Goff, Stephen A.
 ; APPLICANT: Katagiri, Fumiya
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Moughamer, Todd
 ; APPLICANT: Provart, Nicholas
 ; APPLICANT: Ricke, Darrell
 ; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
 ; FILE REFERENCE: 70030-NP
 ; CURRENT APPLICATION NUMBER: US/10/259,165
 ; CURRENT FILING DATE: 2002-09-26
 ; PRIOR APPLICATION NUMBER: US 60/370,620
 ; PRIOR FILING DATE: 2002-04-04
 ; PRIOR APPLICATION NUMBER: US 60/368,327
 ; PRIOR FILING DATE: 2002-03-27
 ; PRIOR APPLICATION NUMBER: US 60/325,277
 ; PRIOR FILING DATE: 2001-09-26
 ; NUMBER OF SEQ ID NOS: 782
 ; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta

; SEQ ID NO 426
 ; LENGTH: 337
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 US-10-259-165-426
 Query Match 72.0%; Score 946; DB 14; Length 337;
 Best Local Similarity 70.3%; Pred. No. 1.5e-66;
 Matches 182; Conservative 31; Mismatches 44; Indels 2; Gaps 1;
 QY 2 SENVDLLLDVAPLSGLGTAGGVTALIKRSTIPTKTQTFYTSNQPGLVQVYE 61
 DB 79 NEKVDLLLDVTPLSGLGTAGGVTALIPRNTTIPTKKEQVFSTYSNQPGLVQVYE 138
 QY 62 GERAMTKNNLLGRFELSGIPPPAPRGVPOIETVDFIDANGILNVATDKSTGKANKITIT 121
 DB 139 GERTRDNNLLGKFLSGIPPPAPRGVPOITVCFDIDANGILNVSAEDKTTGKKNKITT 198
 QY 122 NDKGRLSKEEIERMVQAEKYKADEVRERVSANAKNALESYAFNMKSASVEDEGLKGIKISE 181
 DB 199 NDKGRLSKEEIERMVQAEKYKSEDEHKKVKESKNALENYAVNMRTIKDEKIASKLPA 258
 QY 182 ADKKKVLDCQEVISWLDANTLAERKDEFEHKKLEQVNCNPIISGLYQAGGPGGFGA 241
 DB 259 ADKKKIEDAIDQAIQWLDGNQLAABEFDKMKLEGCINPIIAKMYQAGADMGMD 318
 QY 242 QG--PKGSGSGPTIEVD 258
 DB 319 DDAPPAGSGAGPKIEVD 337

RESULT 62
 US-10-259-165-214
 ; Sequence 214, Application US/10259165
 ; Publication No. US20030135888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhu, Tong
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Chang, Hur-song
 ; APPLICANT: Briggs, Steven P.
 ; APPLICANT: Cooper, Bret
 ; APPLICANT: Glazebrook, Jane
 ; APPLICANT: Goff, Stephen A.
 ; APPLICANT: Katagiri, Fumiya
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Moughamer, Todd
 ; APPLICANT: Provart, Nicholas
 ; APPLICANT: Ricke, Darrell
 ; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
 ; FILE REFERENCE: 70030-NP
 ; CURRENT APPLICATION NUMBER: US/10/259,165
 ; CURRENT FILING DATE: 2002-09-26
 ; PRIOR APPLICATION NUMBER: US 60/370,620
 ; PRIOR FILING DATE: 2002-04-04
 ; PRIOR APPLICATION NUMBER: US 60/368,327
 ; PRIOR FILING DATE: 2002-03-27
 ; PRIOR APPLICATION NUMBER: US 60/325,277
 ; PRIOR FILING DATE: 2001-09-26
 ; NUMBER OF SEQ ID NOS: 782
 ; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
 ; SEQ ID NO 214
 ; LENGTH: 649
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 US-10-259-165-214

Query Match 72.0%; Score 946; DB 14; Length 649;
 Best Local Similarity 70.3%; Pred. No. 3.6e-66;
 Matches 182; Conservative 31; Mismatches 44; Indels 2; Gaps 1;
 QY 2 SENVDLLLDVAPLSGLGTAGGVTALIKRSTIPTKTQTFYTSNQPGLVQVYE 61
 DB 391 NEKVDLLLDVTPLSGLGTAGGVTALIPRNTTIPTKKEQVFSTYSNQPGLVQVYE 450

Qy	62	GERAMTKONNLLGRFELSGIPAPRGVQIETVPFDIDANGILANTATDKSTGKANKITIT	121
		:	
Db	451	GERTRDRNNLLGKFELSGIPAPRGVQITVCFDIDANGILANSAEDKTTGGQNKITIT	510
		:	
Qy	122	NDKGRLSKBEIERMVOEABKYAEBDEVORERVSAKNALESYAFNMKSAAVEDEGLKGKISE	181
		:	
Db	511	NDKGRLSKBEIERMVOEABKYSEDEEHKKVKVESNALENAYVMRTIKDEKIASKLPA	570
		:	
Qy	182	ADKKKVLDKQEVI SWLDANTLAEKDEPEHKKKELEBQCNPDI ISGLVQGAGGPQGGFGA	241
		:	
Db	571	ADKKKTIEDAIQAIQLWDGNLAEADEFDDMKKELEGICNPITAKMTQAGADMAGMWDE	630
		:	
Qy	242	QG--PKGGSGSGFTIEVD	258
Db	631	DDAPPAGSGGAGPKTIEVD	649

```

RESULT 63
US-10-259-165-350
; Sequence 350, Application US/10259165
; Publication No. US2003013588A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Wang, Xun
; APPLICANT: Chang, Hur-song
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
; FILE REFERENCE: 70030-NP
; CURRENT APPLICATION NUMBER: US/10/259,165
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/368,327
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 350
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-259-165-350

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QY      242  QG--PKGSGSGPTIEEYD 258
      | | | | | | | | | |
      | | | | | | | | | |
Db      631  DDAPPAGSGAGPKIEEYD 649

RESULT 64
US-10-437-963-196148
; Sequence 196148, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437, 963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 196148
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_92027C.1.pgp
US-10-437-963-196148

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RESULT 65
US-10-767-701-47021
; Sequence 47021, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 47021
; LENGTH: 486

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Query Match	71.7%;	Score 942;	DB 15;	Length 282;
Best Local Similarity	71.3%;	Pred. No. 2.5e-66;		
Matches 181;	Conservative 28;	Mismatches 43;	Indels 2;	Gaps 1;

QY	7	DLLLDVAPLSGLGTAGGVTWTLIKNSNTPKTOTIFTTYSNDQPGVLIQVYGEGRAM	66
DB	29	DLLLLDVTPLSGLGTAGGVTWVLIPNTTIPYKKEQVFSTYSDNQGVLIQVYGEETR	88
QY	67	TKONNLLGRFELSGIPPPAGPVGQIYVTFDIDANGILNVTATDKSTGKANKKITITNDKGR	126
DB	89	TRDNNLLIGKPELSGIPPPAGPVGQITVCFDIDANGILNVSAAEKTTGCKNKKITITNDKGR	148
QY	127	LSKKEETRMVQEAQKYKABEVORYSKNALESYAFNMKSAVEDSGLAGKTISEADKKK	186
DB	149	LSKKEETKMVQEAQKYKABEDHKKYEAQNTLNTYAINRWNTIKDDKTIASKLSADDDKKK	208
QY	187	VLDKCOEIVISWLDANTLAEKDEFEHKRKELEQVCNPIISGLYQAGGPGPGFGAQGPKG	246
DB	209	IEDAIEQAIQWLDGNOIAEADPEDKMKELIESINPIIAKMYQAGAGDAGAMDEQGPAA	268


```
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 59160
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3912-003-H10_FLI.pep
US-10-425-114-59160

Query Match          71.5%; Score 939; DB 15; Length 653;
Best Local Similarity 69.5%; Pred. No. 1.3e-65;
Matches 180; Conservative 32; Mismatches 45; Indels 2; Gaps 1;

Qy      2  SENVDLLLDVAPLSGLGTAGGVTALIKRNSTIPTKTQITFTTYSNDQPGVLIQVYE 61
Db      395  NEKVQDLLLDVTPLSGLGTAGGVTMLIPRNTTIPTKKEQVFSTYSNDQPGVLIQVYE 454

Qy      62  GERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db      455  GERTRTRDNNLLGKFLSGIPPPAPRGVPQITVCDFIDANGILNVSAEDKTTGQKNKITIT 514

Qy      122  NDKGRLSKEEIERMVQAEKYKAEDVQREVRSNAKNALESYAFNMKSAAVEDGLKGKISE 181
Db      515  NDKGRLSKEEIERMVQAEKYKSEDEHKKVSKNSLENYAYNMRNTIKDEKIASKLA 574

Qy      182  ADKKKVLDKQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGGP--GPGGF 239
Db      575  DDKKKIEDAIDAAISWLDANQLAEDEFDDKMKELSLCNPITAKMYQAGADMGSGGM 634

Qy      240  GAQPKGGSGSGPTIEVD 258
Db      635  DEDAPAGSGGPGKIEVD 653

RESULT 75
US-10-425-114-60382
; Sequence 60382, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 60382
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3591-002-D10_FLI.pep
US-10-425-114-60382

Query Match          71.5%; Score 939; DB 15; Length 653;
Best Local Similarity 69.5%; Pred. No. 1.3e-65;
Matches 180; Conservative 32; Mismatches 45; Indels 2; Gaps 1;

Qy      2  SENVDLLLDVAPLSGLGTAGGVTALIKRNSTIPTKTQITFTTYSNDQPGVLIQVYE 61
Db      395  NEKVQDLLLDVTPLSGLGTAGGVTMLIPRNTTIPTKKEQVFSTYSNDQPGVLIQVYE 454

Qy      62  GERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db      455  GERTRTRDNNLLGKFLSGIPPPAPRGVPQITVCDFIDANGILNVSAEDKTTGQKNKITIT 514

Qy      122  NDKGRLSKEEIERMVQAEKYKAEDVQREVRSNAKNALESYAFNMKSAAVEDGLKGKISE 181
Db      515  NDKGRLSKEEIERMVQAEKYKSEDEHKKVSKNSLENYAYNMRNTIKDEKIASKLA 574

Qy      182  ADKKKVLDKQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGGP--GPGGF 239
Db      575  DDKKKIEDAIDAAISWLDANQLAEDEFDDKMKELSLCNPITAKMYQAGADMGSGGM 634

Qy      240  GAQPKGGSGSGPTIEVD 258
Db      635  DEDAPAGSGGPGKIEVD 653

RESULT 76
US-10-425-114-62531
; Sequence 62531, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 62531
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700476808_FLI.pep
US-10-425-114-62531

Query Match          71.5%; Score 939; DB 15; Length 653;
Best Local Similarity 69.5%; Pred. No. 1.3e-65;
Matches 180; Conservative 32; Mismatches 45; Indels 2; Gaps 1;

Qy      2  SENVDLLLDVAPLSGLGTAGGVTALIKRNSTIPTKTQITFTTYSNDQPGVLIQVYE 61
Db      395  NEKVQDLLLDVTPLSGLGTAGGVTMLIPRNTTIPTKKEQVFSTYSNDQPGVLIQVYE 454

Qy      62  GERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db      455  GERTRTRDNNLLGKFLSGIPPPAPRGVPQITVCDFIDANGILNVSAEDKTTGQKNKITIT 514

Qy      122  NDKGRLSKEEIERMVQAEKYKAEDVQREVRSNAKNALESYAFNMKSAAVEDGLKGKISE 181
Db      515  NDKGRLSKEEIERMVQAEKYKSEDEHKKVSKNSLENYAYNMRNTIKDEKIASKLA 574

Qy      182  ADKKKVLDKQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGGP--GPGGF 239
Db      575  DDKKKIEDAIDAAISWLDANQLAEDEFDDKMKELSLCNPITAKMYQAGADMGSGGM 634

Qy      240  GAQPKGGSGSGPTIEVD 258
Db      635  DEDAPAGSGGPGKIEVD 653

RESULT 77
US-10-425-114-62532
; Sequence 62532, Application US/10425114
```

```
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 59160
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3912-003-H10_FLI.pep
US-10-425-114-59160

Query Match          71.5%; Score 939; DB 15; Length 653;
Best Local Similarity 69.5%; Pred. No. 1.3e-65;
Matches 180; Conservative 32; Mismatches 45; Indels 2; Gaps 1;

Qy      2  SENVDLLLDVAPLSGLGTAGGVTALIKRNSTIPTKTQITFTTYSNDQPGVLIQVYE 61
Db      395  NEKVQDLLLDVTPLSGLGTAGGVTMLIPRNTTIPTKKEQVFSTYSNDQPGVLIQVYE 454

Qy      62  GERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db      455  GERTRTRDNNLLGKFLSGIPPPAPRGVPQITVCDFIDANGILNVSAEDKTTGQKNKITIT 514

Qy      122  NDKGRLSKEEIERMVQAEKYKAEDVQREVRSNAKNALESYAFNMKSAAVEDGLKGKISE 181
Db      515  NDKGRLSKEEIERMVQAEKYKSEDEHKKVSKNSLENYAYNMRNTIKDEKIASKLA 574

Qy      182  ADKKKVLDKQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGGP--GPGGF 239
Db      575  DDKKKIEDAIDAAISWLDANQLAEDEFDDKMKELSLCNPITAKMYQAGADMGSGGM 634

Qy      240  GAQPKGGSGSGPTIEVD 258
Db      635  DEDAPAGSGGPGKIEVD 653

RESULT 76
US-10-425-114-62531
; Sequence 62531, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 62531
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700476808_FLI.pep
US-10-425-114-62531

Query Match          71.5%; Score 939; DB 15; Length 653;
Best Local Similarity 69.5%; Pred. No. 1.3e-65;
Matches 180; Conservative 32; Mismatches 45; Indels 2; Gaps 1;

Qy      2  SENVDLLLDVAPLSGLGTAGGVTALIKRNSTIPTKTQITFTTYSNDQPGVLIQVYE 61
Db      395  NEKVQDLLLDVTPLSGLGTAGGVTMLIPRNTTIPTKKEQVFSTYSNDQPGVLIQVYE 454

Qy      62  GERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db      455  GERTRTRDNNLLGKFLSGIPPPAPRGVPQITVCDFIDANGILNVSAEDKTTGQKNKITIT 514

Qy      122  NDKGRLSKEEIERMVQAEKYKAEDVQREVRSNAKNALESYAFNMKSAAVEDGLKGKISE 181
Db      515  NDKGRLSKEEIERMVQAEKYKSEDEHKKVSKNSLENYAYNMRNTIKDEKIASKLA 574

Qy      182  ADKKKVLDKQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGGP--GPGGF 239
Db      575  DDKKKIEDAIDAAISWLDANQLAEDEFDDKMKELSLCNPITAKMYQAGADMGSGGM 634

Qy      240  GAQPKGGSGSGPTIEVD 258
Db      635  DEDAPAGSGGPGKIEVD 653

RESULT 77
US-10-425-114-62532
; Sequence 62532, Application US/10425114
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Query Match 71.5%; Score 939; DB 15; Length 653;

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; OTHER INFORMATION: Clone ID: UC-ZMFLMO17203G05_FLI.pep
US-10-425-114-69239

Query Match          71.5%; Score 939; DB 15; Length 653;
Best Local Similarity 69.5%; Pred. No. 1.3e-65;
Matches 180; Conservative 32; Mismatches 45; Indels 2; Gaps 1;

Qy      2 SENVQDLLLLDVAPLSGLGTAGGVMTALIKRNSTIPTKQTQIIFTTYSNDNPGVLIOYVE 61
Db      395 NEKVQDLLLLLDVTPLSLGLETAGGVMTLIPRNTTIPTKKKEQVPSTYSNDNPGVLIOYVE 454

Qy      62 GERAMTKONLLGRFELSGIPPAPRGVPQIEVTFDDIDANGILNVATDTKSTGKANKITIT 121
Db      455 GERTRDRNNLLGKFELSGIPPAPRGVPQIVTCFDDIDANGILNVASBDKTTGQKNKITIT 514

Qy      122 NDKGRLSKEBIEIRMVQAEKYKADEVDQRERVSNAKNALESYAFNMKSAREDEGLKGKISE 181
Db      515 NDKGRLSKEBIEIRMVQDAEKYKSEDEBEHKKVKESKNSLENYAVNRWTIKDEKTASKLAA 574

Qy      182 ADKKVKLDKCQEVISWLDANTLAEKDFEHKRKELEQVCNPPIISGLYQGAGGP--GPGGF 239
Db      575 DDKKKIEDAIDAAISWLDANOLAEADFFDKMKLESLCNPPIIAKMYOGAGADMGGSGGM 634

Qy      240 GAQPKGGSGSGPTIEVD 258
Db      635 DEAPAGSGGFGPKIEVD 653

RESULT 82
US-10-425-114-69306
; Sequence 69306, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 69306
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17099C05_FLI.pep
US-10-425-114-69306

Query Match          71.5%; Score 939; DB 15; Length 653;
Best Local Similarity 69.5%; Pred. No. 1.3e-65;
Matches 180; Conservative 32; Mismatches 45; Indels 2; Gaps 1;

Qy      2 SENVQDLLLLDVAPLSGLGTAGGVMTALIKRNSTIPTKQTQIIFTTYSNDNPGVLIOYVE 61
Db      395 NEKVQDLLLLLDVTPLSLGLETAGGVMTLIPRNTTIPTKKKEQVPSTYSNDNPGVLIOYVE 454

Qy      62 GERAMTKONLLGRFELSGIPPAPRGVPQIEVTFDDIDANGILNVATDTKSTGKANKITIT 121
Db      455 GERTRDRNNLLGKFELSGIPPAPRGVPQIVTCFDDIDANGILNVASBDKTTGQKNKITIT 514

Qy      122 NDKGRLSKEBIEIRMVQAEKYKADEVDQRERVSNAKNALESYAFNMKSAREDEGLKGKISE 181
Db      515 NDKGRLSKEBIEIRMVQDAEKYKSEDEBEHKKVKESKNSLENYAVNRWTIKDEKTASKLAA 574

Qy      182 ADKKVKLDKCQEVISWLDANTLAEKDFEHKRKELEQVCNPPIISGLYQGAGGP--GPGGF 239
Db      575 DDKKKIEDAIDAAISWLDANOLAEADFFDKMKLESLCNPPIIAKMYOGAGADMGGSGGM 634
```

Qy 240 GAQPKGSGSGPTIEVD 258
 Db 635 DEDAPAGSGGPGKIEVD 653

RESULT 83

US-10-425-114-70649
 ; Sequence 70649, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 70649
 ; LENGTH: 653
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: UC-ZMFLMO17042B02_FLI.pep
 US-10-425-114-70649

Query Match 71.5%; Score 939; DB 15; Length 653;
 Best Local Similarity 69.5%; Pred. No. 1.3e-65;
 Matches 180; Conservative 32; Mismatches 45; Indels 2; Gaps 1;

Qy 2 SENVODLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQIFTTYSNQPGLIQVYE 61
 Db 395 NEKVQDLLLLDVTPLSGLGTAGVMTLIPRNTTIPTKKEQVFSTYSNQPGLIQVYE 454
 Qy 62 GERAMTKDNNLLGRFELSGIPPPAPRGVPQIETVTFDIDANGILNVATDKSTGKANKITIT 121
 Db 455 GERTRTRDNNLLGKFLSGIPPPAPRGVPQITVCFDIDANGILNVSAEDKTTGQKNKITIT 514
 Qy 122 NDKGRLSKEEIERMVQAEKYKAEDVQREVSANNALESYAFNMKSAAVEDEGLKGKISE 181
 Db 515 NDKGRLSKEEIERMVQAEKYKSEDEHKKVSKNSLENYAYNMRTIKDEKIASKLA 574
 Qy 182 ADKKKVLDKQEVISWLDANTLAEKDFEHRKELEQVCNPIISGLYQAGGP--GPGGF 239
 Db 575 DDKKKTIEDAIDAAISWLDANQLAEDEFDDMKKELESCLNPIIAKMYQAGADMGGSGGM 634

Qy 240 GAQPKGSGSGPTIEVD 258
 Db 635 DEDAPAGSGGPGKIEVD 653

RESULT 84

US-10-425-114-72128
 ; Sequence 72128, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 72128

; LENGTH: 653
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB3591-108-G8_FLI.pep
 US-10-425-114-72128

Query Match 71.5%; Score 939; DB 15; Length 653;
 Best Local Similarity 69.5%; Pred. No. 1.3e-65;
 Matches 180; Conservative 32; Mismatches 45; Indels 2; Gaps 1;

Qy 2 SENVODLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQIFTTYSNQPGLIQVYE 61
 Db 395 NEKVQDLLLLDVTPLSGLGTAGVMTLIPRNTTIPTKKEQVFSTYSNQPGLIQVYE 454
 Qy 62 GERAMTKDNNLLGRFELSGIPPPAPRGVPQIETVTFDIDANGILNVATDKSTGKANKITIT 121
 Db 455 GERTRTRDNNLLGKFLSGIPPPAPRGVPQITVCFDIDANGILNVSAEDKTTGQKNKITIT 514
 Qy 122 NDKGRLSKEEIERMVQAEKYKAEDVQREVSANNALESYAFNMKSAAVEDEGLKGKISE 181
 Db 515 NDKGRLSKEEIERMVQAEKYKSEDEHKKVSKNSLENYAYNMRTIKDEKIASKLA 574
 Qy 182 ADKKKVLDKQEVISWLDANTLAEKDFEHRKELEQVCNPIISGLYQAGGP--GPGGF 239
 Db 575 DDKKKTIEDAIDAAISWLDANQLAEDEFDDMKKELESCLNPIIAKMYQAGADMGGSGGM 634

US-10-425-114-72427
 ; Sequence 72427, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 72427
 ; LENGTH: 653
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 700466311_FLI.pep
 US-10-425-114-72427

Query Match 71.5%; Score 939; DB 15; Length 653;
 Best Local Similarity 69.5%; Pred. No. 1.3e-65;
 Matches 180; Conservative 32; Mismatches 45; Indels 2; Gaps 1;

Qy 2 SENVODLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQIFTTYSNQPGLIQVYE 61
 Db 395 NEKVQDLLLLDVTPLSGLGTAGVMTLIPRNTTIPTKKEQVFSTYSNQPGLIQVYE 454
 Qy 62 GERAMTKDNNLLGRFELSGIPPPAPRGVPQIETVTFDIDANGILNVATDKSTGKANKITIT 121
 Db 455 GERTRTRDNNLLGKFLSGIPPPAPRGVPQITVCFDIDANGILNVSAEDKTTGQKNKITIT 514
 Qy 122 NDKGRLSKEEIERMVQAEKYKAEDVQREVSANNALESYAFNMKSAAVEDEGLKGKISE 181
 Db 515 NDKGRLSKEEIERMVQAEKYKSEDEHKKVSKNSLENYAYNMRTIKDEKIASKLA 574


```
Qy 182 ADKKVLDKQEVISWLDANTLAEDFHEHKKRKELEQVNCNPIISGLYQAGAGP--GPGGF 239
Db 575 DDKKKIEDAIDAAISWLDANQLAEADFDKMKELSLCNPIIAKMYQAGADMGSGGGM 634
Qy 240 GAQPKGSGSGPTIEVD 258
Db 635 DEDAPAGSGGPGKIEVD 653

RESULT 86
US-10-425-114-72533
; Sequence 72533, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 72533
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700477929_FLI.pap
US-10-425-114-72533

Query Match 71.5%; Score 939; DB 15; Length 653;
Best Local Similarity 69.5%; Pred. No. 1.3e-65;
Matches 180; Conservative 32; Mismatches 45; Indels 2; Gaps 1;

Qy 2 SENVQDILLDVPISLGLETAGGVTALIKRNSTIPTKQTQIPTTYSNDQPGVLIQVYE 61
Db 395 NEKVQDILLDVPISLGLETAGGVTALIPRNTTPTTKEQVFSTYSNDQPGVLIQVYE 454
Qy 62 GERAMTKNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 455 GERTRDNNLLKGFELSGIPPPAPRGVPQITVCFDIDANGILNVSAEDKTTGQKNKITIT 514
Qy 122 NDKGRLSKEIERMVQEAQYKAEDVQREVSNAKNALESYAFNMKSAAVEDGLKGKISE 181
Db 515 NDKGRLSKEIERMVQEAQYKAEDVQREVSNAKNALESYAFNMKSAAVEDGLKGKISE 574
Qy 182 ADKKVLDKQEVISWLDANTLAEDFHEHKKRKELEQVNCNPIISGLYQAGAGP--GPGGF 239
Db 575 DDKKKIEDAIDAAISWLDANQLAEADFDKMKELSLCNPIIAKMYQAGADMGSGGGM 634
Qy 240 GAQPKGSGSGPTIEVD 258
Db 635 DEDAPAGSGGPGKIEVD 653

RESULT 87
US-10-425-114-38995
; Sequence 38995, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
```

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; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 38995
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3067-050-E8_FLI.pap
US-10-425-114-38995

Query Match 71.4%; Score 938; DB 15; Length 652;
Best Local Similarity 69.9%; Pred. No. 1.5e-65;
Matches 181; Conservative 30; Mismatches 46; Indels 2; Gaps 1;

Qy 2 SENVQDILLDVPISLGLETAGGVTALIKRNSTIPTKQTQIPTTYSNDQPGVLIQVYE 61
Db 394 NEKVQDILLDVPISLGLETAGGVTALIPRNTTPTTKEQVFSTYSNDQPGVLIQVYE 453
Qy 62 GERAMTKNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 454 GERTRDNNLLKGFELSGIPPPAPRGVPQITVCFDIDANGILNVSAEDKTTGQKNKITIT 513
Qy 122 NDKGRLSKEIERMVQEAQYKAEDVQREVSNAKNALESYAFNMKSAAVEDGLKGKISE 181
Db 514 NDKGRLSKEIERMVQEAQYKAEDVQREVSNAKNALESYAFNMKSAAVEDGLKGKISE 573
Qy 182 ADKKVLDKQEVISWLDANTLAEDFHEHKKRKELEQVNCNPIISGLYQAGAGP--GPGGF 239
Db 574 DDKKKIEDAIDAAISWLDANQLAEADFDKMKELSLCNPIIAKMYQAGADMGSGGGM 633
Qy 240 GAQPKGSGSGPTIEVD 258
Db 634 DEDAPAGSGGPGKIEVD 652

RESULT 88
US-10-425-114-55225
; Sequence 55225, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 55225
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17391H02_FLI.pap
US-10-425-114-55225

Query Match 71.4%; Score 938; DB 15; Length 652;
Best Local Similarity 69.9%; Pred. No. 1.5e-65;
Matches 181; Conservative 30; Mismatches 46; Indels 2; Gaps 1;

Qy 2 SENVQDILLDVPISLGLETAGGVTALIKRNSTIPTKQTQIPTTYSNDQPGVLIQVYE 61
Db 394 NEKVQDILLDVPISLGLETAGGVTALIPRNTTPTTKEQVFSTYSNDQPGVLIQVYE 453
Qy 62 GERAMTKNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 454 GERTRDNNLLKGFELSGIPPPAPRGVPQITVCFDIDANGILNVSAEDKTTGQKNKITIT 513
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Query Match          71.4%; Score 938; DB 15; Length 652;
Best Local Similarity 69.9%; Pred. No. 1.5e-65;
Matches 181; Conservative 30; Mismatches 46; Indels 2; Gaps 1;

QY      2  SENVDLLLLDVAPLSLGLETAGGVMTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVYE 61
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      394 NEKVODLLLLLVTPLSLGLETAGGVMTVLIPRNTIITPKKEQVFSTISNDQPGVLIQVIE 453
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      62  GERAMTKDNLLGRFELSGIPAPRGPVQIIEVTFDIDANGILNVATDKSTGKANKITIT 121
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      454 GERTTRDNLLGKFLSGIPAPRGPVQITVCFDIDANGILNVSAEDKTTQCKNKITIT 513
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      122 NDKGRLSKEETERMVQGAEKYKAEDEVQREVSRAKNALESYAFNMKSAVEDEGLKGKISE 181
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      514 NDKGRLSKEETERMVQGAEKYKSEDEBHKKKVBAKNSLENTYNNMNTIKDKSIASKUPA 573
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      182 ADKKVLPDKQEVISWLDANTLAFKDFEHRKRELEQVCNPIISGLYQAGAGP--GPGGF 239
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      574 DDKKIEDAIDAAISWLDANQLAEAFEDFKKELSLNCNPIIAKMYQAGAGEDMGAGGM 633
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      240 GAQGPKGSGSGPTIEVD 258
      : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      634 DEDAPAGSGGPGPKIEVD 652
      : ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 90
US-10-425-114-61345
; Sequence 61345, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E

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Query Match	71.4%;	Score 938;	DB 15;	Length 652;
Best Local Similarity	69.9%;	Pred. No. 1.5e-46;		
Matches 181;	Conservative 30;	Mismatches 46;	Indels 2;	Gaps 1
QY	2	SENVDLLLLLDVAPLSLGLTAGGVTALIKRSTIPTKOTQFTFTYSDNQPGVLIQVYE	61	
Db	394	NEKVQDLLLLLDVPLSLGLTAGGVTMLVLPRTTPTKKEQVPSYSDNQPGVLIQVYE	453	
QY	62	GERANTKNNLLGRPELSGIPPAARGVQPIQEVTFPDANGILNVATYDTSKSTGKANKITIT	121	
Db	454	GERTRDNNLLGRPELSGIPPAARGVQPIQVTCFDANGILNVSAEDKTTGQGNKITIT	513	
QY	122	NDKGRLSKEEIERVMVQAEKYKABDEYQRESRSAQNALESYAFNMKSAVEDEGLKGKISE	181	
Db	514	NDKGRLSKEEIEKMWQAEKYKSEDEEHKKVKAQNSLENYSYNMENTIKDEKIASKLPA	573	
QY	182	ADDKVAVLDCQEVTSWLDANTLAEKDFEHRKKELEQVCNPIISGLYQAGGP--GPGGF	239	
Db	574	DKKKKIEIDAIALSWLDANQLAEADFEDMKKELSLCNPPIIAKMYQAGGEDMGAGGM	633	
QY	240	GAQGPKGSGSGPTIEEYD	258	
Db	634	DEDAPAGSGGPGKIEEYD	652	

Query Match 71.4%; Score 938; DB 15; Length 652;
Best Local Similarity 69.9%; Pred. No. 1.5e-65;
Matches 181; Conservative 36; Mismatches 46; Indels 2; Gaps 1

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QY 62 GERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 454 GERTTRDNNLLGRFELSGIPPPAPRGVPOITVCFDIDANGILNVASAEKDTTGGKNTIT 513
QY 122 NDKGRLSKEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAAVEDEGLKGKISE 181
Db 514 NDKGRLSKEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAAVEDEGLKGKISE 573
QY 182 ADKKKVLDKQEVISWLDANTLAEKDEFEHKKRKELEQVNCNPIISGLYQGAGGP--GPGGF 239
Db 574 DDKKKIEDAIDAAISWLDANQLAEAFEDFKMKESLNCNPIIAKMYQGAGEDMGGAGGM 633
QY 240 GAQPKGGSGSGPTIEVD 258
Db 634 DEDAPAGSGGPGKIEVD 652

RESULT 92
US-10-425-114-63240
; Sequence 63240, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 63240
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3180-031-A4_FLI.pep
US-10-425-114-63240

Query Match 71.4%; Score 938; DB 15; Length 652;
Best Local Similarity 69.9%; Pred. No. 1.5e-65;
Matches 181; Conservative 30; Mismatches 46; Indels 2; Gaps 1;

QY 2 SENVDLLLDVAPLSGLTAGVMTALIKRSTIPTKTOTFTTYSNPNQGVLIQVYE 61
Db 394 NEKVQDLLLDVTPLSGLTAGVMTVLIPRNTTPTKKEQVFSTYSNPNQGVLIQVYE 453
QY 62 GERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 454 GERTTRDNNLLGRFELSGIPPPAPRGVPOITVCFDIDANGILNVASAEKDTTGGKNTIT 513
QY 122 NDKGRLSKEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAAVEDEGLKGKISE 181
Db 514 NDKGRLSKEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAAVEDEGLKGKISE 573
QY 182 ADKKKVLDKQEVISWLDANTLAEKDEFEHKKRKELEQVNCNPIISGLYQGAGGP--GPGGF 239
Db 574 DDKKKIEDAIDAAISWLDANQLAEAFEDFKMKESLNCNPIIAKMYQGAGEDMGGAGGM 633
QY 240 GAQPKGGSGSGPTIEVD 258
Db 634 DEDAPAGSGGPGKIEVD 652

US-10-425-114-63505
; Sequence 63505, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 63505
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73249A05_FLI.pep
US-10-425-114-63505

Query Match 71.4%; Score 938; DB 15; Length 652;
Best Local Similarity 69.9%; Pred. No. 1.5e-65;
Matches 181; Conservative 30; Mismatches 46; Indels 2; Gaps 1;
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```
QY 62 GERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 454 GERTTRDNNLLGRFELSGIPPPAPRGVPOITVCFDIDANGILNVASAEKDTTGGKNTIT 513
QY 122 NDKGRLSKEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAAVEDEGLKGKISE 181
Db 514 NDKGRLSKEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAAVEDEGLKGKISE 573
QY 182 ADKKKVLDKQEVISWLDANTLAEKDEFEHKKRKELEQVNCNPIISGLYQGAGGP--GPGGF 239
Db 574 DDKKKIEDAIDAAISWLDANQLAEAFEDFKMKESLNCNPIIAKMYQGAGEDMGGAGGM 633
QY 240 GAQPKGGSGSGPTIEVD 258
Db 634 DEDAPAGSGGPGKIEVD 652

US-10-425-114-63457
; Sequence 63457, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 63457
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73159A10_FLI.pep
US-10-425-114-63457

Query Match 71.4%; Score 938; DB 15; Length 652;
Best Local Similarity 69.9%; Pred. No. 1.5e-65;
Matches 181; Conservative 30; Mismatches 46; Indels 2; Gaps 1;

QY 2 SENVDLLLDVAPLSGLTAGVMTALIKRSTIPTKTOTFTTYSNPNQGVLIQVYE 61
Db 394 NEKVQDLLLDVTPLSGLTAGVMTVLIPRNTTPTKKEQVFSTYSNPNQGVLIQVYE 453
QY 62 GERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 454 GERTTRDNNLLGRFELSGIPPPAPRGVPOITVCFDIDANGILNVASAEKDTTGGKNTIT 513
QY 122 NDKGRLSKEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAAVEDEGLKGKISE 181
Db 514 NDKGRLSKEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAAVEDEGLKGKISE 573
QY 182 ADKKKVLDKQEVISWLDANTLAEKDEFEHKKRKELEQVNCNPIISGLYQGAGGP--GPGGF 239
Db 574 DDKKKIEDAIDAAISWLDANQLAEAFEDFKMKESLNCNPIIAKMYQGAGEDMGGAGGM 633
QY 240 GAQPKGGSGSGPTIEVD 258
Db 634 DEDAPAGSGGPGKIEVD 652

US-10-425-114-63505
; Sequence 63505, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 63505
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73249A05_FLI.pep
US-10-425-114-63505

Query Match 71.4%; Score 938; DB 15; Length 652;
Best Local Similarity 69.9%; Pred. No. 1.5e-65;
Matches 181; Conservative 30; Mismatches 46; Indels 2; Gaps 1;
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```

QY 2  SENVDLLLDVAPLSGLTAGGVTALIKRNSTIPTKQIIFTTSDNQPGVLIQVYE 61
Db 394  NEKVQDLLLDVTPLSGLTAGGVTMLIPRNTTIPTKKEQVFSTYSDNQPGVLIQVYE 453
QY 62  GERAMTKDNLGKRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITIT 121
Db 454  GERTRTRDNLGKRFELSGIPAPRGVPOITVCFDIDANGILNVSAEDKTTGQKNKITIT 513
QY 122  NDKGRLSKEEIERMVQAEKYKAEDVORERSAKNALESYAFNMKSAYEDELKKGKISE 181
Db 514  NDKGRLSKEEIERMVQAEKYKAEDVORERSAKNALESYAFNMKSAYEDELKKGKISE 181
QY 182  ADKKVLDKQEVISWLDANTLAEKDPEHKKRKELEQVCNPIISGLYQAGGPP--GPGGF 239
Db 574  DDKKKIEDAIDAAISWLDANQLAEDEFEDKMKELSLCNPIIAKMYQAGAGDMGGAGGM 633
QY 240  GAQGPKGSGSGPTIEVD 258
Db 634  DEDAPAGSGGPGPKIEVD 652

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RESULT 95

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US-10-425-114-65274
; Sequence 65274, Application US/10425114
; Publication No. US20040034889A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 65274
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4748-005-H4_FLI.pep
US-10-425-114-65274

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```

Query Match 71.4%; Score 938; DB 15; Length 652;
Best Local Similarity 69.9%; Pred. No. 1.5e-65;
Matches 181; Conservative 30; Mismatches 46; Indels 2; Gaps 1;

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QY 2  SENVDLLLDVAPLSGLTAGGVTALIKRNSTIPTKQIIFTTSDNQPGVLIQVYE 61
Db 394  NEKVQDLLLDVTPLSGLTAGGVTMLIPRNTTIPTKKEQVFSTYSDNQPGVLIQVYE 453
QY 62  GERAMTKDNLGKRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITIT 121
Db 454  GERTRTRDNLGKRFELSGIPAPRGVPOITVCFDIDANGILNVSAEDKTTGQKNKITIT 513
QY 122  NDKGRLSKEEIERMVQAEKYKAEDVORERSAKNALESYAFNMKSAYEDELKKGKISE 181
Db 514  NDKGRLSKEEIERMVQAEKYKAEDVORERSAKNALESYAFNMKSAYEDELKKGKISE 181
QY 182  ADKKVLDKQEVISWLDANTLAEKDPEHKKRKELEQVCNPIISGLYQAGGPP--GPGGF 239
Db 574  DDKKKIEDAIDAAISWLDANQLAEDEFEDKMKELSLCNPIIAKMYQAGAGDMGGAGGM 633
QY 240  GAQGPKGSGSGPTIEVD 258
Db 634  DEDAPAGSGGPGPKIEVD 652

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RESULT 96

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US-10-437-963-193938

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; Sequence 193938, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barabazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 193938
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_90028C.1.pep
US-10-437-963-193938

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```

Query Match 70.7%; Score 928.5; DB 16; Length 649;
Best Local Similarity 69.4%; Pred. No. 8.7e-65;
Matches 179; Conservative 33; Mismatches 45; Indels 1; Gaps 1;

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QY 2  SENVDLLLDVAPLSGLTAGGVTALIKRNSTIPTKQIIFTTSDNQPGVLIQVYE 61
Db 392  NEKVQDLLLDVTPLSGLTAGGVTMLIPRNTTIPTKKEQVFSTYSDNQPGVLIQVYE 451
QY 62  GERAMTKDNLGKRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITIT 121
Db 452  GERTRTRDNLGKRFELSGIPAPRGVPOITVCFDIDANGILNVSAEDKTTGQKNKITIT 511
QY 122  NDKGRLSKEEIERMVQAEKYKAEDVORERSAKNALESYAFNMKSAYEDELKKGKISE 181
Db 512  NDKGRLSKEEIERMVQAEKYKAEDVORERSAKNALESYAFNMKSAYEDELKKGKISE 181
QY 182  ADKKVLDKQEVISWLDANTLAEKDPEHKKRKELEQVCNPIISGLYQAGGPPGFGA 241
Db 572  DDKKKIEDAIDAAISWLDANQLAEDEFEDKMKELSLCNPIIAKMYQAGAGDMGGGMD 631
QY 242  QGP-KGGSGSGPTIEVD 258
Db 632  DAPAGSGGPGPKIEVD 649

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RESULT 97

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US-10-425-114-54413
; Sequence 54413, Application US/10425114
; Publication No. US20040034889A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 54413
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73199A09_FLI.pep

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US-10-425-114-54413
Query Match      70.1%; Score 920.5; DB 15; Length 461;
Best Local Similarity 69.2%; Pred. No. 2.4e-64;
Matches 180; Conservative 32; Mismatches 45; Indels 3; Gaps 2;

Qy  2  SENVDLLLDVAPLSLGLETAGGVTALIKRNTIPTKQTQIPTTYSNDQPGVLIQVYE 61
Db  202 NEKVQDLLLLDVTPSLGLETAGGVTALIPRNTIPTKKEQVFTSYSDNQPGVLIQVYE 261

Qy  62  GERAMTKNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 121
Db  262 GERAMTKNNLLGRFELSGIPAPRGVPQITVCFDIDANGILNVSADKTTGQKNKITIT 321

Qy  122 NDKGRLSKEIERMVQAEKTKAEDEVQRRVRSNAKNALESYAFNMKSAVEDGLKGKISE 181
Db  322 NDKGRLSKEIERMVQAEKTKAEDEBHKKKVDKNSLENYAYNMRNTIKDDKIASKLGA 381

Qy  182 ADKKVLDKCOEVTISWLDANTLAEDFEHKKRKELEOVNPIISGLYQAGGPP--GPGGF 239
Db  382 DDKKRIENAVDGAISWLDNSQLAEVDFEDKMKKELEGICNPITAKMYQAGADMGAAAGM 441

Qy  240 GAQGP-KGGSGSGPTIEVD 258
Db  442 DEDAPAAAGGSAAGPKIEVD 461

RESULT 98
US-10-425-114-57892
; Sequence 57892, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 57892
; LENGTH: 658
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17117B05_FLI.pep
US-10-425-114-57892
Query Match      69.9%; Score 918.5; DB 15; Length 658;
Best Local Similarity 69.2%; Pred. No. 5.5e-64;
Matches 180; Conservative 31; Mismatches 46; Indels 3; Gaps 2;

Qy  2  SENVDLLLDVAPLSLGLETAGGVTALIKRNTIPTKQTQIPTTYSNDQPGVLIQVYE 61
Db  399 NEKVQDLLLLDVTPSLGLETAGGVTALIPRNTIPTKKEQVFTSYSDNQPGVLIQVYE 458

Qy  62  GERAMTKNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 121
Db  459 GERAMTKNNLLGRFELSGIPAPRGVPQITVCFDIDANGILNVSADKTTGQKNKITIT 518

Qy  122 NDKGRLSKEIERMVQAEKTKAEDEVQRRVRSNAKNALESYAFNMKSAVEDGLKGKISE 181
Db  519 NDKGRLSKEIERMVQAEKTKAEDEBHKKKVDKNSLENYAYNMRNTIKDDKIASKLGA 578

Qy  182 ADKKVLDKCOEVTISWLDANTLAEDFEHKKRKELEOVNPIISGLYQAGGPP--GPGGF 239
Db  579 DDKKRIENAVDGAISWLDNSQLAEVDFEDKMKKELEGICNPITAKMYQAGADMGAAAGM 638

Qy  240 GAQGP-KGGSGSGPTIEVD 258

US-10-425-114-57892
Query Match      69.9%; Score 918.5; DB 15; Length 658;
Best Local Similarity 69.2%; Pred. No. 5.5e-64;
Matches 180; Conservative 31; Mismatches 46; Indels 3; Gaps 2;

Qy  2  SENVDLLLDVAPLSLGLETAGGVTALIKRNTIPTKQTQIPTTYSNDQPGVLIQVYE 61
Db  399 NEKVQDLLLLDVTPSLGLETAGGVTALIPRNTIPTKKEQVFTSYSDNQPGVLIQVYE 458

Qy  62  GERAMTKNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 121
Db  459 GERAMTKNNLLGRFELSGIPAPRGVPQITVCFDIDANGILNVSADKTTGQKNKITIT 518

Qy  122 NDKGRLSKEIERMVQAEKTKAEDEVQRRVRSNAKNALESYAFNMKSAVEDGLKGKISE 181
Db  519 NDKGRLSKEIERMVQAEKTKAEDEBHKKKVDKNSLENYAYNMRNTIKDDKIASKLGA 578

Qy  182 ADKKVLDKCOEVTISWLDANTLAEDFEHKKRKELEOVNPIISGLYQAGGPP--GPGGF 239
Db  579 DDKKRIENAVDGAISWLDNSQLAEVDFEDKMKKELEGICNPITAKMYQAGADMGAAAGM 638

Qy  240 GAQGP-KGGSGSGPTIEVD 258

US-10-425-114-65502
; Sequence 65502, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 65502
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4766-015-H12_FLI.pep
US-10-425-114-65502
Query Match      69.4%; Score 912.5; DB 15; Length 653;
Best Local Similarity 68.8%; Pred. No. 1.6e-63;
Matches 179; Conservative 32; Mismatches 46; Indels 3; Gaps 2;

Qy  2  SENVDLLLDVAPLSLGLETAGGVTALIKRNTIPTKQTQIPTTYSNDQPGVLIQVYE 61
Db  394 NEKVQDLLLLDVTPSLGLETAGGVTALIPRNTIPTKKEQVFTSYSDNQPGVLIQVYE 453

Qy  62  GERAMTKNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 121
Db  454 GERAMTKNNLLGRFELSGIPAPRGVPQITVCFDIDANGILNVSADKTTGQKNKITIT 513

Qy  122 NDKGRLSKEIERMVQAEKTKAEDEVQRRVRSNAKNALESYAFNMKSAVEDGLKGKISE 181
Db  514 NDKGRLSKEIERMVQAEKTKAEDEBHKKKVDKNSLENYAYNMRNTIKDDKIASKLGA 573

Qy  182 ADKKVLDKCOEVTISWLDANTLAEDFEHKKRKELEOVNPIISGLYQAGGPP--GPGGF 239
Db  574 DDKKRIENAVDGAISWLDNSQLAEVDFEDKMKKELEGICNPITAKMYQAGADMGAAAGM 633

Qy  240 GAQGP-KGGSGSGPTIEVD 258
Db  634 DEDAPAAAGGSAAGPKIEVD 653

RESULT 100
US-10-451-467A-536
; Sequence 536, Application US/10451467A
; Publication No. US20040161840A1
; GENERAL INFORMATION:
; APPLICANT: CONTRERAS, ROLAND HENRI
; APPLICANT: EBERHARDT, INES
; APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
; APPLICANT: REEKMAN, RIEKA JOSEPHINA
; TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
; FILE REFERENCE: JAB-1667
; CURRENT APPLICATION NUMBER: US/10/451,467A
; CURRENT FILING DATE: 2003-06-19
; PRIOR FILING DATE: 2003-06-19
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-01-04
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: EP 01870002.1
; PRIOR APPLICATION NUMBER: EP 01870003.9
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Search completed: April 6, 2005, 17:37:18
Job time : 152 secs